

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13, Search time 263.185 Seconds
(without alignments)
866.886 Million cell updates/sec

Title: US-09-788-051-4

Perfect score: 3354
Sequence: 1 MWGLVRLLLMLGSMGCMGR.....LPSCQLPLGIPALGIVLCAS 636

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2002273 segs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_23Sep04:*

1: Geneseqp1980s:*\n2: Geneseqp1990s:*\n3: Geneseqp2000s:*\n4: Geneseqp2001s:*\n5: Geneseqp2002s:*\n6: Geneseqp2003as:*\n7: Geneseqp2003bs:*\n8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3354	100.0	636	7	ADD29445 Human cad
2	3259	97.2	620	7	ADD29448 Human cad
3	2746.5	81.9	781	5	ABBS3296 Human pol
4	2746.5	81.9	781	5	AAM48736 Human cad
5	2746.5	81.9	781	5	ABG34078 Human pro
6	2746.5	81.9	781	6	ABR40114 Human cel
7	2746.5	81.9	781	6	ADA01365 Human pro
8	2746.5	81.9	781	6	ADA43795 Human sec
9	2746.5	81.9	781	6	ADA43563 Human sec
10	2746.5	81.9	781	6	ADA01238 Human pro
11	2746.5	81.9	781	7	ADA01122 Human sec
12	2746.5	81.9	781	7	ADA43679 Human sec
13	2746.5	81.9	781	7	ADA06941 Human pro
14	2746.5	81.9	781	7	ADA08429 Human hum
15	2746.5	81.9	781	7	ADP99722 Human pro
16	2746.5	81.9	781	7	ADP87005 Human pro
17	2746.5	81.9	781	7	ADP66160 Human sec
18	2746.5	81.9	781	7	ADP99838 Human pro
19	2746.5	81.9	781	7	ADP99493 Novel hum
20	2746.5	81.9	781	7	ADP66044 Human sec
21	2746.5	81.9	781	7	ADG23442 Human tra
22	2746.5	81.9	781	7	ADG26135 Human pro
23	2746.5	81.9	781	7	ADG04962 Human pro
24	2746.5	81.9	781	7	ADG11268 Human pro
25	2746.5	81.9	781	7	ADD88199 Human pro

26	2746.5	81.9	781	7	ADP95494 Human sec
27	2746.5	81.9	781	7	ADP06424 Human pro
28	2746.5	81.9	781	7	ADP38199 Human pro
29	2746.5	81.9	781	7	ADP88315 Human pro
30	2746.5	81.9	781	7	ADP90896 Human sec
31	2746.5	81.9	781	7	ADP99451 Human sec
32	2746.5	81.9	781	7	ADG06544 Human pro
33	2746.5	81.9	781	7	ADG05495 Human pro
34	2746.5	81.9	781	7	ADP82496 Human pro
35	2746.5	81.9	781	8	ADP51749 Human sec
36	2746.5	81.9	781	8	ADP51865 Human sec
37	2746.5	81.9	781	8	ADP37723 Human sec
38	2746.5	81.9	781	8	ADP37607 Human sec
39	2746.5	81.9	781	8	ADP95378 Human sec
40	2746.5	81.9	781	8	ADP38078 Human pro
41	2746.5	81.9	781	8	ADP76167 Human pro
42	2746.5	81.9	781	8	ADP39490 Human pro
43	2746.5	81.9	781	8	ADP04294 Human pro
44	2746.5	81.9	781	8	ADP39891 Human pro
45	2746.5	81.9	781	8	ADP19756 Human pro

ALIGNMENTS

RESULT 1	ADD29445	standard; protein; 636 AA.
XX	ADD29445:	
AC	ADD29445:	
XX	15-JAN-2004 (first entry)	
DT		
XX		
DE	Human cadherin-like protein amino acid sequence.	
XX		
KW	cadherin-like protein; transmembrane protein; cadherin domain;	
KW	homotypic cell-cell adhesion; cytotactin; osteopontin; cancer;	
KW	osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;	
KW	metastatic tumour; human.	
OS	Homo sapiens.	
XX		
FT	key	Location/Qualifiers
FT	Peptide	1..16
FT	Protein	17..636
FT		/label= Signal_peptide
XX		/label= Mature_human_cadherin-like_protein
PN	US2003144491-A1.	
XX		
PD	31-JUL-2003.	
XX		
PF	16-FEB-2001; 2001US-00788051.	
XX		
PR	03-FEB-2000; 2000US-00496914.	
PR	27-APR-2000; 2000US-00560875.	
XX		
PA	(GDB/) GDBOLE S D.	
PA	(KUC/) KUO C.	
PA	(ARTE/) ARTERBURN M C.	
PA	(YEUN/) YEUNG G.	
PA	(PALE/) PALENCIA S.	
PA	(TANG/) TANG Y T.	
PA	(LITC/) LIT C.	
PA	(DRMA/) DRMANAC R T.	
XX		
PI	Godbole SD, Xuo C, Arterburn MC, Yeung G, Palencia S, Tang YT,	
PI	Liu C, Drmanac RT,	
XX		
DR	WPI: 2003-829799/77.	
DR	N-PSDB; ADD29461, ADD29446.	
XX		
PT	Novel isolated human secreted cadherin-like polypeptide useful for	

PT treating diseases such as cancers, osteoporosis, Paget's disease,
 PT osteomalacia, hyperostosis, osteopetrosis.
 XX Claim 11; SEQ ID NO 4; 63pp; English.
 XX This invention relates to a novel isolated human secreted cadherin-like
 CC protein and the DNA sequence which encodes it. Cadherins are a family of
 CC transmembrane proteins which share a common cadherin domain in their
 CC extracellular region. The extracellular portion mediates homotypic cell-
 CC cell adhesion that is calcium dependent. Modulators of the protein of the
 CC invention may have cytostatic or osteopathic activity. The invention may
 CC allow development of therapeutics useful for the treatment of diseases
 CC such as cancers, osteoporosis, Paget's disease, osteomalacia,
 CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
 CC invention may also be useful as markers for prognosis of metastatic
 CC tumours. The present sequence is that of the human secreted cadherin-like
 CC protein of the invention.
 CC
 XX Sequence 636 AA;
 SQ
 Query Match 100.0%; Score 3354; DB 7; Length 636;
 Best Local Similarity 100.0%; Pred. No. 1,1e-272;
 Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNGIVRLILAMLGWGMGRLAARAPARAWAGSRHHPGALLIRTRRSWYWNQFVIEEYAGP 60
 DB 1 MNGIVRLILAMLGWGMGRLAARAPARAWAGSRHHPGALLIRTRRSWYWNQFVIEEYAGP 60
 QY 61 EPLVIGKLSHDVDEGEGETKYLITGEGAGTFFVIDEATGNIHVTKSLDREKQYVLLAQ 120
 DB 61 EPLVIGKLSHDVDEGEGETKYLITGEGAGTFFVIDEATGNIHVTKSLDREKQYVLLAQ 120
 QY 121 AVDRASNRPLEPSEFFIIKGGDINDNPPIPLGPHATVPEMSNVGTSVQVTAHADDP 180
 DB 121 AVDRASNRPLEPSEFFIIKGGDINDNPPIPLGPHATVPEMSNVGTSVQVTAHADDP 180
 QY 121 AVDRASNRPLEPSEFFIIKGGDINDNPPIPLGPHATVPEMSNVGTSVQVTAHADDP 180
 DB 121 AVDRASNRPLEPSEFFIIKGGDINDNPPIPLGPHATVPEMSNVGTSVQVTAHADDP 180
 QY 181 SYGSAKLVTVLDTGLPFPSVDPTGVYRTALPMDRETEBEFLVYQADMGHGGIS 240
 DB 181 SYGSAKLVTVLDTGLPFPSVDPTGVYRTALPMDRETEBEFLVYQADMGHGGIS 240
 QY 181 SYGSAKLVTVLDTGLPFPSVDPTGVYRTALPMDRETEBEFLVYQADMGHGGIS 240
 DB 181 SYGSAKLVTVLDTGLPFPSVDPTGVYRTALPMDRETEBEFLVYQADMGHGGIS 240
 QY 241 GSTTWTWTLSPVNDNPKFPQSLYQFSVETAGCGTLVGRADDPDLGNALMAYSIID 300
 DB 241 GSTTWTWTLSPVNDNPKFPQSLYQFSVETAGCGTLVGRADDPDLGNALMAYSIID 300
 QY 301 GEGEAFSISTDLOGRDGLTVRKPDPESQSYSPFVKAATNLIDPAYLRGPFDVVS 360
 DB 301 GEGEAFSISTDLOGRDGLTVRKPDPESQSYSPFVKAATNLIDPAYLRGPFDVVS 360
 QY 301 GEGEAFSISTDLOGRDGLTVRKPDPESQSYSPFVKAATNLIDPAYLRGPFDVVS 360
 DB 301 GEGEAFSISTDLOGRDGLTVRKPDPESQSYSPFVKAATNLIDPAYLRGPFDVVS 360
 QY 361 VRVAVODAPPEPATTOAAHLLTVPENKAPGTLVGQISAAALDPSASPIRSILPHSDPER 420
 DB 361 VRVAVODAPPEPATTOAAHLLTVPENKAPGTLVGQISAAALDPSASPIRSILPHSDPER 420
 QY 421 CFSIQPEEGTHTAAPLDREARAWNTLTALTELGWSMGERGVPLVAEWSAPAPQ 480
 DB 421 CFSIQPEEGTHTAAPLDREARAWNTLTALTELGWSMGERGVPLVAEWSAPAPQ 480
 QY 421 CFSIQPEEGTHTAAPLDREARAWNTLTALTELGWSMGERGVPLVAEWSAPAPQ 480
 DB 421 CFSIQPEEGTHTAAPLDREARAWNTLTALTELGWSMGERGVPLVAEWSAPAPQ 480
 QY 481 RSPVGSVAVGIPQDSSAQRVQVAIQTLDDNDNAPQLABEYDFVCDSPAAGQLIVIRA 540
 DB 481 RSPVGSVAVGIPQDSSAQRVQVAIQTLDDNDNAPQLABEYDFVCDSPAAGQLIVIRA 540
 QY 541 LDRDEVNSSHVSFQGLGPDANFTVQDNRDLPAWFPHLMASASSMLWPEERGNQPA 600
 DB 541 LDRDEVNSSHVSFQGLGPDANFTVQDNRDLPAWFPHLMASASSMLWPEERGNQPA 600
 QY 541 LDRDEVNSSHVSFQGLGPDANFTVQDNRDLPAWFPHLMASASSMLWPEERGNQPA 600
 DB 541 LDRDEVNSSHVSFQGLGPDANFTVQDNRDLPAWFPHLMASASSMLWPEERGNQPA 600
 QY 601 SQGSSSLPCGRPLGALPSCQLPLGIPALGIVLCAS 636
 DB 601 SQGSSSLPCGRPLGALPSCQLPLGIPALGIVLCAS 636
 DB 601 SQGSSSLPCGRPLGALPSCQLPLGIPALGIVLCAS 636

AC ADD29448;
 XX 15-JAN-2004 (first entry)
 DT Human cadherin-like mature protein.
 XX
 DE
 XX cadherin-like protein; transmembrane protein; cadherin domain;
 KW homotypic cell-cell adhesion; cytostatic; osteopathic; cancer;
 KW osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
 KW metastatic tumour; human.
 XX
 OS Homo sapiens.
 XX
 PN US2003144491-A1.
 XX
 PD 31-JUL-2003.
 XX
 PF 16-FEB-2001; 2001US-00788051.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 XX
 PA (GODB/) GODBOLE S D.
 PA (KUOC/) KUO C.
 PA (ARTE/) ARTERBURN M C.
 PA (YEUN/) YEUNG G.
 PA (PALE/) PALENCIA S.
 PA (TANG/) TANG Y T.
 PA (LIUC/) LIU C.
 PA (DRMA/) DRMANAC R T.
 PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT,
 PI Liu C, Drmanac RT;
 PI MPI, 2003-829799/77.
 DR
 PT Novel isolated human secreted cadherin-like polypeptide useful for
 PT treating diseases such as cancers, osteoporosis, Paget's disease,
 PT osteomalacia, hyperostosis, osteopetrosis.
 XX
 PS Claim 11; SEQ ID NO 7; 63pp; English.
 XX
 CC This invention relates to a novel isolated human secreted cadherin-like
 CC protein and the DNA sequence which encodes it. Cadherins are a family of
 CC transmembrane proteins which share a common cadherin domain in their
 CC extracellular region. The extracellular portion mediates homotypic cell-
 CC cell adhesion that is calcium dependent. Modulators of the protein of the
 CC invention may have cytostatic or osteopathic activity. The invention may
 CC allow development of therapeutics useful for the treatment of diseases
 CC such as cancers, osteoporosis, Paget's disease, osteomalacia,
 CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
 CC invention may also be useful as markers for prognosis of metastatic
 CC tumours. The present sequence is that of the mature human secreted
 CC cadherin-like protein which was used during the exemplification of the
 CC invention.
 CC
 XX Sequence 620 AA;
 SQ
 Query Match 97.2%; Score 3259; DB 7; Length 620;
 Best Local Similarity 100.0%; Pred. No. 1e-264;
 Matches 620; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 CMGRLAARAWAGSRHHPGALLIRTRRSWYWNQFVIEEYAGPEPLIGKLSHDVDRGE 76
 DB 1 CMGRLAARAWAGSRHHPGALLIRTRRSWYWNQFVIEEYAGPEPLIGKLSHDVDRGE 76
 QY 77 GRITKYLITGEGAGTFFVIDEATGNIHVTKSLDREKQYVLLAQAVDRASNRPLEPSEF 136
 DB 77 GRITKYLITGEGAGTFFVIDEATGNIHVTKSLDREKQYVLLAQAVDRASNRPLEPSEF 136
 QY 137 IIKGGDINDNPPIPLGPHATVPEMSNVGTSVQVTAHADDPSSYNSAKLVTVLDTGL 196
 DB 137 IIKGGDINDNPPIPLGPHATVPEMSNVGTSVQVTAHADDPSSYNSAKLVTVLDTGL 196
 QY 121 IIKGGDINDNPPIPLGPHATVPEMSNVGTSVQVTAHADDPSSYNSAKLVTVLDTGL 180
 DB 121 IIKGGDINDNPPIPLGPHATVPEMSNVGTSVQVTAHADDPSSYNSAKLVTVLDTGL 180

QY 197 PFESVDPQTGVRTALPNMDRETOEBELVYVIAQKMGHNGLSGTTVTTLSDVNDNP 256
 DB 181 PFESVDPQTGVRTALPNMDRETOEBELVYVIAQKMGHNGLSGTTVTTLSDVNDNP 240
 QY 257 PKFQSLYQSFVETAPGTLVGRIRAPQDDLDGNLMASTIIDGSGRPFSTLQGR 316
 DB 241 PKFQSLYQSFVETAPGTLVGRIRAPQDDLDGNLMASTIIDGSGRPFSTLQGR 300
 QY 317 DGLTVAKPLDPEQSORSYSFRVETNTLIDPAVLRGPFQDVASVRAVADAPPAFTQ 376
 DB 301 DGLTVAKPLDPEQSORSYSFRVETNTLIDPAVLRGPFQDVASVRAVADAPPAFTQ 360
 QY 377 AAHTLTPENKAPGTLVGOISADLDSPASPFRYSILPHSDPERCFSTIQEBEGTHTAP 436
 DB 361 AAHTLTPENKAPGTLVGOISADLDSPASPFRYSILPHSDPERCFSTIQEBEGTHTAP 420
 QY 437 LDRERAMHNLTVLATELGSMGPERGWPVLVAEMGAPAPQPSRVSAGVIGPDDSA 496
 DB 421 LDRERAMHNLTVLATELGSMGPERGWPVLVAEMGAPAPQPSRVSAGVIGPDDSA 480
 QY 497 QASRVQVAIQTLDENDNAPOLAEFYDTFVCDSPAAGQLIOVIRALDDEVGNSSHVSFOG 556
 DB 481 QASRVQVAIQTLDENDNAPOLAEFYDTFVCDSPAAGQLIOVIRALDDEVGNSSHVSFOG 540
 QY 557 PLGSDANFTVQDNNDLPAMFHPLMASASWLMHPAERGQOPASOGKSSLPQGRPGA 616
 DB 541 PLGSDANFTVQDNNDLPAMFHPLMASASWLMHPAERGQOPASOGKSSLPQGRPGA 600
 QY 617 LPSCQLPGIPALGIVLCAS 636
 DB 601 LPSCQLPGIPALGIVLCAS 620

RESULT 3
 ABB53296
 ID ABB53296 standard; protein; 781 AA.

XX AC ABB53296;

DT 12-FEB-2002 (first entry)

DE Human polypeptide #36.

XX Human; nootropic; neuroprotective; anticonvulsant; antidepressant;
 neuroleptic; tranquilizer; antiarrhythmic; cardiac; antidiabetic;
 antiinflammatory; antihypertensive; hepatotropic; vitamin; antidiabetic;
 nephrotropic; anorectic; cytoskeletal; vaccine; neurological disease;
 cardiovascular disease; respiratory disease; liver disease;
 renal disease; skeletal muscle disease; gastrointestinal disease;
 placental disease; testicular cancer; male fertility; pancreatic disease.

XX Homo sapiens.

PN WO200181363-A1.

PD 01-NOV-2001.

PF 26-APR-2001; 2001WO-US013360.

PR 27-APR-2000; 2000US-0199963P.

PR 11-MAY-2000; 2000US-020336P.

PR 25-MAY-2000; 2000US-0207087P.

PR 26-MAY-2000; 2000US-0207546P.

XX (SMTK) SMITHKLINE BEECHAM CORP.

XX (SMTK) SMITHKLINE BEECHAM PLC.

XX Agarwal P, Murdock FR, Rizvi SK, Smith RF, Xiang Z, Kabnick KS;
 XX Lai Y, Xie Q;
 XX WPI; 2002-041392/05.
 DR N-PSDB; ABA90361.

XX Novel polypeptides and polynucleotides useful as a vaccine for preventing
 PT and treating diseases associated with the polypeptide, e.g. Alzheimer's
 PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.

PS Claim 1; Page 108-109; 116pp; English.

XX The invention relates to an isolated polypeptide comprising a 277, 480,
 CC 583, 581, 628, 424, 639, 229, 310, 841, 241, 359, 382, 185, 586, 1026,
 CC 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 225,
 CC 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
 CC given in the specification. The polypeptides, modulators of the
 CC polypeptides and antibodies against the polypeptides are useful for
 CC treating diseases such as neurological and psychiatric diseases including
 CC Alzheimer's, paraneuronal disease, Huntington's disease, myotonic
 CC dystrophy, anorexia and depression; cardiovascular diseases including
 CC congestive heart failure, Hodgkin's disease and myocardial infarction;
 CC respiratory diseases including asthma, chronic obstructive pulmonary
 CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
 CC diseases including hypercholesterolemia, cirrhosis, viral and nonviral
 CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
 CC renal disease including renal failure, acute tubular necrosis and
 CC glomerulonephritis; skeletal muscle diseases including Duchenne's
 CC disease, hypoglycemia and obesity; gastrointestinal diseases including
 CC myotonia congenita and intestinal obstruction; lymph diseases including
 CC lymphoglycemia; diseases of placenta including choriocarcinoma; diseases
 CC of testes including testicular cancer, male reproductive diseases
 CC including low testosterone and male infertility; and disease of pancreas
 CC including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The
 CC present sequence is a polypeptide of the invention

XX Sequence 781 AA;

Query Match 81.9%; Score 2746.5; DB 5; Length 781;
 Best Local Similarity 84.8%; Pred No. 1.8e-221;
 Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MMGLVRLILAMLGWCMGRLLAPARAWGSRHFGPALLRTRRSMWNQFVIEYAGP 60
 DB 1 MMGLVRLILAMLGWCMGRLLAPARAWGSRHFGPALLRTRRSMWNQFVIEYAGP 60
 QY 61 EPLTIGKHSVDYDRGGRKTYLLTGEAGTVAVIDEATNIHVTSLDREKAOYVLAQ 120
 DB 61 EPLTIGKHSVDYDRGGRKTYLLTGEAGTVAVIDEATNIHVTSLDREKAOYVLAQ 120
 QY 121 AVDRASNRPLEPSEPIIKQDINDNPIPLPGPYHATVPENSNVTSYQVTAHADDP 180
 DB 121 AVDRASNRPLEPSEPIIKQDINDNPIPLPGPYHATVPENSNVTSYQVTAHADDP 180
 QY 181 SYGNSAKLYTYVLDGIPFSVVPQGVRTALPNMDRETOEBELVYVIAQKMGHNGLS 240
 DB 181 SYGNSAKLYTYVLDGIPFSVVPQGVRTALPNMDRETOEBELVYVIAQKMGHNGLS 240
 QY 241 GSTTIVTSLSDVNDNPKFPQSLYQSFVETAPGTLVGRIRAPQDDLDGNLMASTIID 300
 DB 241 GSTTIVTSLSDVNDNPKFPQSLYQSFVETAPGTLVGRIRAPQDDLDGNLMASTIID 300
 QY 301 GEGSEAFSISTDIQGRDGLTVAKPLDPEQSORSYSFRVETNTLIDPAVLRGPFQDVAS 360
 DB 301 GEGSEAFSISTDIQGRDGLTVAKPLDPEQSORSYSFRVETNTLIDPAVLRGPFQDVAS 360
 QY 361 VRYAVODAPPPAPFTQAAHYLTPENKAPGTLVGOISADLDSPASPFRYSILPHSDPR 420
 DB 361 VRYAVODAPPPAPFTQAAHYLTPENKAPGTLVGOISADLDSPASPFRYSILPHSDPR 420
 QY 421 CFSIQEBEGTHTAPLDRERAMHNLTVLATELGSMGPERGWPVLVAEMGAPAPQ 480
 DB 421 CFSIQEBEGTHTAPLDRERAMHNLTVLATELGSMGPERGWPVLVAEMGAPAPQ 480
 QY 481 RSPVGSAGVIGPDDSAQASRVQVAIQTLDENDNAPOLAEFYDTFVCDSPAAGQLIOVIRA 540
 DB 481 RSPVGSAGVIGPDDSAQASRVQVAIQTLDENDNAPOLAEFYDTFVCDSPAAGQLIOVIRA 540
 DR -----DSSQASRVQVAIQTLDENDNAPOLAEFYDTFVCDSPAAGQLIOVIRA 502

QY 541 LDRDEGVNSSHVSFGPLGPDANFTVODNRD-----LPA-----WF 576
 DB 503 LDRDEGVNSSHVSFGPLGPDANFTVODNRGASLLPSPAPPRHAPYVPIELMDWG 562
 QY 577 HPLMASASWLH-----WPPAERGQAPASOG 603
 DB 563 QPALSTATVTVSVCRQCPDGSVASCPFEAHLISAAGLSTG 602
 RESULT 4
 ID AAM48736 standard; protein; 781 AA.
 AAM48736
 AC AAM48736;
 XX 28-MAR-2002 (first entry)
 DT
 XX Human cadherin family member 57805 protein SEQ ID NO 2.
 DE
 XX Human; cadherin 57805; osteopathic; hepatotropic; antibacterial;
 KW antidiabetic; neuroprotective; antiarthritic; antifibrotic;
 KW dermatological; immunosuppressive; antinflammatory; antipruritic;
 KW antiasmatic; antiallergic; antileprotic; haemostatic; antipruritic;
 KW antihypertensive; antiatherosclerotic; cardiant; antiarrhythmic;
 KW anorectic; immunomodulatory; vasotropic; virucide; cytostatic; liver;
 KW thrombolytic; analgesic; anabolic; immune disorder; cardiovascular;
 KW viral; pain; metabolism; osteoporosis; diabetes mellitus; arthritis;
 KW osteoarthritis; multiple sclerosis; Crohn's disease; asthma; allergy;
 KW thrombus; inflammation; infection; ischaemia; irritable bowel syndrome;
 KW gene therapy.
 XX Homo sapiens.
 OS
 XX WO200190145-A2.
 EN
 XX 29-NOV-2001.
 PD
 XX 18-MAY-2001; 2001WO-US016013.
 PE
 XX 19-MAY-2000; 2000US-0205674P.
 PR
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 XX Curtis RAJ;
 PI
 XX WPI; 2002-083082/11.
 DR N-PSDB; ABA96406; ABA96407.
 DR
 XX New human cadherin family protein and polynucleotides, useful for
 PT diagnosing and treating disorders e.g obstructive jaundice, multiple
 PT sclerosis, encephalomyelitis and atherosclerosis and to identify
 PT modulators of therapeutic use.
 PT
 XX Claim 9; Page 105; 119pp; English.
 PS
 XX The invention relates to human cadherin family polypeptide designated
 CC 57805 with osteopathic, hepatotropic, antibacterial, antidiabetic,
 CC neuroprotective, antiarthritic, antifibrotic, dermatological,
 CC immunosuppressive, antinflammatory, antipruritic, antiasmatic,
 CC antiallergic, antileprotic, haemostatic, antipruritic, antihypertensive,
 CC hypotensive, antiatherosclerotic, cardiant, antiarrhythmic, anorectic,
 CC immunomodulatory, vasotropic, virucide, cytostatic, thrombolytic,
 CC analgesic and anabolic activity. The 57805 molecules are useful for
 CC diagnosing and treating disorders which include disorders associated with
 CC bone metabolism, immune disorders, cardiovascular disorders, liver
 CC disorders, viral diseases, pain or metabolic disorders. Especially bone
 CC metabolism including osteoporosis, rickets, osteosclerosis, cirrhosis;
 CC immune disorders including autoimmune disease including diabetes mellitus
 CC arthritis, including rheumatoid arthritis and osteoarthritis, multiple
 CC sclerosis, systemic lupus, dermatitis, psoriasis, Crohn's disease,
 CC asthma, thrombocytopaenia, Graves' disease, graft-versus-host disease,
 CC allergy; cardiovascular disorders, thrombus, hypertension,
 CC atherosclerosis, arrhythmias and cardiomyopathy; liver disorders.

CC glycogen storage disease, vascular disorders, chronic heart failure,
 CC portal vein thrombosis; viral diseases; metabolic or pain disorders
 CC include obesity, anorexia nervosa and diabetes, inflammation, infection
 CC and ischaemia, irritable bowel syndrome. The polynucleotides are also
 CC useful in gene therapy
 CC
 XX
 SQ Sequence 781 AA;
 Query Match 81.9%; Score 2746.5; DB 5; Length 781;
 Best Local Similarity 84.8%; Pred. No. 1.8e-221;
 Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;
 QY 1 MNGVLRLLAAMLGCMGCRGLAAPARAWAGREHPGLALTRRSWMVNOFFVBEVAGP 60
 DB 1 MNGVLRLLAAMLGCMGCRGLAAPARAWAGREHPGLALTRRSWMVNOFFVBEVAGP 60
 QY 61 EPLLIGKLSVDVDRGEGRTKYLITGEGAGTVFVIDEATGNIHVTKSLDREKQAYVLLAQ 120
 DB 61 EPLLIGKLSVDVDRGEGRTKYLITGEGAGTVFVIDEATGNIHVTKSLDREKQAYVLLAQ 120
 QY 121 AVDRASNPPLPPEPSEFIIKQGDINDNPPIFPLGPHVATVPMMSVGTSVQVTAHADDP 180
 DB 121 AVDRASNPPLPPEPSEFIIKQGDINDNPPIFPLGPHVATVPMMSVGTSVQVTAHADDP 180
 QY 181 SYGNSAKLVYTVLDGLPFFSVDPQTGVVTRAIIPNMDRETQEEFLVVIQAKDMGGMGLS 240
 DB 181 SYGNSAKLVYTVLDGLPFFSVDPQTGVVTRAIIPNMDRETQEEFLVVIQAKDMGGMGLS 240
 QY 241 GSTTATVTLSDVNDNPPKPFPOSILYQSVETAGAGTIVGRIRADDPDGLGNALMAYSLD 300
 DB 241 GSTTATVTLSDVNDNPPKPFPOSILYQSVETAGAGTIVGRIRADDPDGLGNALMAYSLD 300
 QY 301 GEGSEAFSISTDLQGRDGLTVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFKXVAS 360
 DB 301 GEGSEAFSISTDLQGRDGLTVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFKXVAS 360
 QY 361 VRVAVQDAPBPAPATQAAVHLTVPENKAPGTLVQGISAADIDSPASIRISILPHSPER 420
 DB 361 VRVAVQDAPBPAPATQAAVHLTVPENKAPGTLVQGISAADIDSPASIRISILPHSPER 420
 QY 421 CFSIQPEEGTHTTAPLDREARAWNTLVATELGMSGWERGVPLVAVMSAPAPQ 480
 DB 421 CFSIQPEEGTHTTAPLDREARAWNTLVATELGMSGWERGVPLVAVMSAPAPQ 480
 QY 481 RSPVGSAGVIGIPQSSAQSARVQVAIQTLBENDNAPQALAEFYDFVCDSPAAGQLIQVIRA 540
 DB 481 RSPVGSAGVIGIPQSSAQSARVQVAIQTLBENDNAPQALAEFYDFVCDSPAAGQLIQVIRA 540
 QY 455 -----DSSAQSRVQVAIQTLBENDNAPQALAEFYDFVCDSPAAGQLIQVIRA 502
 DB 455 -----DSSAQSRVQVAIQTLBENDNAPQALAEFYDFVCDSPAAGQLIQVIRA 502
 QY 541 LDRDEGVNSSHVSFGPLGPDANFTVODNRD-----LPA-----WF 576
 DB 503 LDRDEGVNSSHVSFGPLGPDANFTVODNRGASLLPSPAPPRHAPYVPIELMDWG 562
 QY 577 HPLMASASWLH-----WPPAERGQAPASOG 603
 DB 563 QPALSTATVTVSVCRQCPDGSVASCPFEAHLISAAGLSTG 602
 RESULT 5
 ID ABG34078 standard; protein; 781 AA.
 ABG34078
 AC ABG34078;
 XX 15-JUL-2002 (first entry)
 DT
 XX Human Pro peptide #49.
 DE
 XX Human; PRO; secreted protein; transmembrane protein; genetic disorder;
 KW tumour; cancer.
 XX
 OS Homo sapiens.
 EN WO200224888-A2.

XX 28-MAR-2002.
 PD 29-AUG-2001; 2001WO-US027099.
 XX
 PF
 XX 01-SEP-2000; 2000US-0229896P.
 PR 05-SEP-2000; 2000US-0230621P.
 PR 22-SEP-2000; 2000US-0235147P.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 12-JAN-2001; 2001US-0261878P.
 PR 16-JAN-2001; 2001US-0261910P.
 PR 16-JAN-2001; 2001US-0261939P.
 PR 16-JAN-2001; 2001US-0262150P.
 PR 25-JAN-2001; 2001US-0264395P.
 PR 02-FEB-2001; 2001US-0266421P.
 PR 09-FEB-2001; 2001US-0267623P.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 09-MAR-2001; 2001US-0274399P.
 PR 03-APR-2001; 2001US-0280982P.
 PR 04-APR-2001; 2001US-0282125P.
 PR 04-APR-2001; 2001US-0282199P.
 PR 09-MAY-2001; 2001US-0290589P.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 XX
 XX (GETH) GENENTECH INC.
 PA Baker KP, Bacon DL, Filvarcoff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;
 PI Fong S;
 XX WPI; 2002-362426/39.
 DR N-PSDB; ABR70009.
 XX
 PT New PRO polypeptides and polynucleotides encoding the polypeptides,
 PT useful in gene therapy, chromosome identification, tissue typing, or for
 PT genetic analysis of individuals with genetic disorders.
 XX
 XX Claim 11; Fig 98; 218pp; English.
 XX
 CC This invention relates to the cDNA and protein sequences of novel
 CC secreted and transmembrane polypeptides PRO polypeptides. The invention
 CC also comprises a method for producing the proteins of the invention by
 CC recombinant means and antibodies specific for the protein of the
 CC invention. The antibody may be used for detecting the PRO proteins of the
 CC invention and may be used to modify their activity. polynucleotides may
 CC be used as hybridisation probes for a cDNA library to isolate the full-
 CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation
 CC probes for mapping the gene which encodes that PRO and for genetic
 CC analysis of individuals with genetic disorders, in assays to identify
 CC other proteins or molecules involved in binding reaction, to generate
 CC transgenic animals or knock-out animals which in turn are useful in the
 CC development and screening of therapeutically useful reagents, for
 CC chromosome identification, and tissue typing. The PRO polypeptides are
 CC useful in gene therapy, and as molecular weight markers for protein
 CC electrophoresis purposes. The sequences may also be used to detect
 CC overexpression on PRO polypeptides in cancerous tumours and for screening
 CC for differentially expressed genes using microarray technology. The
 CC present sequence represents a human PRO protein of the invention
 XX
 XX Sequence 781 AA;
 SQ

Query Match 81.9%; Score 2746.5; DB 5; Length 781;
 Best Local Similarity 84.8%; Pred No. 1.8e-221;
 Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

OY 1 MMGLVLLIAMIQSGWCMGRLLAARAWAGSRHHPGALLTRRSWVNOFFVIEEYAGP 60
 DB 1 MMGLVLLIAMIQSGWCMGRLLAARAWAGSRHHPGALLTRRSWVNOFFVIEEYAGP 60

OY 61 EPLLIGKLSHDVDRGEGRTKYLITGEGAGTVFVIDEATGNTHVTKSLDRERKAQVLLAQ 120
 DB 61 EPLLIGKLSHDVDRGEGRTKYLITGEGAGTVFVIDEATGNTHVTKSLDRERKAQVLLAQ 120
 OY 121 AVDRASNPRLPEPSEFIKGGDINDNPPIFGPYHATVPEMSNVTGVIQVTAHADDP 180
 DB 121 AVDRASNPRLPEPSEFIKGGDINDNPPIFGPYHATVPEMSNVTGVIQVTAHADDP 180
 OY 181 SYGSAKLYTVLDGIPFESVDPQTGVYRTAIPNMDRETQEEFLVYIQAKMGHMGIS 240
 DB 181 SYGSAKLYTVLDGIPFESVDPQTGVYRTAIPNMDRETQEEFLVYIQAKMGHMGIS 240
 OY 241 GSTTVTVLSDVNDNPPKFPQSLVQFSVETAGPTLVGRRAQDPDGDNALMAYSILD 300
 DB 241 GSTTVTVLSDVNDNPPKFPQSLVQFSVETAGPTLVGRRAQDPDGDNALMAYSILD 300
 OY 301 GEGSEAFSISTDLQGRDGLITVRKPLDEESQSYSFVEAINTLIDPAYLRGPFKYAS 360
 DB 301 GEGSEAFSISTDLQGRDGLITVRKPLDEESQSYSFVEAINTLIDPAYLRGPFKYAS 360
 OY 361 VRYAVODAPERPAPFTQAAVHLTVPENKAQGLTVGQISAADLSPASPIRYSILPHSDPR 420
 DB 361 VRYAVODAPERPAPFTQAAVHLTVPENKAQGLTVGQISAADLSPASPIRYSILPHSDPR 420
 OY 421 CFSIOPEEGTITTAAPLDREARAMHNLTVLATELGMSWGPBERGWYLLVAEWSAPAPQ 480
 DB 421 CFSIOPEEGTITTAAPLDREARAMHNLTVLATELGMSWGPBERGWYLLVAEWSAPAPQ 480
 OY 481 RSPVGSAGVIFODSSAQASRVQVAIQTLDENNDNAPQAEPTVTFVCDSPAAPQILQVIRA 540
 DB 481 RSPVGSAGVIFODSSAQASRVQVAIQTLDENNDNAPQAEPTVTFVCDSPAAPQILQVIRA 540
 OY 455 -----DSSAQASRVQVAIQTLDENNDNAPQAEPTVTFVCDSPAAPQILQVIRA 502
 DB 455 -----DSSAQASRVQVAIQTLDENNDNAPQAEPTVTFVCDSPAAPQILQVIRA 502
 OY 541 LDRDEVGNSSHVSPQGLPDANFTVQDNRD-----LPA-----WF 576
 DB 541 LDRDEVGNSSHVSPQGLPDANFTVQDNRD-----LPA-----WF 576
 OY 503 LDRDEVGNSSHVSPQGLPDANFTVQDNRDSSALILPSPRAPPRHAFYVILMWG 562
 DB 503 LDRDEVGNSSHVSPQGLPDANFTVQDNRDSSALILPSPRAPPRHAFYVILMWG 562
 OY 577 HPLMASASSWLH-----WPPAERGNQAPASOG 603
 DB 577 HPLMASASSWLH-----WPPAERGNQAPASOG 603
 OY 563 QPALSSTATVTVSVCRQPDGVSASCPFAHLSAAGLSYG 602
 DB 563 QPALSSTATVTVSVCRQPDGVSASCPFAHLSAAGLSYG 602

RESULT 6
 ABR40114
 ID ABR40114 standard; protein; 781 AA.
 XX
 AC ABR40114;
 XX
 DT 04-JUL-2003 (first entry)
 XX
 DE Human cell adhesion and extracellular matrix protein, CADCM-11.
 XX
 XX Human; anti-HIV; antiallergic; cerebroprotective; antiparkinsonian;
 KW anticonvulsant; nootropic; neuroprotective; immunosuppressive;
 KW dermatological; anti-inflammatory; cytosolic; antiatherosclerotic;
 KW gene therapy; cell adhesion; extracellular matrix; CADCM;
 KW immune system disorder; AIDS; allergy; neurological disorder; stroke;
 KW Parkinson's disease; epilepsy; developmental disorder; Down's syndrome;
 KW cerebral palsy; connective tissue disorder; systemic lupus erythematosus;
 KW genetic disorder; Alport's syndrome; cell proliferative disorder; cancer;
 KW atherosclerosis.
 XX
 OS Homo sapiens.
 XX
 XX WC02003027230-A2.
 PN
 XX
 PD 03-APR-2003.
 XX
 PF 02-AUG-2002; 2002WO-US024649.
 XX
 XX 03-AUG-2001; 2001US-0309964P.
 PR 03-AUG-2001; 2001US-0310119P.
 PR 17-AUG-2001; 2001US-0313091P.
 PR 31-AUG-2001; 2001US-0316771P.

07-SEP-2001; 2001US-0317896P.
PR 21-SEP-2001; 2001US-0324781P.
PR 05-OCT-2001; 2001US-0327606P.
PR 12-OCT-2001; 2001US-0328960P.
PR 09-NOV-2001; 2001US-0344471P.
PR 17-MAY-2002; 2002US-0381291P.
(INCY-) INCYTE GENOMICS INC.
XX
XX Burford N, Warren BA, Duggan EM, Mason PM, Richardson TW, Yue H;
PI Forsythe TJ, Elliott VS, Griffin JA, Gorvad AE, Azinza Y,
PI Kallikch DA, Xu Y, Honchell CD, Baughn ME, Gietzen KO, Lee S;
PI Walla NK, Tang YT, Nguyen DS, Becha SD, Lee SY, Ramkumar J;
XX
XX WPI; 2003-354645/33.
DR N-PSDB; ACC00402.
XX
XX
XX New human cell adhesion and extracellular matrix proteins (CADECM),
PT useful for diagnosing, treating or preventing disorders associated with
PT aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies
PT or stroke.
XX
XX
XX Claim 1; Page 192-194; 234pp; English.
XX
XX
XX The present invention relates to novel human cell adhesion and
XX extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding
XX sequences (ACC00392-ACC00413 and ABR40104-ABR40125). The coding sequences
XX and proteins are useful in diagnosing, treating and preventing disorders
XX associated with aberrant expression of CADECM, such as immune system
XX disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,
XX Parkinson's disease or epilepsy), developmental disorders (e.g. Down's
XX syndrome or cerebral palsy), connective tissue disorders (e.g. systemic
XX lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell
XX proliferative disorders (e.g. cancer or atherosclerosis)
XX
XX
XX Sequence 781 AA:
81.9%; Score 2746.5; DB 6; Length 781;
Query Match Best Local Similarity 84.8%; Pred. No. 1.8e-221;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;
QY 1 MMGLVRLILAWLGGMGCMGRLLAARAMAGSREHPGALRTTRSWWVNFVIEYAGP 60
DB 1 MMGLVRLILAWLGGMGCMGRLLAARAMAGSREHPGALRTTRSWWVNFVIEYAGP 60
QY 61 EPTVLIGLHSDVDGEGRTKYLITGEGAGTVFIDEATGNIHTKSLDREKQYVLLAQ 120
DB 61 EPTVLIGLHSDVDGEGRTKYLITGEGAGTVFIDEATGNIHTKSLDREKQYVLLAQ 120
QY 121 AVDRASNRPLEPSEPFIIKQDINDNPIPLGPHYATVEMSNVGSVYQVTAHDADP 180
DB 121 AVDRASNRPLEPSEPFIIKQDINDNPIPLGPHYATVEMSNVGSVYQVTAHDADP 180
QY 181 SYGSASAKLVYTVLDGLPFESVDPOGTGVRTAIPNMDRETOEBELVYIOAKMGSHGGLS 240
DB 181 SYGSASAKLVYTVLDGLPFESVDPOGTGVRTAIPNMDRETOEBELVYIOAKMGSHGGLS 240
QY 241 GSTTAVTTLSDVDNPKFPQSLYQSFVETAGPGLTVGLRQDDPLDGNLMAYSILD 300
DB 241 GSTTAVTTLSDVDNPKFPQSLYQSFVETAGPGLTVGLRQDDPLDGNLMAYSILD 300
QY 301 GEGSEAFSISTDIQGRDGLTVKKPLDFESQRSYFRVETANTLIDPAVLRGPFKDVAS 360
DB 301 GEGSEAFSISTDIQGRDGLTVKKPLDFESQRSYFRVETANTLIDPAVLRGPFKDVAS 360
QY 361 VRAVAVODAPPEPAFTQAAHYLTPENKAPETLVGOISADLDSPASPIYSLIPSDPR 420
DB 361 VRAVAVODAPPEPAFTQAAHYLTPENKAPETLVGOISADLDSPASPIYSLIPSDPR 420
QY 421 CFSIQPEEGTITTAAPLDREARAMNLTVALTELGMSQGERGVWVLLVAEMSAAPAPQ 480
DB 421 CFSIQPEEGTITTAAPLDREARAMNLTVALTELGMSQGERGVWVLLVAEMSAAPAPQ 480
454

481 RSPVSAVIGIPDSSAQAQSRVQVATQTLIDENDNAPQALAEPTDTPVCSAARQGLIQVIRA 540
DB 455 -----DSSAQASRVQVATQTLIDENDNAPQALAEPTDTPVCSAARQGLIQVIRA 502
QY 541 LDRDEVGNSSHVSPGCPGPANFTVQDNRD-----LPA-----WF 576
DB 503 LDRDEVGNSSHVSPGCPGPANFTVQDNRDGASLILPSRAPPRAPRVLPVLEMDWG 562
QY 577 HPLMASASMTLH-----WEPAREGNQAPAG 603
DB 563 QPALSTATVTVSVCRCPDGSVASCPWPAHLASAGLSTG 602
RESULT 7
ADA01366
ID ADA01366 strand; protein; 781 AA.
XX
XX ADA01366;
XX
XX 06-NOV-2003 (first entry)
XX
XX
XX Human PRO polypeptide #49.
XX
XX Human; PRO, secreted polypeptide; transmembrane polypeptide;
XX tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
XX adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
XX microvascular endothelial cell; endothelial cell tube formation;
XX sports-related joint problem; articular cartilage defect; osteoarthritis;
XX rheumatoid arthritis; osteopathic; anti-rheumatic; antiarthritic.
XX
XX Homo sapiens.
XX
XX US2003068779-A1.
XX
XX 10-APR-2003.
XX
XX 16-SEP-2002; 2002US-00245107.
XX
XX 09-MAY-2001; 2001US-0290589P.
XX 29-AUG-2001; 2001WO-US027099.
XX 18-JUL-2002; 2002US-00197942.
XX
XX (GENTH) GENENTECH INC.
XX
XX Baker KP, Baton DL, Filvaroff E, Goddard A, Grimaldi JC,
XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
XX Fong S;
XX WPI; 2003-625484/59.
XX N-PEDB; ADA01365.
XX
XX Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
XX stimulating proliferation of human microvascular endothelial cells, and
XX PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
XX cells.
XX
XX Claim 11; Fig 98; 307pp; English.
XX
XX The invention relates to isolated human PRO polypeptides (secreted and
XX transmembrane polypeptides) and the polynucleotides encoding them. The
XX invention also relates to an antibody which specifically binds to a PRO
XX polypeptide, a method for stimulating the release of tumour necrosis
XX factor-alpha (TNF-alpha) from human blood, a method for stimulating the
XX proliferation or differentiation of chondrocyte cells and a method for
XX detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
XX colon, breast, prostate, rectal, cervical and liver tumours). The
XX polynucleotides are useful in molecular biology, including uses as
XX hybridisation probes, in chromosome and gene mapping, in generating
XX antisense RNA and DNA and in gene therapy. The polynucleotides may also
XX be used in preparing PRO polypeptides by recombinant techniques and in
XX generating either transgenic animals or knock-out animals which are
XX useful in the development and screening of therapeutically useful
XX reagents. The PRO polypeptides or antibodies are used in preparing a

medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for inducing endothelial cell tube formation and for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence represents a human PRO polypeptide of the invention.

SO Sequence 781 AA;

Query Match 81.9%; Score 2746.5; DB 6; Length 781;
Best Local Similarity 84.8%; Pred. No. 1.8e-221;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MMGLVRLLLAWLGWGMCKGRLAAPARAWAGSREHHPGALLRTRRSWVWVNFVIEEYAGP 60
DB 1 MMGLVRLLLAWLGWGMCKGRLAAPARAWAGSREHHPGALLRTRRSWVWVNFVIEEYAGP 60
QY 61 EPLVIGKLHSDVDGEGRTKYLITGEGAGTVFVIDEATGNIHVTSKSLDREKQYVLLAQ 120
DB 61 EPLVIGKLHSDVDGEGRTKYLITGEGAGTVFVIDEATGNIHVTSKSLDREKQYVLLAQ 120
QY 121 AVDAASRNPLEPSEEFITKQDINDNPIPLGPHYATVPEMSWVGTSVIQTVAHDDP 180
DB 121 AVDAASRNPLEPSEEFITKQDINDNPIPLGPHYATVPEMSWVGTSVIQTVAHDDP 180
QY 181 SYGSAKLVTYVLDGLPFPSVDPQTGVVTRAI PMNDEBTOEELVVI QAKDMGGMGLS 240
DB 181 SYGSAKLVTYVLDGLPFPSVDPQTGVVTRAI PMNDEBTOEELVVI QAKDMGGMGLS 240
QY 241 GSTTWTYVLSVWVNNPKFPOSTVQSVETAGSGTIVGRADDPDGNALMAYSLD 300
DB 241 GSTTWTYVLSVWVNNPKFPOSTVQSVETAGSGTIVGRADDPDGNALMAYSLD 300
QY 301 GEGSEAFSISTDLQGRDGLTVRKPLDPESQSRYSFVEATNTLIDPAYLRGPFKDVAS 360
DB 301 GEGSEAFSISTDLQGRDGLTVRKPLDPESQSRYSFVEATNTLIDPAYLRGPFKDVAS 360
QY 361 VRVAVQAPPEPPATQAAVHTLVENKAPGTLVQISADDDSPASIRISILPHSPER 420
DB 361 VRVAVQAPPEPPATQAAVHTLVENKAPGTLVQISADDDSPASIRISILPHSPER 420
QY 421 CFSIQPEBGTHTTAFLDREARAHNLTVLATELGWSMGRGWVPLVAVMSAPAPQ 480
DB 421 CFSIQPEBGTHTTAFLDREARAHNLTVLATELGWSMGRGWVPLVAVMSAPAPQ 480
QY 481 RSPVGSAGVIGPDDSSAQAQRVQVAIQTLIDENDNAPQLAEPYDTVCDSPAAGQLIQVIRA 540
DB 481 RSPVGSAGVIGPDDSSAQAQRVQVAIQTLIDENDNAPQLAEPYDTVCDSPAAGQLIQVIRA 540
QY 541 LDRDEVGSSHVSRQGLGPANFTVOONRP-----LPA-----WF 576
DB 541 LDRDEVGSSHVSRQGLGPANFTVOONRP-----LPA-----WF 576
QY 576 HPLMASASSWLH-----MPPAERGQAPASOG 603
DB 576 HPLMASASSWLH-----MPPAERGQAPASOG 603
QY 603 QPALSSSTATVTVASVCRQCPDGSVASCMPEALMSAAGSTG 602
DB 603 QPALSSSTATVTVASVCRQCPDGSVASCMPEALMSAAGSTG 602

RESULT 8
ADA43795 ID ADA43795 standard; protein; 781 AA.

ADA43795; AC

20-NOV-2003 (first entry)

Human secreted/transmembrane polypeptide PRO34009.
Human; PRO; secreted protein; transmembrane protein;
endothelial cell tube formation; chondrocyte cell differentiation;
microvascular endothelial cell; tumour; lung tumour; colon tumour;
breast tumour; prostate tumour; rectal tumour; kidney tumour;
liver tumour; cytostatic; vaccine.

XX Homo sapiens.
OS US2003064474-A1.
PN 03-APR-2003.
PD 16-SEP-2002; 2002US-00245859.
PP 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX (GENENTECH INC.
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
XX Fong S;
XX MPI; 2003-605867/57.
XX N-PSDB; ADA43794.
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX Claim 11; Fig 98; 308pp; English.
XX The invention relates to an isolated secreted/transmembrane (PRO)
XX polypeptide, having at least 80% sequence identity to a sequence selected
XX from any one of the 57 amino acid sequences given in specification, or to
XX a sequence encoded by a nucleic acid molecule selected from any one of
XX the nucleic acids deposited under any of the ATCC accession numbers given
XX in specification, or a sequence having at least 80% identity to PRO
XX lacking its associated signal peptide, an extracellular domain of PRO
XX with or without its associated signal peptide. Also included are vectors,
XX transformed host cells, anti-PRO antibodies, the nucleic acids encoding
XX PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
XX administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
XX PRO1275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
XX an oligonucleotide probe derived from any one of the above nucleotide
XX sequences. PRO6018 polypeptide is useful for stimulating the
XX proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
XX and PRO21383 polypeptides are useful for stimulating the proliferation of
XX human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
XX polypeptides are useful for inhibiting the proliferation of human
XX microvascular endothelial cells. PRO polypeptides are useful for
XX detecting the presence of tumour in a mammal, including tumours of lung,
XX colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
XX PRO189, PRO4499, PRO6308, PRO10275, PRO21207, PRO20933 and
XX PRO34274 polypeptides are useful for inducing endothelial cell tube
XX formation. PRO or the antibody are useful in the preparation of a
XX medicament for treating a condition responsive to PRO polypeptide. The
XX oligonucleotide probes are useful for isolating genomic and cDNA
XX nucleotide sequences, for measuring or detecting the expression of an
XX associated gene, and as antisense probes. PRO nucleic acid is useful as a
XX hybridisation probe, in chromosome and gene mapping, in the generation of
XX antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
XX PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
XX present sequence represents a PRO protein.

SO Sequence 781 AA;

Query Match 81.9%; Score 2746.5; DB 6; Length 781;
Best Local Similarity 84.8%; Pred. No. 1.8e-221;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MMGLVRLLLAWLGWGMCKGRLAAPARAWAGSREHHPGALLRTRRSWVWVNFVIEEYAGP 60
DB 1 MMGLVRLLLAWLGWGMCKGRLAAPARAWAGSREHHPGALLRTRRSWVWVNFVIEEYAGP 60
QY 61 EPLVIGKLHSDVDGEGRTKYLITGEGAGTVFVIDEATGNIHVTSKSLDREKQYVLLAQ 120
DB 61 EPLVIGKLHSDVDGEGRTKYLITGEGAGTVFVIDEATGNIHVTSKSLDREKQYVLLAQ 120

QY 121 AYDRASNPLEPSEFIIKGGDINDNPPILPFGYHATVEMSNVGTSVIQTVAHADDDP 180
 Db 121 AYDRASNPLEPSEFIIKGGDINDNPPILPFGYHATVEMSNVGTSVIQTVAHADDDP 180
 QY 181 SYGNSAKLVYTVLGLPFPSVDPTGVRTAIPMDRETOBEFLVVIQAOMGSHMGGS 240
 Db 181 SYGNSAKLVYTVLGLPFPSVDPTGVRTAIPMDRETOBEFLVVIQAOMGSHMGGS 240
 QY 241 GSTTIVTVLSDVNDNPKFPQSLYQFSVETAGBGLVGLRAQDDPDLGNALMAYSIID 300
 Db 241 GSTTIVTVLSDVNDNPKFPQSLYQFSVETAGBGLVGLRAQDDPDLGNALMAYSIID 300
 QY 301 GEGSEAFSISTDLQGRGGLTVKRPDLFESQRSYSPVEATNTLIDPAYLRGPFQDVAS 360
 Db 301 GEGSEAFSISTDLQGRGGLTVKRPDLFESQRSYSPVEATNTLIDPAYLRGPFQDVAS 360
 QY 361 VRVAVDAPPEPPTQAAYHLYPENKAPGTLVGOISADLSPASIRYSILPHSDPER 420
 Db 361 VRVAVDAPPEPPTQAAYHLYPENKAPGTLVGOISADLSPASIRYSILPHSDPER 420
 QY 421 CFSIQPEEGTHTTAAPLDREKRAMHNTLVLTATELIGMSWGPERGVPLVAEMGAPAPPO 480
 Db 421 CFSIQPEEGTHTTAAPLDREKRAMHNTLVLTATELIGMSWGPERGVPLVAEMGAPAPPO 480
 QY 481 RSPVGSAVGLPQDSSAASRVOVAIQTLDENDNAPQLAEPYDTFVCDAPGQLIQTIRA 540
 Db 481 RSPVGSAVGLPQDSSAASRVOVAIQTLDENDNAPQLAEPYDTFVCDAPGQLIQTIRA 540
 QY 541 LDRDEVGNSSHVSGPLGPDANFTVODNFD-----LPA-----WF 576
 Db 541 LDRDEVGNSSHVSGPLGPDANFTVODNFD-----LPA-----WF 576
 QY 577 HPLMASASSWLH-----WPARRGNGAPASOG 603
 Db 577 HPLMASASSWLH-----WPARRGNGAPASOG 603
 QY 563 OPALSTHTVTVSVCRQDPGGSVASCPEAHLSAAGLSTG 602
 Db 563 OPALSTHTVTVSVCRQDPGGSVASCPEAHLSAAGLSTG 602

RESULT 9
 ADA43563
 ID ADA43563 standard; protein; 781 AA.
 AC ADA43563;
 XX
 XX 20-NOV-2003 (first entry)
 DT
 XX Human secreted/transmembrane polypeptide PRO34009.
 DE
 XX Human: PRO: secreted protein; transmembrane protein;
 KW endothelial cell tube formation; chondrocyte cell differentiation;
 KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KW liver tumour; cytostatic; vaccine.
 XX
 XX Homo sapiens.
 OS
 XX
 XX US2003073196-A1.
 EN
 XX 17-APR-2003.
 PD
 XX 18-SEP-2002; 2002US-00246210.
 PF
 XX 04-APR-2001; 2001US-0282199P.
 PR 29-AUG-2001; 2001MO-US027093.
 PR 18-JUL-2002; 2002US-00197942.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
 PI Fong S;
 XX WPI; 2003-743814/70.

DR N-PSDB; ADA43562.
 XX
 XX New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
 PT PRO21383 useful for stimulating the proliferation or differentiation of
 PT chondrocyte cells and detecting the presence of a tumor in a mammal.
 PT
 XX
 XX Claim 11, Fig 98, 307pp; English.
 PS
 XX
 XX The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acids deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide. Also included are vectors,
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO189, PRO499, PRO6308, PRO6000,
 CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO3133, PRO20080
 CC and PRO21383 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumour in a mammal, including tumours of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence represents a PRO protein.
 CC
 XX
 XX Sequence 781 AA;
 SQ
 QY 1 MMGLVRLLLAAGMGCMGRIAPARAWAGSREHPGALLRTRRSWTNQPFIYEYAGP 60
 Db 1 MMGLVRLLLAAGMGCMGRIAPARAWAGSREHPGALLRTRRSWTNQPFIYEYAGP 60
 QY 61 EPLVIGKLHSDVDGEGRTKYLITGEGAGTVFVDEATGNIHVTKSLDREKQYVLLAQ 120
 Db 61 EPLVIGKLHSDVDGEGRTKYLITGEGAGTVFVDEATGNIHVTKSLDREKQYVLLAQ 120
 QY 121 AYDRASNPLEPSEFIIKGGDINDNPPILPFGYHATVEMSNVGTSVIQTVAHADDDP 180
 Db 121 AYDRASNPLEPSEFIIKGGDINDNPPILPFGYHATVEMSNVGTSVIQTVAHADDDP 180
 QY 181 SYGNSAKLVYTVLGLPFPSVDPTGVRTAIPMDRETOBEFLVVIQAOMGSHMGGS 240
 Db 181 SYGNSAKLVYTVLGLPFPSVDPTGVRTAIPMDRETOBEFLVVIQAOMGSHMGGS 240
 QY 241 GSTTIVTVLSDVNDNPKFPQSLYQFSVETAGBGLVGLRAQDDPDLGNALMAYSIID 300
 Db 241 GSTTIVTVLSDVNDNPKFPQSLYQFSVETAGBGLVGLRAQDDPDLGNALMAYSIID 300
 QY 301 GEGSEAFSISTDLQGRGGLTVKRPDLFESQRSYSPVEATNTLIDPAYLRGPFQDVAS 360
 Db 301 GEGSEAFSISTDLQGRGGLTVKRPDLFESQRSYSPVEATNTLIDPAYLRGPFQDVAS 360
 QY 361 VRVAVDAPPEPPTQAAYHLYPENKAPGTLVGOISADLSPASIRYSILPHSDPER 420
 Db 361 VRVAVDAPPEPPTQAAYHLYPENKAPGTLVGOISADLSPASIRYSILPHSDPER 420

Query Match 81.9%; Score 2746.5; DB 6; Length 781;
 Best Local Similarity 84.8%; Pred. No. 1.8e-221;
 Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

```

Db 361 VRVAVQDAPPEPPAFTQAALHTLPENKAPGTLVQGISADLDSPASPIRYSILPHSDPER 420
QY 421 CFSIQPEEGTHTTAAPLDREARAHNLTVALTELGMKSGWPERGWPLIVAEWSAPAPQ 480
Db 421 CFSIQPEEGTHTTAAPLDREARAHNLTVALTEL----- 454
QY 481 RSPVGSANVGIPQSSAQSARVQVAIQTLDENNDNAPOLAEPYDTFVCDASAPGQLIOYIRA 540
Db 455 -----DSSAQASRVQVAIQTLDENNDNAPOLAEPYDTFVCDASAPGQLIOYIRA 502
QY 541 LDRDEVGNSSHVSFCQPLGPDANFTVQDNRD-----LPA-----WF 576
Db 503 LDRDEVGNSSHVSFCQPLGPDANFTVQDNRDGASALLPSRPAPPAPRHAPLYPIELMDWG 562
QY 577 HPLMASASSWLH-----WPAERGNQSPASQ 603
Db 563 QPALSTATVTVSVCRQCPDGSVASCPPEAHLSPAAGLSTG 602

RESULT 10
ADA01238
ID ADA01238 standard; protein; 781 AA.
XX
AC ADA01238;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human PRO polypeptide #49.
XX
KM Human; PRO; secreted polypeptide; transmembrane polypeptide;
KM tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
KM cancer; lung; colon; breast; prostate; rectum; kidney; liver;
KM microvascular endothelial cell; endothelial cell tube formation.
OS Homo sapiens.
XX
FN US2003068782-A1.
XX
PD 10-APR-2003;
XX
PF 16-SEP-2002; 2002US-00245851.
XX
PR 27-APR-1999; 98US-0131271P.
PR 29-OCT-1999; 98US-0162506P.
PR 02-DEC-1999; 99WO-US028551.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
PA (GENTH) GENENTECH INC.
XX
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI Gurney AL, Smith V, Stephan JP, Matanabe CK, Wood WI, Zhang Z,
PI Fong S;
XX
DR WPI; 2003-625487/59.
DR N-PSDB; ADA01237.
XX
PT Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
PT preparation of a medicament for treating a condition responsive to PRO
PT polypeptide, and as therapeutic agents e.g. vaccines.
XX
PS Claim 11; Fig 98; 308bp; English.
XX
CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
CC prostate, rectal, kidney and liver tumours). The polynucleotides are
CC useful in molecular biology, including uses as hybridisation probes, in
CC chromosome and gene mapping, in generating antisense RNA and DNA and in

```

```

CC gene therapy. The polynucleotides may also be used in preparing PRO
CC polypeptides by recombinant techniques and in generating either
CC transgenic animals or knock-out animals which are useful in the
CC development and screening of therapeutically useful reagents. The PRO
CC polypeptides or antibodies are used in preparing a medicament for
CC treating a condition responsive to the polypeptides or antibodies, such
CC as tumours, for stimulating and inhibiting proliferation of human
CC microvascular endothelial cells and for inducing endothelial cell tube
CC formation. This sequence represents a human PRO polypeptide of the
CC invention.
XX
SQ Sequence 781 AA;
XX
Query Match 81.9%; Score 2746.5; DB 6; Length 781;
Best Local Similarity 84.8%; Pred. No. 1.8e-221;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MMGLVRLLLAMLGWCMGRLLAPAPAMAGSREHPGALLRTRRSVMNQFVIEYAGP 60
Db 1 MMGLVRLLLAMLGWCMGRLLAPAPAMAGSREHPGALLRTRRSVMNQFVIEYAGP 60
QY 61 EPLYLIGKLSDDVDRGGRTRKYLITGAGTAVVIDEATGNHVTSLDREKAQVYLAAQ 120
Db 61 EPLYLIGKLSDDVDRGGRTRKYLITGAGTAVVIDEATGNHVTSLDREKAQVYLAAQ 120
QY 121 AVDRASNRPLEPPESEFIINGQDINDNPIFPLGPYHATVPENSNVGTSVIQTADADDP 180
Db 121 AVDRASNRPLEPPESEFIINGQDINDNPIFPLGPYHATVPENSNVGTSVIQTADADDP 180
QY 121 AYDRASNRPLEPPESEFIINGQDINDNPIFPLGPYHATVPENSNVGTSVIQTADADDP 180
Db 121 AYDRASNRPLEPPESEFIINGQDINDNPIFPLGPYHATVPENSNVGTSVIQTADADDP 180
QY 181 SYGNSAKLYTTLVDGIPFSSVDPQTGVFRTAIPNMDREFQEFVLVIQAKMGHNGGJS 240
Db 181 SYGNSAKLYTTLVDGIPFSSVDPQTGVFRTAIPNMDREFQEFVLVIQAKMGHNGGJS 240
QY 241 GSTTAVTSLDVNDNPKPFQSLYQFSVETAGPGLTVRLRAQDDLDGNLMAYSIID 300
Db 241 GSTTAVTSLDVNDNPKPFQSLYQFSVETAGPGLTVRLRAQDDLDGNLMAYSIID 300
QY 301 GEGSEAFSISTDIQGRDGLTVRKPLDFESQNSYSFRVATNTLIDPAYLRGPFQDVS 360
Db 301 GEGSEAFSISTDIQGRDGLTVRKPLDFESQNSYSFRVATNTLIDPAYLRGPFQDVS 360
QY 361 VRVAVQDAPPEPPAFTQAALHTLPENKAPGTLVQGISADLDSPASPIRYSILPHSDPER 420
Db 361 VRVAVQDAPPEPPAFTQAALHTLPENKAPGTLVQGISADLDSPASPIRYSILPHSDPER 420
QY 421 CFSIQPEEGTHTTAAPLDREARAHNLTVALTELGMKSGWPERGWPLIVAEWSAPAPQ 480
Db 421 CFSIQPEEGTHTTAAPLDREARAHNLTVALTEL----- 454
QY 481 RSPVGSANVGIPQSSAQSARVQVAIQTLDENNDNAPOLAEPYDTFVCDASAPGQLIOYIRA 540
Db 455 -----DSSAQASRVQVAIQTLDENNDNAPOLAEPYDTFVCDASAPGQLIOYIRA 502
QY 541 LDRDEVGNSSHVSFCQPLGPDANFTVQDNRD-----LPA-----WF 576
Db 503 LDRDEVGNSSHVSFCQPLGPDANFTVQDNRDGASALLPSRPAPPAPRHAPLYPIELMDWG 562
QY 577 HPLMASASSWLH-----WPAERGNQSPASQ 603
Db 563 QPALSTATVTVSVCRQCPDGSVASCPPEAHLSPAAGLSTG 602

RESULT 11
ADA01122
ID ADA01122 standard; protein; 781 AA.
XX
AC ADA01122;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human secreted/transmembrane polypeptide PRO34009.
XX
KM Human; PRO; secreted protein; transmembrane protein;

```


KW endothelial cell tube formation; chondrocyte cell differentiation;
 KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KW liver tumour; cytostatic; vaccine.
 XX Homo sapiens.
 XX OS
 XX US2003068780-A1.
 XX PN
 XX 10-APR-2003.
 XX PD
 XX 16-SEP-2002; 2002US-00245143.
 XX PF
 XX 02-AUG-2000; 2000US-0222695P.
 XX PR 20-JUN-2001; 2001WO-US019692.
 XX PR 29-AUG-2001; 2001WO-US027099.
 XX PR 18-JUL-2002; 2002US-00197942.
 XX PA (GENTH) GENENTECH INC.
 XX PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S;
 XX DR MPI, 2003-625485/59.
 XX DR N-PDB; ADA01121.
 XX PT Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
 PT preparation of a medicament for treating a condition responsive to PRO
 PT polypeptide, and as therapeutic agents e.g. vaccines.
 XX PS Claim 11, Fig 98; 307pp; English.
 XX XX
 CC The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acids deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide. Also included are vectors,
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO189, PRO499, PRO6308, PRO6000,
 CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
 CC and PRO21383 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumour in a mammal, including tumours of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO499, PRO6308, PRO6000, PRO10275, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence represents a PRO protein.
 XX
 XX Sequence 781 AA;
 XX SQ
 Query Match 81.9%; Score 2746.5; DB 7; Length 781;
 Best Local Similarity 84.8%; Pred. No. 1.8e-221;
 Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;
 QY 1 MGVLRLLIAMIWGCMGRLLAPARANAGSRHHPGALLTRRSVMNQFVIEEYAGP 60

DB 1 MGVLRLLIAMIWGCMGRLLAPARANAGSRHHPGALLTRRSVMNQFVIEEYAGP 60
 QY 61 EPLLIGKLSVDVDRGGRTRKYLITGEGAGTVFVIDEATGNHTVTKSLDREKAQYVLLAQ 120
 DB 61 EPLLIGKLSVDVDRGGRTRKYLITGEGAGTVFVIDEATGNHTVTKSLDREKAQYVLLAQ 120
 QY 121 AVDRASNPPLRPSSEFIKQDINDNPEIPLGAPYHAHPMSVNGSVIQTVAHDADDP 180
 DB 121 AVDRASNPPLRPSSEFIKQDINDNPEIPLGAPYHAHPMSVNGSVIQTVAHDADDP 180
 QY 181 SYGNSAKLVYTVLDLPPEFSVDPQTGVVRIAIPNMDRETOEFLVVIQAKMGHMGSL 240
 DB 181 SYGNSAKLVYTVLDLPPEFSVDPQTGVVRIAIPNMDRETOEFLVVIQAKMGHMGSL 240
 QY 241 GSTTIVTVLSDVNDNPPKFPQSLVQFSVETAGPTLVGRLRADPDLDGNALMAYSLD 300
 DB 241 GSTTIVTVLSDVNDNPPKFPQSLVQFSVETAGPTLVGRLRADPDLDGNALMAYSLD 300
 QY 301 GEGSEAFSISTDLQGRDGLTVRKXLDPESSORSYFVEATNTLIDPAYLRGPFKVAS 360
 DB 301 GEGSEAFSISTDLQGRDGLTVRKXLDPESSORSYFVEATNTLIDPAYLRGPFKVAS 360
 QY 361 VRVAVQDAPPEPPAFQAAVHITVPENKAEGTLVQGISADLDSAPSIRVISILHSDPER 420
 DB 361 VRVAVQDAPPEPPAFQAAVHITVPENKAEGTLVQGISADLDSAPSIRVISILHSDPER 420
 QY 421 CFSIQEGCTHTAFLDREARAHNLTVLATELGWSGSPERGWPVLVAEWSAPAPQ 480
 DB 421 CFSIQEGCTHTAFLDREARAHNLTVLATELGWSGSPERGWPVLVAEWSAPAPQ 480
 QY 481 RSPVGSAGVIGDSSAQASRVOVAIQTLDENDNAPQLAEPYDTFVCSAPGQIIQYIRA 540
 DB 481 RSPVGSAGVIGDSSAQASRVOVAIQTLDENDNAPQLAEPYDTFVCSAPGQIIQYIRA 540
 QY 541 LDRDVGNSHVSRFGCPIDPANTFYQDNRP-----LPA-----WF 576
 DB 541 LDRDVGNSHVSRFGCPIDPANTFYQDNRP-----LPA-----WF 576
 QY 503 LDRDVGNSHVSRFGCPIDPANTFYQDNRGASLLIPSPAPPRHAPVLTETLMDWG 562
 DB 503 LDRDVGNSHVSRFGCPIDPANTFYQDNRGASLLIPSPAPPRHAPVLTETLMDWG 562
 QY 577 HPLMASASWMLH-----WPAERGNQAPASOG 603
 DB 577 HPLMASASWMLH-----WPAERGNQAPASOG 603
 QY 563 QPALSTATVTVSVRCQPDGSVASCWPEAHLTAAGISTG 602
 DB 563 QPALSTATVTVSVRCQPDGSVASCWPEAHLTAAGISTG 602
 RESULT 12
 ID ADA43679
 ADAA3679; protein: 781 AA.
 AC
 XX ADAA3679;
 XX DT 20-NOV-2003 (first entry)
 XX DE Human secreted/transmembrane polypeptide PRO34009.
 XX KW Human; PRO; secreted protein; transmembrane protein;
 KW endothelial cell tube formation; chondrocyte cell differentiation;
 KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KW liver tumour; cytostatic; vaccine.
 XX OS Homo sapiens.
 XX XX
 XX US2003073190-A1.
 XX PN
 XX 17-APR-2003.
 XX PD
 XX 09-SEP-2002; 2002US-00238283.
 XX PF
 XX 01-JUL-1998; 98US-0091358P.
 XX PR 02-JUN-1999; 99WO-US012252.
 XX PR 20-JUL-1999; 99US-0144758P.
 XX PR 28-JUL-1999; 99US-0146222P.
 XX PR 25-AUG-1999; 99US-00380137.

PR 30-MAR-2000; 2000OWO-US008439.
 PR 02-JUN-2000; 2000OWO-US015264.
 PR 29-AUG-2001; 2001OWO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX
 PA (GETH) GENENTECH INC.
 PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S;
 XX WPI, 2003-585304/55.
 DR N-PSDB; ADA43678.
 XX
 PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
 PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
 PT generating antisense RNA and DNA, and in gene therapy.
 XX
 PS Claim 11, Fig 98, 352pp; English.
 XX
 CC The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acids deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide. Also included are vectors,
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO189, PRO439, PRO6308, PRO6000,
 CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO2133, PRO20080
 CC and PRO21383 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumour in a mammal, including tumours of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence represents a PRO protein.
 XX
 SQ Sequence 781 AA;
 Query Match 81.9%; Score 2746.5; DB 7; Length 781;
 Best Local Similarity 84.8%; Pred. No. 1.8e-221;
 Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

Db 181 SYGNSAKLYVTLDGLPFPSVDPTGVTATLNNDRTOEFLVLIQAKMGHMGSL 240
 QY 241 GSTTAVTTLSDVNDNPKPFQSLIOPSVYETAGPTLVLRAPQPDLDGNALMAVSLD 300
 Db 241 GSTTAVTTLSDVNDNPKPFQSLIOPSVYETAGPTLVLRAPQPDLDGNALMAVSLD 300
 QY 301 GEGSEAFSISTDIQGRDGLTVRKPIDEFSQSYSFREVAATNTLIDPAYLRGPFQDVAS 360
 Db 301 GEGSEAFSISTDIQGRDGLTVRKPIDEFSQSYSFREVAATNTLIDPAYLRGPFQDVAS 360
 QY 361 VRAVODAPBPAPFPAAYHLLTPENKAPGTLVGOISAADLSPASPIRYSILPSPDPR 420
 Db 361 VRAVODAPBPAPFPAAYHLLTPENKAPGTLVGOISAADLSPASPIRYSILPSPDPR 420
 QY 421 CFSIQPEEGTHTPAFLDREARAWNLTVLATELGMSWGPBGWVPLVAEWSAPAAPQ 480
 Db 421 CFSIQPEEGTHTPAFLDREARAWNLTVLATELGMSWGPBGWVPLVAEWSAPAAPQ 480
 QY 481 RSPVGSAGVLPDSSQASRRVQVATOTLDENNAIPQAPPTFVCDASAPGOLIQVRA 540
 Db 455 -----DSSAQASRRVQVATOTLDENNAIPQAPPTFVCDASAPGOLIQVRA 502
 QY 541 LDEDEVNGNSHVSFOGPIPDANFTVQDNRD-----LPA-----WF 576
 Db 503 LDEDEVNGNSHVSFOGPIPDANFTVQDNRDGASLILPSRAPPRHAFYLVPIELMDWG 562
 QY 577 HPLMASASLWH-----WPAERNGNPASGC 603
 Db 563 QPALSTATVTVVCRCPDGSVASCPEAHLSAAGLSIG 602
 RESULT 13
 ADA06941
 ID ADA06941 standard; protein; 781 AA.
 AC ADA06941;
 XX
 DT 06-NOV-2003 (first entry)
 DE Human PRO polypeptide #49.
 XX
 KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
 KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver;
 KW microvascular endothelial cell; endothelial cell tube formation;
 KW bone disorder; cartilage disorder; sports injury; proteoglycan;
 KW cartilage; sports-related joint problem; articular cartilage defect;
 KW osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder;
 KW thalassemia; immune system cell infiltration; cancer; vulnerability;
 KW antianemic; osteopathic; antirheumatic; antiarthritic.
 OS Homo sapiens.
 FN US2003066781-A1.
 XX
 PD 10-APR-2003.
 XX
 PF 16-SEP-2002; 2002US-00245771.
 XX
 PR 03-AUG-1999; 99US-0146643P.
 PR 15-MAY-2000; 2000OWO-US013358.
 PR 29-AUG-2001; 2001OWO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX
 PA (GETH) GENENTECH INC.
 PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S;
 XX WPI, 2003-625486/59.
 DR N-PSDB; ADA06940.
 XX

PT Novel secreted and transmembrane polypeptides, PRO polypeptides useful
PT for stimulating proliferation or differentiation of chondrocyte cells and
PT inducing endothelial cell tube formation.

PS Claim 11, Fig 98; 307pp; English.

CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptides or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for inducing endothelial cell
CC tube formation and for treating various bone and/or cartilage disorders
CC such as sports injuries and arthritis. PRO polypeptides which stimulate
CC the release of proteoglycans from cartilage are useful for treating
CC sports-related joint problems, articular cartilage defects,
CC osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful
CC for treating various mammalian haemoglobin-associated disorders such as
CC various thalassemias and conditions which may benefit from enhanced
CC local immune system cell infiltration. This sequence represents a human
CC PRO polypeptide of the invention.

XX Sequence 781 AA;

Query Match 81.9%; Score 2746.5; DB 7; Length 781;
Best Local Similarity 84.8%; Pred. No. 1.8e-221;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MMGLVRLILAMTGGCMGRLAAPARAWAGSREHPGALLRTRRSWTWNOFFVIEBYAGP 60
DB 1 MMGLVRLILAMTGGCMGRLAAPARAWAGSREHPGALLRTRRSWTWNOFFVIEBYAGP 60
QY 61 EPLVIGKLSHSDVDGEGRTKYLITGEGAGTFFVDEATGNIHTKSLDREKQYVLLAQ 120
DB 61 EPLVIGKLSHSDVDGEGRTKYLITGEGAGTFFVDEATGNIHTKSLDREKQYVLLAQ 120
QY 121 AVDRASRPLEPPEPFIITKQDINDNPPIPLGPHATVPEKSNVGTSVIQTAAHADDP 180
DB 121 AVDRASRPLEPPEPFIITKQDINDNPPIPLGPHATVPEKSNVGTSVIQTAAHADDP 180
QY 181 SYGNSAKLVTVLGLPFESVDPQTGVVCTAIPMDREPEELVVIQAADMGGHNGIS 240
DB 181 SYGNSAKLVTVLGLPFESVDPQTGVVCTAIPMDREPEELVVIQAADMGGHNGIS 240
QY 241 GSTTAVTVLSDVNDNPKEPPOSIVQSFVETAGGTIVGLRAQDDPLGDNALMAYSILD 300
DB 241 GSTTAVTVLSDVNDNPKEPPOSIVQSFVETAGGTIVGLRAQDDPLGDNALMAYSILD 300
QY 301 GEGSEARSISTDLOGRGLITVRKPLDPESSORSYSPVEATNTLIPAYIRRGEPDVAS 360
DB 301 GEGSEARSISTDLOGRGLITVRKPLDPESSORSYSPVEATNTLIPAYIRRGEPDVAS 360
QY 361 VRVAVODAPPEPFAFQAHLTVPENKAPGTLVGOISAAALDPSAPSRIRSIIPHSDPER 420
DB 361 VRVAVODAPPEPFAFQAHLTVPENKAPGTLVGOISAAALDPSAPSRIRSIIPHSDPER 420
QY 421 CFSTIQPEEGTHTTAAPLDREKRAMHNTTVLATELGMSWGERGWPLVAWMSAPAAPQ 480
DB 421 CFSTIQPEEGTHTTAAPLDREKRAMHNTTVLATELGMSWGERGWPLVAWMSAPAAPQ 480
QY 481 RSPVGSAGVIPDSSAQASRVOVAIQTLDENDNAPQLAEBYDTFVCDSSAPQGLIQVIRA 540

DB 455 -----DSSAQASRVOVAIQTLDENDNAPQLAEBYDTFVCDSSAPQGLIQVIRA 502
QY 541 LDRDEVGNSSHYVFCGPGPDANFTVQDNRP-----LPA-----WF 576
DB 503 LDRDEVGNSSHYVFCGPGPDANFTVQDNRPASLLPSRPAPRHAFTVPIELMDWG 562
QY 577 HPLMASASWLH-----WPAERGNOPASQG 603
DB 563 GPALSTATVTVSVRCQCPDGSVASCWPEAHLASAGLSTG 602

RESULT 14

ADA08429
ID ADA08429 standard; protein; 781 AA.

XX ADA08429;

DT 06-NOV-2003 (first entry)

DE Novel human secreted and transmembrane protein PRO34009.

XX osteopathic; antirheumatic; antiarthritic; gene therapy;

KM cell proliferation stimulator;

KM chondrocyte cell differentiation stimulator;

KM secreted and transmembrane protein; PRO human; PRO1313; PRO20080;

KM PRO21383; human microvascular endothelial cell proliferation; PRO6071;

KM PRO4387; PRO6006; PRO2406; PRO2556; PRO698; PRO1002; PRO4316; tumour;

KM adrenal tumour; lung tumour; colon tumour; breast tumour;

KM sports-related joint problem; articular cartilage defect; osteoarthritis;

KM rheumatoid arthritis; tissue typing.

XX Homo sapiens.

XX US2003068783-A1.

XX 10-APR-2003.

XX 16-SEP-2002; 2002US-00245883.

XX 09-MAY-2001; 2001US-0290589P.

XX 29-AUG-2001; 2001WO-US027099.

XX 18-JUL-2002; 2002US-00197942.

XX (GENT) GENENTECH INC.

XX Baker KP, Baton DL, Filvaroff E, Goddard A, Grimaldi JC,

XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WT, Zhang Z,

XX Fong S;

XX WPI; 2003-625488/59.

XX N-PSDB; ADA08428.

XX Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for

XX stimulating proliferation of human microvascular endothelial cells, and

XX PRO6018 polypeptide useful for stimulating proliferation of chondrocyte

XX cells.

PS Claim 11, Fig 98; 308pp; English.

XX The invention describes an isolated PRO (secreted and transmembrane)

XX polypeptide (1). PRO6018 polypeptide is useful for stimulating the

XX proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080,

XX or PRO21383 polypeptide is useful for stimulating the proliferation of

XX human microvascular endothelial cells. PRO6071, PRO4487, or PRO6006

XX polypeptide is useful for inhibiting the proliferation of human

XX microvascular endothelial cells. PRO polypeptides such as PRO240, PRO256,

XX PRO698, PRO1002, PRO4316, etc., are useful for detecting the presence of

XX tumour in a mammal which involves comparing the level of expression of

XX the above mentioned polypeptides in a test sample of cells taken from the

XX mammal, and a control sample of normal cells of the same cell type, where

XX a higher level of expression of the PRO polypeptide in the test sample as

CC compared to the control sample is indicative of the presence of tumour in
 CC the mammal, the tumour being adrenal tumour, lung tumour, colon tumour,
 CC breast tumour, prostate tumour, rectal tumour, cervical tumour or liver
 CC tumour. PRO6018 polypeptide is useful for treating sports-related joint
 CC problems, articular cartilage defects, osteoarthritis, or rheumatoid
 CC arthritis. PRO polypeptides are useful as molecular weight markers for
 CC protein electrophoresis. (I) is also useful for screening compounds to
 CC identify those that mimic the PRO polypeptide (agonists) or prevent the
 CC effect of the PRO polypeptide (antagonists). The polynucleotide (II)
 CC encoding (I) is useful as hybridisation probes, in chromosome and gene
 CC mapping and in the generation of anti-sense RNA and DNA. PRO nucleic acid
 CC is also useful for the preparation of PRO polypeptides. The full-
 CC length native sequence of PRO gene or its portions may be used as
 CC hybridisation probes for a cDNA library to isolate the full-length PRO
 CC cDNA or to isolate still other cDNAs. Nucleotide sequences encoding PRO
 CC can also be used to construct hybridisation probes for mapping the gene
 CC which encodes that PRO and for the genetic analysis of individuals with
 CC genetic disorders. (II) encoding (I) or its modified forms can also be
 CC used to generate either transgenic animals or knockout animals which in
 CC turn are useful in the development and screening of therapeutically
 CC useful reagents. (II) encoding PRO polypeptides are also useful in gene
 CC therapy techniques to treat conditions associated with aberrant
 CC expression or activity of (I). The PRO polypeptides and nucleic acid
 CC molecules are useful for tissue typing. This is the amino acid sequence
 CC of a novel human secreted and transmembrane PRO polypeptide.

XX Sequence 781 AA:

Query Match 81.9%; Score 2746.5; DB 7; Length 781;
 Best Local Similarity 84.8%; Pred. No. 1.8e-221;
 Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MGVRLILAMIGMCMGRIAAPARAWAGSRHHPGALLTRRSWNNQFVIEEYAGP 60
 DB 1 MGVRLILAMIGMCMGRIAAPARAWAGSRHHPGALLTRRSWNNQFVIEEYAGP 60
 QY 61 EPLVIGKLSHSDVDGEGRTKYLITGEGAGTVEIDEAGNIHVKSLDREKAAVYLLAQ 120
 DB 61 EPLVIGKLSHSDVDGEGRTKYLITGEGAGTVEIDEAGNIHVKSLDREKAAVYLLAQ 120
 QY 121 AVDRASNPRLPEPSEFIKGGDINDNPIPLGPHATVPMSNVGTSVIQTAHADDP 180
 DB 121 AVDRASNPRLPEPSEFIKGGDINDNPIPLGPHATVPMSNVGTSVIQTAHADDP 180
 QY 181 SYGSAKIVYVLDGLPFFSVDPOTGVRTAIPMMDETOEFLVVIQAKMGSHMGLS 240
 DB 181 SYGSAKIVYVLDGLPFFSVDPOTGVRTAIPMMDETOEFLVVIQAKMGSHMGLS 240
 QY 241 GSTTIVTILSDVNDNPKFPQSLQFVSVERTAGETLVGRADDPDLGNALMAVSLD 300
 DB 241 GSTTIVTILSDVNDNPKFPQSLQFVSVERTAGETLVGRADDPDLGNALMAVSLD 300
 QY 301 GEGSARFISITDLQGRDGLITVRKLPDESORSISFRFEATNTLIDPAYLRGPFKVAS 360
 DB 301 GEGSARFISITDLQGRDGLITVRKLPDESORSISFRFEATNTLIDPAYLRGPFKVAS 360
 QY 361 VRVAQDAPEPPAFQAAYHLTVPENKAPGTLVQGISADADSPASPRYSIILHSPER 420
 DB 361 VRVAQDAPEPPAFQAAYHLTVPENKAPGTLVQGISADADSPASPRYSIILHSPER 420
 QY 421 CFSIQPEEGTHTAAPLDRERAMNLTVALTEL----- 454
 DB 421 CFSIQPEEGTHTAAPLDRERAMNLTVALTEL----- 454
 QY 481 RSPVSAAGVIGPQDSASQASRVQVAIQTDENDNAPQALPEPDTFVCSAAFGQILQYIRA 540
 DB 481 RSPVSAAGVIGPQDSASQASRVQVAIQTDENDNAPQALPEPDTFVCSAAFGQILQYIRA 540
 QY 545 -----DSSAQSRVQVAIQTDENDNAPQALPEPDTFVCSAAFGQILQYIRA 502
 DB 545 -----DSSAQSRVQVAIQTDENDNAPQALPEPDTFVCSAAFGQILQYIRA 502
 QY 541 LDRDEVGNSSHVSGFQPLGPDPANFTVQDNRD-----LPA-----WF 576
 DB 541 LDRDEVGNSSHVSGFQPLGPDPANFTVQDNRD-----LPA-----WF 576
 QY 503 LDRDEVGNSSHVSGFQPLGPDPANFTVQDNRDGASALLPSRPAPPRHAPLVLPTELDWG 562
 DB 503 LDRDEVGNSSHVSGFQPLGPDPANFTVQDNRDGASALLPSRPAPPRHAPLVLPTELDWG 562
 QY 577 HPLMASASASWHL-----WPPARNGNPAGSG 603
 DB 577 HPLMASASASWHL-----WPPARNGNPAGSG 603

DB 563 GPALSTATVTVSVCRCPPDGSVASCWPEAHLSAAGLSYG 602

RESULT 15

ID ADB99722 standard; protein, 781 AA.

ADB99722;

04-DEC-2003 (first entry)

Human PRO polypeptide SEQ ID 98.

Human; PRO; secreted polypeptide; transmembrane polypeptide;

tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;

adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;

microvascular endothelial cell; endothelial cell tube formation;

sports-related joint problem; articular cartilage defect; osteoarthritis;

rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.

Homo sapiens.

US2003082728-A1.

01-MAY-2003.

16-SEP-2002; 2002US-00245185.

07-JUL-1998; 98US-0091878P.

02-JUN-1999; 99MO-US012252.

25-AUG-1999; 99US-00380137.

29-AUG-2001; 2001MO-US027099.

18-JUL-2002; 2002US-00197942.

(GENTH) GENENTECH INC.

Baker KP, Eaton DL, Filvaroff E, Grimaldi JC;

Gurney AL, Smith V, Stephan JP, Maranabe CK, Wood WI, Zhang Z;

Fong S;

WPI; 2003-743898/70.

N-PSDB; ADB99721.

New isolated, secreted and transmembrane PRO polypeptides and nucleic

acids, useful for diagnosing, preventing and/or treating tumors, such as

lung, colon, breast, prostate, rectal, kidney or liver tumors.

claim 11; Fig 98; 308pp; English.

The invention relates to isolated human PRO polypeptides (secreted and

transmembrane polypeptides) and the polynucleotides encoding them. The

invention also relates to an antibody which specifically binds to a PRO

polypeptide, a method for stimulating the release of tumour necrosis

factor-alpha (TNF-alpha) from human blood, a method for stimulating the

proliferation or differentiation of chondrocyte cells and a method for

detecting the presence of a tumour in a mammal (e.g. adrenal, lung,

colon, breast, prostate, rectal, cervical and liver tumours). The

polynucleotides are useful in molecular biology, including uses as

hybridisation probes, in chromosome and gene mapping, in generating

antisense RNA and DNA and in gene therapy. The polynucleotides may also

be used in preparing PRO polypeptides by recombinant techniques and in

generating either transgenic animals or knock-out animals which are

useful in the development and screening of therapeutically useful

reagents. The PRO polypeptides or antibodies are used in preparing a

medicament for treating a condition responsive to the polypeptides or

antibodies, such as tumours, for stimulating and inhibiting proliferation

of human microvascular endothelial cells, for inducing endothelial cell

tube formation and for treating sports-related joint problems, articular

cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence

represents a human PRO polypeptide of the invention.

Sequence 781 AA:

Query Match 81.9%; Score 2746.5; DB 7; Length 781;
 Best Local Similarity 84.8%; Pred. No. 1.8e-221;
 Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

```

QY      1 MMGLVRLILLAMLGWGCCKGRLAAPARAWAGSREHPGALLRTRRSWTWNOFFVIEEYAGP 60
DB      1 MMGLVRLILLAMLGWGCCKGRLAAPARAWAGSREHPGALLRTRRSWTWNOFFVIEEYAGP 60
QY      61 EPLVIGKLHSDVDRGEGRTKYLITGEGAGTVFVIDEATGNHVTKSLDREKAKQYVLLAQ 120
DB      61 EPLVIGKLHSDVDRGEGRTKYLITGEGAGTVFVIDEATGNHVTKSLDREKAKQYVLLAQ 120
QY      121 AVDRASNPLEPPESEFIITKQDINDNPFIPLGPHATVPMSNVGTSVIQVTAHDADDP 180
DB      121 AVDRASNPLEPPESEFIITKQDINDNPFIPLGPHATVPMSNVGTSVIQVTAHDADDP 180
QY      181 SYGNSAKLYTVTLGDLPEFSYDPOTGVVRTAIPMDRETOEELVVIQAKDMGSHGGLS 240
DB      181 SYGNSAKLYTVTLGDLPEFSYDPOTGVVRTAIPMDRETOEELVVIQAKDMGSHGGLS 240
QY      241 GSTVTVTTLSDVNDNPPKFPQSLYQFSVETAGPGLVGRRAQDPDLGNALMAYSILD 300
DB      241 GSTVTVTTLSDVNDNPPKFPQSLYQFSVETAGPGLVGRRAQDPDLGNALMAYSILD 300
QY      301 GEGSEAFSISTDLQGRGLTVRRKPLDPESGRSYFVEATNTLIDPAYLRGPFKDYAS 360
DB      301 GEGSEAFSISTDLQGRGLTVRRKPLDPESGRSYFVEATNTLIDPAYLRGPFKDYAS 360
QY      361 VRVAVODAPBPAPFTQAAVHLTVPENKAPGTLVQGISADLDSFASPIRYSILPHSDPER 420
DB      361 VRVAVODAPBPAPFTQAAVHLTVPENKAPGTLVQGISADLDSFASPIRYSILPHSDPER 420
QY      421 CFSIQPEEGTHTTAAPLDREKARAWHNTLVLTETELGMSGPEPGWPLLVAMNSAPAAPQ 480
DB      421 CFSIQPEEGTHTTAAPLDREKARAWHNTLVLTETELGMSGPEPGWPLLVAMNSAPAAPQ 480
QY      481 RSPVGSAAVGIPODSSAQSRVQVAIQTLIDENDNAPQLABPYDFVCDSAPGQLIOYIRA 540
DB      481 RSPVGSAAVGIPODSSAQSRVQVAIQTLIDENDNAPQLABPYDFVCDSAPGQLIOYIRA 540
QY      541 LDRDEVGNSSHVSFQGPLGPDANFTVQDNRD-----LPA-----WP 576
DB      541 LDRDEVGNSSHVSFQGPLGPDANFTVQDNRD-----LPA-----WP 576
QY      577 HPLMASASSWLH-----WPPAERGNGQPASOG 603
DB      577 HPLMASASSWLH-----WPPAERGNGQPASOG 603
QY      603 QPALSTRTVTTSVCRQPDGSAVSCWPEZAHLSAAGLSTG 602
DB      603 QPALSTRTVTTSVCRQPDGSAVSCWPEZAHLSAAGLSTG 602

```

Search completed: December 8, 2004, 10:13:02
 Job time : 266.185 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 51.4357 Seconds

(without alignments)
1189.717 Million cell updates/sec

Title: US-09-788-051-4

Perfect score: 3354
Sequence: 1 MWGLVRLLLMLGSGMGCMGR.....LPSCQLPLGIPALGIVLCAS 636

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1602	47.8	796	2	A38992
2	1596	47.6	796	2	A53584
3	1593	47.5	796	2	148277
4	1593	47.5	796	2	149556
5	1529.5	45.6	793	2	D38992
6	1442	43.0	789	2	152701
7	1441	43.0	790	2	137016
8	1432.5	42.7	785	2	150180
9	1412.5	42.1	790	2	G02678
10	1400	41.7	790	2	150178
11	1389.5	41.4	790	2	151638
12	1368.5	40.8	794	2	159372
13	940.5	28.0	784	1	IUHU5C
14	604	18.0	913	1	IUCHCR
15	601	17.9	906	1	IUMSCN
16	594.5	17.7	906	1	IUXUC2
17	594	17.7	906	1	IUCHCN
18	592	17.7	877	1	IUBOCN
19	591	17.6	912	1	IUCHCN
20	589	17.6	913	1	A47543
21	586	17.5	887	1	IUCHCL
22	581	17.3	882	1	IUTUCE
23	581	17.3	905	1	IUXUC1
24	574.5	17.1	712	1	IUMSCT
25	574.5	17.1	717	2	I51206
26	567	16.9	916	2	B38992
27	563.5	16.8	713	2	B38992
28	552.5	16.5	814	2	G02878
29	535	16.0	2809	2	T30213

30	531	15.8	732	1	IUCHCB
31	531	15.8	783	2	I50116
32	524	15.6	884	1	IUMSCE
33	523.5	15.6	896	2	I45858
34	521	15.5	884	2	S34438
35	519	15.5	871	2	S47518
36	512	15.3	3034	2	T14119
37	510.5	15.2	826	2	B55363
38	510.5	15.2	896	2	A55363
39	507	15.1	730	1	IUMSCM
40	502.5	15.0	822	1	IUMSCP
41	502	15.0	829	1	IUTUCP
42	486	14.8	3097	2	T00021
43	481	14.6	840	2	I37281
44	491	14.6	894	2	I37282
45	487	14.5	770	2	B48910

ALIGNMENTS

RESULT 1					
A38992					
cadherin 11 precursor - human					
N/Alternate names: OB-cadherin, osteoblast					
C/Species: Homo sapiens (man)					
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 03-Jul-2004					
C/Accession: A38992					
R/Suzuki, S.; Sano, K.; Tanihara, H.					
Cell Regul. 2, 261-270, 1991					
A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous					
A/Reference number: S24305; NUID:91283540; PMID:2059658					
A/Accession: A38992					
A/Status: Preliminary; translated from GB/EMBL/DBJ					
A/Molecule type: mRNA					
A/Residues: 1-796 <SUZ>					
A/Cross-references: UNIPROT:P55287; GB:L34056; NID:9506403; PIDN:AAA5622.1; PID:950640					
C/Genetics:					
A/Gene: GDB:CDH11; OB					
A/Cross-references: GDB:512891; OMIM:600023					
A/Map position: 16q22.1-16q22.1					
C/Superfamily: cadherin repeat homology					
C/Keywords: calcium binding; cell adhesion; duplication					
F/56-159/Domain: cadherin repeat homology <CR1>					
F/162-268/Domain: cadherin repeat homology <CR2>					
F/271-383/Domain: cadherin repeat homology <CR3>					
F/386-488/Domain: cadherin repeat homology <CR4>					
Query Match					
Best Local Similarity 47.8%; Score 1602; DB 2; Length 796;					
Matches 323; Conservative 98; Mismatches 134; Indels 86; Gaps 10;					
QY	17	CMGRLA-----APAR-----AMAGSRE--HGGPALRFRBSWMNQFVIEYAGPEVY	63		
DB	13	CLMLCHSNAFAFERGHLRPFHGHGHEKQCVLQSKRGVMWQFVIEBYTPDHY	72		
QY	64	LICKLHSDVDGSEGRKRYLTLTGAGTGVVIDEATGNHVTKSLDREKAQVYLLAQAVD	123		
DB	73	LVRLLHSDIDSGDGNIKYILSGGAGTILFVIDRKSNGIHATKILDRBBAQYLLMAQAVD	132		
QY	124	RASNRPLEPSPSEITINGODINDNPRIFPLGPRYAATPEMSNVGTSTVIOVTAHADDPSTG	183		
DB	133	RDNRPLPEPSEITIVAVQDINDNPPFLHETTYANVPESSNVGTSTVIOVTAHADDPSTG	192		
QY	184	NSAKLVYTVVDGLPFFSVDPQGTGVATAPNMDRETQEEFLVYIQAQMGHNGSLSGST	243		
DB	193	NSAKLVYSILLEGPIYSVEAQGTIIRTPALPNDRKAKEHYHVYIQAQMGHNGSLSGST	252		
QY	244	TVTVTLSDVNDNPPKPPQSIYQFSVETAGPGTLVGRLAQDPDLGDNALMAYSIIDSGG	303		
DB	253	KVITITLVNDNPPKPPQRIYQMSVSEAAVPGEEVGRVAKQDDIGENGLVYTNIVDQGG	312		
QY	304	SEAFSTLTDQGDGLITVKKPLDPFSQRSYSPREVAATNTLIDPAVLRGPFQVAVSVH	363		

```
Db      313 MESFETITDYTOEGLVILKKPVPDEFERAVSLKVEANVHIDPKFISNGEPKOTVTKI 372
Qy      364 AVQADPEPPAFTQAAVHLTVPENKAPGLVQGISAADLSPASPIRISILPHSPERCF 423
Db      373 SVEDEBPMTLASIYHEVOENAAAGVGRVAKPDPDANSPIRISIDRHDLDFIT 432
Qy      424 IQPEGIHTAAPLDREARAHNLTVLATELGWGWGPERGVVPLVEMSAAPAPQSRSP 483
Db      423 INPEDGFITKTKPLDRETAWLNTVFAAEI-----463
Qy      484 VGSAGVIFQDSSAASRQVAILQTLDENDNAFQALPEYDTFVCS-----AARQOLQIVR 539
Db      464 -----NHRHQAQVPAIRVLVDVNDAPKFAAYPEGICEDQTKPLSNQPIVTIS 514
Qy      540 ALDRDEVGNSSHVSFGCP--LGPDAFTVQDNRLPA-----WPHPLM 581
Db      545 ADDQDDTANGPRFFISLPEIINHNTVDRNRNTAGVYARRGFSRQKODLYLPIVI 574
Qy      582 ASASGWLHWPAAERGNQAPAGCKSSLP-CG-RLPGLPSC 620
Db      575 -----SDGIPMSSTNTLITKVCQGVNGALLSC 604
```

RESULT 2

```
A53584
OB-cadherin precursor - mouse
C.Species: Mus musculus (house mouse)
C.Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C.Accession: A53584
R.Okazaki, M.; Takeshita, S.; Kawai, S.; Kikuno, R.; Tsujimura, A.; Kudo, A.; Amano, E.
J. Biol. Chem. 269, 12092-12098, 1994
A.Title: Molecular cloning and characterization of OB-cadherin, a new member of cadherin
A.Reference number: A53584; MUID:94216322; PMID:8163513
A.Accession: A53584
A.Residues: 1-796 <OKA>
A.Status: preliminary
A.Molecule type: mRNA
A.Cross-references: UNIPROT:P55288; GB:D21253; NID:g994774; PID:BA04797.1; PID:g994775
A.CSuperfamily: cadherin, cadherin repeat homology
C.Keywords: transmembrane protein
F156-159/Domain: cadherin repeat homology <CR1>
F162-268/Domain: cadherin repeat homology <CR2>
F186-488/Domain: cadherin repeat homology <CR4>
```

Query Match 47.6%; Score 1596; DB 2; Length 796;

Best Local Similarity 50.7%; Pred. No. 2.7e-98;

Matches 317; Conservative 97; Mismatches 127; Indels 84; Gaps 8;

```
Qy      31 SREHP-----GPALLRTRSRWVWNOFVIEEYAGPEPVLIGKLSHDVDRGERT 79
Db      29 SHLHPSFGHHEKKEGQVLRSKRGWVWNOFVIEEYTGDPVLVGRLHSDIDSGDNI 88
Qy      80 KYLLTGEGAGTVFVIDATGNIHVTKSLDREKAQVYLLAQAVDRASNRPLEPSEFIIK 139
Db      89 KYLLSGEGAGTIFVIDKSGNIHATKTLDRERAAQYLLMAQAVDRNTNRPLEPSEFIVK 148
Qy      140 GQDINDNPPIPLPGPHATVPEKSNVGTSVIQTAAHDADPSSYGNASKLYVTYVLDGLPF 199
Db      149 VQDINDNPPEFLHETIYANVPERSNVGTSVIQTASADDPPTYGNASKLYVSLIEQPIF 208
Qy      200 SYDPQTGVATPAINMRETOEELVVIQAKMGKNGSGSTTVTVLSDVNDNPPKF 259
Db      209 SVEAQGTGIRTAIPNMREAKEEHVVIQAKMGKNGSGSTTVTVLSDVNDNPPKF 268
Qy      260 POSLYQSVSVETAGPTLVGRRAQDPDLGDNALMAVSIIDGEGSEAFISTDLQGRDL 319
Db      269 POSLYQSVSVETAGPTLVGRRAQDPDLGDNALMAVSIIDGEGSEAFISTDLQGRDL 319
Qy      320 LTVKRPDLDFESQSYRVEATNTLIDPAVLRGPFKDVASVAVQADPEPPAFTQAAV 379
Db      329 VKLKPVDPEFKRAVSLKIEANVHIDPKFISNGEPKOTVTKISVEDADEPMTLASPY 388
```

```
Qy      380 HLTVPENKAPGLVQGISAADLSPASPIRISILPHSPERCFISIOPEEGTHTAAPLDR 439
Db      389 IHEVOENAAAGTVGRVAKPDPDANSPIRISIDRHDLDFITINPEDGFIKTKPLDR 448
Qy      440 EAAAHNLTVLATELGWGWGPERGVVPLVEMSAAPAPQSRSPVGSAGVIFQDSSAAS 499
Db      449 EETAMLNLSVFAAEI-----NHRHQA 470
Qy      500 RQVAVIQTLDENDNAFQALPEYDTFVCSAAP-----GQLQIVRALDRDEVGNSSHVSFQ 555
Db      471 KVPVAVIRVLVDVNDAPKFAAYPEGICEDHPKALSNQPIYTVASADQDDTANGPRFFIS 530
Qy      556 GP--LGPDAFTVQDNRLPA-----WPHPLMASASSWLHWPAAERGN 597
Db      531 LPPEIHNHNPFTVRNRNTAGVYARRGFSRQKODLYLPIVI-----SDGII 579
Qy      598 OPASQCKSSLP-CG-RLPGLPSC 620
Db      580 PMSSTNTLITKVCQGVNGALLSC 604
```

RESULT 3

148277

cadherin-11 - mouse

C.Species: Mus musculus (house mouse)

C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C.Accession: 148277

R.Hoffmann, I.; Balling, R.

Dev. Biol. 169, 337-346, 1995

A.Title: Cloning and expression analysis of a novel mesodermally expressed cadherin.

A.Reference number: 148277; MUID:95269866; PMID:7750649

A.Accession: 148277

A.Status: preliminary; translated from GB/EMBL/DDBJ

A.Molecule type: mRNA

A.Residues: 1-796 <RES>

A.Cross-references: UNIPROT:P55288; EMBL:X77557; NID:6442796; PID:CAA54674.1; PID:g666666

A.CSuperfamily: cadherin, cadherin repeat homology

F156-159/Domain: cadherin repeat homology <CDH>

Query Match 47.5%; Score 1593; DB 2; Length 796;

Best Local Similarity 50.6%; Pred. No. 4.3e-98;

Matches 316; Conservative 98; Mismatches 127; Indels 84; Gaps 8;

```
Qy      31 SREHP-----GPALLRTRSRWVWNOFVIEEYAGPEPVLIGKLSHDVDRGERT 79
Db      29 SHLHPSFGHHEKKEGQVLRSKRGWVWNOFVIEEYTGDPVLVGRLHSDIDSGDNI 88
Qy      80 KYLLTGEGAGTVFVIDATGNIHVTKSLDREKAQVYLLAQAVDRASNRPLEPSEFIIK 139
Db      89 KYLLSGEGAGTIFVIDKSGNIHATKTLDRERAAQYLLMAQAVDRNTNRPLEPSEFIVK 148
Qy      140 GQDINDNPPIPLPGPHATVPEKSNVGTSVIQTAAHDADPSSYGNASKLYVTYVLDGLPF 199
Db      149 VQDINDNPPEFLHETIYANVPERSNVGTSVIQTASADDPPTYGNASKLYVSLIEQPIF 208
Qy      200 SYDPQTGVATPAINMRETOEELVVIQAKMGKNGSGSTTVTVLSDVNDNPPKF 259
Db      209 SVEAQGTGIRTAIPNMREAKEEHVVIQAKMGKNGSGSTTVTVLSDVNDNPPKF 268
Qy      260 POSLYQSVSVETAGPTLVGRRAQDPDLGDNALMAVSIIDGEGSEAFISTDLQGRDL 319
Db      269 POSLYQSVSVETAGPTLVGRRAQDPDLGDNALMAVSIIDGEGSEAFISTDLQGRDL 319
Qy      320 LTVKRPDLDFESQSYRVEATNTLIDPAVLRGPFKDVASVAVQADPEPPAFTQAAV 379
Db      329 VKLKPVDPEFKRAVSLKIEANVHIDPKFISNGEPKOTVTKISVEDADEPMTLASPY 388
Qy      380 HLTVPENKAPGLVQGISAADLSPASPIRISILPHSPERCFISIOPEEGTHTAAPLDR 439
Db      389 IHEVOENAAAGTVGRVAKPDPDANSPIRISIDRHDLDFITINPEDGFIKTKPLDR 448
```

QY 440 EAAKMHNLTVLATELGMWKGPERGVPLVLAEMSAAPAPQORSPVGSAGVCIPODSSAQAS 499
DB 449 EETAMNLISVFAADI-----HNRHQT 470
QY 500 RVQVAIQTLDENDNAPOLAEPYDTFVCDASAP-----GQLIQVIRALDRDEVGNSHVSFQ 555
DB 471 KVPVAILVDVNDNAPKFAAPYEGFICESHPKALSNQPIVTVASADDDOTDANGPRIFIS 530
QY 556 GP--LGPDAFVTVDNRLPA-----WFHPLMASASSWLHMPAERGN 597
DB 531 LPEIMNPNFTVNDNNTAGVYARRGGSROKQDFLPLFIVL-----SDGGI 579
QY 598 QPASQKSSSLP-CG-RUPGALPSC 620
DB 580 PPMSTNTLITIKVCGCDVNGALLSC 604

RESULT 4

149556
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 149556
R/Kimura, Y.; Matsunami, H.; Inoue, T.; Shimamura, K.; Uchida, N.; Ueno, T.; Miyazaki, T.
Dev. Biol. 169, 347-358, 1995
A:Title: Cadherin-11 expressed in association with mesenchymal morphogenesis in the head
A:Reference number: 149556; MUID:95269887; PMID:7750650
A:Accession: 149556
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-796 <RES>
A:Cross-references: UNIPROT:P55288; GB:D31963; NID:G974190; PIDN:BA06730.1; PID:G974191
F:56-159/Domain: cadherin repeat homology <CDH>

Query Match 47.5%; Score 1593; DB 2; Length 796;
Best Local Similarity 50.6%; Pred. No. 4.3e-98;
Matches 317; Conservative 95; Mismatches 128; Indels 86; Gaps 8;

QY 31 SREHP-----GPALTRRSWYWNQFYIEEYAGPEPVILGKLSHDVDRGEGRT 79
DB 29 SHLPSPFHGHHEKKEGVQLGSKRGWYNQFYIEETGPDVTVGRILHSDISGQNT 88
QY 80 KYLLTSGAGTVFYIDEATGNIHTKSLDREKAQVYLLAQAVDRASNRPLEPSEFTIK 139
DB 89 KYILSGEGAGTIFVIDKSGNIIHATKTLDRERAOYTLMAQAVDRDTRPLEPSEFTIVK 148
QY 140 GODINDNPPILPGYHATVPEMSNVGTVQVTAHADDPSSYNSAKLVYTVVDGAPFF 199
DB 149 VQDINDNPEPLHETVHANVPERKSNVGTIVQVNASDADDPYNSAKLVYTVVDGAPFF 208
QY 200 SVDPQTVVTRTALPMDRETOEPLVTVIQAQDMGSHGSLGSTTVTVTLSDVNDNPKF 259
DB 209 SVEAQGTIIRTAIPMDREAKEEYHVTVQAQDMGSHGSLGSTTKVITLTDVNDNPKF 268
QY 260 POSLYQSFVETAGGTIVGRILRAODPRLGDNALMAYSLIDGEGSEAFSTIDQGRDL 319
DB 269 POSVQWQVSEAAVGEVGRVAKCPDIGENGLTVYIVDGLIELEITTDYETDGV 328
QY 320 LTVKPLDPESQSYSPFVEATNTLIDPAYLRGPFKDVASVRAVQDAPPEPAFTQAY 379
DB 329 VTKKPVDFETKRASTLKEAANVAIDPKFISNGFKOTVTVKISVEDADEPPEFLPSY 388
QY 380 HLTVPENKAPGLVQCIQAADLDSPASPIRYSILPHSPERCFSIQPEEGTITHTAAPLR 439
DB 389 IHEVQENAAAGTVVGRVAKCPDANSPIRYSIDHTLDRFFITNPEDGFIKTKPDR 448
QY 440 EAAKMHNLTVLATELGMWKGPERGVPLVLAEMSAAPAPQORSPVGSAGVCIPODSSAQAS 499
DB 449 EETAMNLISVFAADI-----HNRHQT 470
QY 500 RVQVAIQTLDENDNAPOLAEPYDTFVCDASAP-----GQLIQVIRALDRDEVGNSHVSFQ 555

DB 471 KVPVAILVDVNDNAPKFAAPYEGFICESHPKALSNQPIVTVASADDDOTDANGPRIFIS 530
QY 556 GP--LGPDAFVTVDNRLPA-----WFHPLMASASSWLHMPAERGN 597
DB 531 LPEIMNPNFTVNDNNTAGVYARRGGSROKQDFLPLFIVL-----SDGGI 579
QY 598 QPASQKSSSLP-CG-RUPGALPSC 620
DB 579 PPMSTNTLITIKVCGCDVNGALLSC 604

RESULT 5

D38992
C:Species: Homo sapiens (man)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
C/Accession: D38992
R/Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous
A:Reference number: S24305; MUID:91283540; PMID:2059658
A:Accession: D38992
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-793 <SUZ>
A:Cross-references: GB:L34060; NID:G506411; PIDN:AAA35628.1; PID:G506412
A:Gene: GDB:CDH8
A:Gene: GDB:CDH8
A:Cross-references: GDB:5822911
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication
F:163-269/Domain: cadherin repeat homology <CDH>

Query Match 45.6%; Score 1529.5; DB 2; Length 793;
Best Local Similarity 47.8%; Pred. No. 7.2e-94;
Matches 299; Conservative 111; Mismatches 135; Indels 81; Gaps 9;

QY 39 LLETRRSWYWNQFYIEEYAGPEPVILGKLSHDVDRGEGRTYLLTGBAGTVFYIDEAT 98
DB 49 LNSKRGWYWNQFYIEEYAGPEPVILGKLSHDVDRGEGRTYLLTGBAGTVFYIDEAT 108
QY 99 GNHVTKSLDREKAQVYLLAQAVDRASNRPLEPSEFTIKGODINDNPPILPGYHAT 158
DB 109 GDHAKRLDRERKAETTLTAQVDMETSKPLEPSEFTIKQDINDNAPFLNGLVYAT 168
QY 159 VPMSNVGTVQVTAHADDPSSYNSAKLVYTVVDGLPFESVDQTVVTRTALPMDRE 218
DB 169 VPMSILGTSYNTVATDADDPYNSAKLVYTVVDGLPFESVDQTVVTRTALPMDRE 228
QY 219 TOEEFVTVQAQDMGSHGSLGSTTVTVTLSDVNDNPKFPOSIXQSFVETAGGTIV 278
DB 229 AKEEYLVTVQAQDMGSHGSLGSTTVTVTLSDVNDNPKFPOSIXQSFVETAGGTIV 288
QY 279 GRLEADPDLGDNALMAYSLIDGEGSEAFSTIDQGRDLTVKPLDPESQSYSPFV 338
DB 289 GRKANDQDQIGENAGSYTIDDDGTALFEISDAQAQGIIRLRKPLDFETKSYTLKD 348
QY 339 EANTTILIDPAYLRGPFKDVASVRAVQDAPPEPAFTQAYLTVPENKAPGLVQCIQA 398
DB 349 EAAVHIDIRFSRGPFKDVATVTVVEADDPVFSSTYVLEHENAALNSVIGQVTA 408
QY 399 ADLDSPASPIRYSILPHSPERCFSIQPEEGTITHTAAPREARAHNLTVLATELGMW 458
DB 409 RQDDITSSPIRFSIDHTLDRQFNINADGKITLATPLDRSLSVWHNTITLATEL----- 464
QY 459 GPERGVPLVLAEMSAAPAPQORSPVGSAGVCIPODSSAQASQVQAIVQLDENDNAPOLA 518
DB 465 -----RNHSGISRPVPAIKVLDVNDNAPFA 490
QY 519 EPYDTFVCDASAPGQLIQVIRALDRDEVGNSHVSFQGLPDP-----ANFTVQDND 571
DB 491 SEYEAFLCENKGGQVITQVNASMDKDPKNGH--FLYGLLEBMVNNRPFTIKKEDNLS 548

QY 572 -----LPAWHPLMASASWLMHPPA-----ENQCPASGCKSSSL-PCG-RALPGA 616
 Db 549 SILAKHNGFNROKOEYVLLPILIT-----SDSGNPLSTSTLTTRVCGCNDGV 597
 QY 617 LPSCQ-----LPLGI---PALGIYLC 634
 Db 598 VQSCVNEAYVLPILGSMGALLIALLAC 623

RESULT 6

152701
 K-cadherin - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C/Accession: 152701
 R.Xing, Y.Y.; Tanaka, M.; Suzuki, M.; Teraishi, H.; Kiyokawa, E.; Naito, Y.; Ohtawara, Cancer Res. 54, 3034-3041, 1994
 A/Title: Isolation of complementary DNA encoding K-cadherin, a novel rat cadherin prefer A/Reference number: 152701; MUID:94243827; PMID:8187093
 A/Accession: 152701
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-769 <RES>
 A/Cross-References: UNIPROT:P55280; GB:D25290; NID:9435460; PIDN:BA04975.1; PID:9435461
 C/Genetics:
 A/Gene: KCAD
 C/Superfamily: cadherin; cadherin repeat homology
 F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 43.0%; Score 1442; DB 2; Length 789;
 Best Local Similarity 43.7%; Pred. No. 4.8e-88;
 Matches 298; Conservative 118; Mismatches 160; Indels 106; Gaps 10;
 7 LLLMLG-----GWGCMGRLLAARAPAW---AGREHGPALLTRRSWV 48
 Db 8 LLLFWGQPYPTSPNPLSKRTSGP-----PAKRRLLELSANRNE---LSKSKSWM 57
 QY 49 NQFVIEEYAGPEVLLIGKLSHDVDRGEGRTKYLITGEAGTVFVIDEATGNITHTKSLD 108
 Db 58 NQFELIEYGSDDQYQYKLSHDODRGDSLKYLITSGDAGDLFIINENGDIOATRLDD 117
 QY 109 REEAQYVLLAQAADRAASNRPLPEPSEFIITKODINDNPIPLGPHATVPEMSVGS 168
 Db 118 REEPVYILRAQAATNRGRVPEPSEFIITKIDINDNEPIFKDYATATVPEMAVGF 177
 QY 169 VIQTADADDPYSYNSAKLVYTVLDGLPFFSVDPQTGVVTAIPMDRETOEFLVVIQ 228
 Db 178 VVQVATDADDPYTGNSAKLVYVILQGPYFVSSESGIITKALLMDRENREGQYVVIQ 237
 QY 229 AKMGGMGLSGSTTVTLSDVNDNPKFPOSILQFVSVEETAGTGLVGRRAODPDL 268
 Db 238 AKMGGMGLSGSTTVTLSDVNDNPKFPOSILQFVSVEETAGTGLVGRRAODPDL 297
 QY 289 GDNALMAYSLIDGSEAFSISTDLQGRDGLTVRKPLDSESQSYSFYEATNTLIDPA 348
 Db 298 GDNALMAYSLIDGSEAFSISTDLQGRDGLTVRKPLDSESQSYSFYEATNTLIDPA 357
 QY 349 YLRGPRKDVASVAVQADPEPPAFTQAAYHLTVENKAPGTLVQGISADLDSASFI 408
 Db 358 FLVGPBKDSATVAVIVDDVDEPPVSKPAYIILQIEDAQINTTISVAQDPDAARNV 417
 QY 409 RYSLIPHSDEPERCSIOPEEGTHTAAPLDREARAHNLTVALTELGMGSEBERGVPL 468
 Db 418 KYVDRTMDRIFFNIDSGSGSIFTKLDRITLHMNTIVATTEL----- 463
 QY 469 VAKMSAPAPPPQSPVGSAGVIGIQQSSAQASRQVAIQTLDENDNAPQLAEPYDTFVCS 528
 Db 464 -----NNPKSSRPVLYIKVLVDVNDNAPFAEFETVCEK 499
 QY 529 AAFGQILQVTRALDRBEVGNSSVSPGPIGPDA-----NFTVQDND 571
 Db 500 AKXDQILQITLHAVDKDDPYSGHQSFS--LAPPAAGSNFTIIONDKONTAGILTRKNGYN 557

QY 572 ---LPAWHPLMASASWLMHPPA-----ENQCPASGCKSSSL-PCGRLP 614
 Db 558 RHEMSTYLLPVLISND-----YVQSSGTIVTVYACDHHGNQSCHAEBALIHPTGLST 613
 QY 615 GALPSCQLPLGIYALGIYLCAS 636
 Db 614 GALVAILCLCTIVLTVVLEFPA 635

RESULT 7

137016
 cadherin-6 - human
 C/Species: Homo sapiens (man)
 C/Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
 C/Accession: 137016
 R.Shimoyama, Y.; Gotch, M.; Terasaki, T.; Kitajima, M.; Hirohashi, S. Cancer Res. 55, 2206-2211, 1995
 A/Title: Isolation and sequence analysis of human cadherin-6 complementary DNA for the A/Reference number: 137016; MUID:95262134; PMID:7743525
 A/Accession: 137016
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-790 <RES>
 A/Cross-References: UNIPROT:P55285; GB:D31784; NID:974184; PIDN:BA06562.1; PID:974185
 C/Genetics:
 A/Gene: GDB:CDH6
 A/Cross-References: GDB:5822908
 C/Superfamily: cadherin; cadherin repeat homology
 F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 43.0%; Score 1441; DB 2; Length 790;
 Best Local Similarity 43.3%; Pred. No. 5.6e-88;
 Matches 294; Conservative 124; Mismatches 161; Indels 100; Gaps 9;
 7 LLLMLG-----GWGCMGRLLAARAPAW---AGREHGPALLTRRSWVNOF 51
 Db 8 LLLFWGQPYPTLSTPSTKRTSGFPAPKR---ALELSGNSKN---ELNSKSKSWMNOF 60
 QY 52 FVIEEYAGPEVLLIGKLSHDVDRGEGRTKYLITGEAGTVFVIDEATGNITHTKSLDRE 111
 Db 61 FLIEEYGSDDQYQYKLSHDODRGDSLKYLITSGDAGDLFIINENGDIOATRLDRE 120
 QY 112 KAQVYLLAQAADRAASNRPLPEPSEFIITKODINDNPIPLGPHATVPEMSVGSVIO 171
 Db 121 KPVYILRAQAATNRGRVPEPSEFIITKIDINDNEPIFKDYATATVPEMSDVGTFVVO 180
 QY 172 VTADADDPYSYNSAKLVYTVLDGLPFFSVDPQTGVVTAIPMDRETOEFLVVIQAKD 231
 Db 181 VTATDADDPYTGNSAKLVYVILQGPYFVSSESGIITKALLMDRENREGQYVVIQAKD 240
 QY 232 MGHNGMGLSGSTTVTLSDVNDNPKFPOSILQFVSVEETAGTGLVGRRAODPDLGN 291
 Db 241 MGHNGMGLSGSTTVTLSDVNDNPKFPOSILQFVSVEETAGTGLVGRRAODPDLGN 300
 QY 292 ALMAYSLIDGSEAFSISTDLQGRDGLTVRKPLDSESQSYSFYEATNTLIDPAYLR 351
 Db 301 AEIYSLIDGSEAFSISTDLQGRDGLTVRKPLDSESQSYSFYEATNTLIDPAYLR 360
 QY 352 RGPEDVASVAVQADPEPPAFTQAAYHLTVENKAPGTLVQGISADLDSASPIRYS 411
 Db 361 LGPFKDSATVAVIVDDVDEPPVSKPAYIILQIEDAQINTTISVATQDDPAARNPVYS 420
 QY 412 ILHSPDERCSIOPEEGTHTAAPLDREARAHNLTVALTELGMGSEBERGVPLIVAE 471
 Db 421 VDRHTMDRIFFNIDSGSGSIFTKLDRITLHMNTIVATTEL----- 463
 QY 472 WSAFAPAPPPQSPVGSAGVIGIQQSSAQASRQVAIQTLDENDNAPQLAEPYDTFVCS 531
 Db 464 -----NNPKSSRPVLYIKVLVDVNDNAPFAEFETVCEK 502
 QY 532 GQILQVTRALDRBEVGNSSVSPGPIGPDA-----NFTVQDND 571
 Db 503 DQILQITLHAVDKDDPYSGHQSFS--LAPPAAGSNFTIIONDKONTAGILTRKNGYNRHE 560

Oy	572	LPAMFPHILMAASASSWILHPPA-----	ERGNOPASOGKSSLPCLRPGAL	617
Db	561	MSYLLPEVVISDDN----YFVOSTGTVTVRVCACDHGNGSCHEALIHPTLSGAL		616
Oy	618	PSCQLPGLPGALGIYTCAS		636
Db	617	VAILLCTVILLVTVLPFAA		635

RESULT 8

150180
cadherin-7 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: 150180
R:Nakagawa, S.; Takeichi, M.
Development 121, 1321-1332, 1995
A:Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-specific
A:Reference number: 150178; MUID:95309115; PMID:7540531
A:Accession: 150180
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-785 <NAK>
A:Cross-References: UNIPROT:Q90763; GB:DA2150; NID:9866000; PIDD:BAAO7721.1; PID:98680001
A:Superfamily: cadherin; cadherin repeat homology
A:156-262/Domain: cadherin repeat homology <CDH>

Query Match	42.7%;	Score 1432.5;	DB 2;	Length 785;
Best Local Similarity	44.8%;	Pred. No. 2e-87;		
Matches 299;	Conservative 170;	Mismatches 110;	Indels 89;	Gaps 10;

```

QY 4 VRLILLMLGGMGCMGRU--AAPARAMGSEHP--GALLARTRRSRWMOOFVLEEYAG 59
Db 11 LLOITIALFL---CLSGMNOAEPKR---SKRPYFOSGRRTTKSRWMOOFVLEEYMG 62
QY 60 PEPYLIGLHSDVDGRGERTKYLTLTGEGAGTVFVIDEATGNIHWTSLDREKAQYVLLA 119
Db 63 SDPLVGLKHLSDVDKGDGSKIYILISGEGASSIIFIIDENTGDIHMTKRLDREGQAYVTLRA 122
QY 120 QAVDRASNRPLPEPSEFIIKGODINDNPPIPLGPGYHAHTVPEKSNVGTSVIQTVAHADDD 179
Db 123 QAHRLTAKKPAVEPSEEFVIKIOTINDNPKFLDGGYTVAGVEMSPVGTSVQVATADDD 182
QY 180 PSYNSAALVYTVL DGLPEFVSVDPOTGVRATAPMDETOEELFVIVQAOKMGHMGGL 239
Db 183 PLYGASAVVSVSIILOGDPYFSVEPKTGIIKTALPMDDEAKDQYVLYVQAOKMGQNGGL 242
QY 240 SGTSTVTVTLSDVNDNPPKFPQSLYQFSVETAGBGLVGRLRADPDLDGNALMAYSIL 299
Db 243 SGTISVTVTLVDVNDNPPRPFRPSQYVNPESLPLASVVAIKKADADVGNAEMEKYLV 302
QY 300 DGESEAFSISTDLQGRDGLTVKRPDLPEBQSRYSFVEAINTLIDPAVYLRGQPFKQVA 359
Db 303 DGDGIGVFKIIVDKTOGEGITTIIOKELDFEAKTSYTLIRIEANMHWVDRPFLSGFSDMT 362
QY 360 SVRAVVOAPAPPRATQAAHLTVPENKAPGLVQGISAAALDPSAPSRISILPHSDE 419
Db 363 TVKIIIEVDDEPVPVTSRLYSVNVSEAAKVGIIITVAAHPDANSDSVRSIDRNTDLS 422
QY 420 RCFSIQPEEGTIIHTAAPLDREARAWHNLTVLATELGWGCBERGWVPLVIAEWSAPAAP 479
Db 423 RYFNINDANSGITTAKSILDRETNVHNITVLAME----- 456
QY 480 QRSFVGAAGVGIPODSSAQASRVQVAIQTLDERNDNAPQLAEPYDTVTCDSAAFGQILQYTR 539
Db 457 -----SOMFAQIGRGYVAITILBIDINDNAPEFAMEYTVVCENAPGQIIOKIS 504
QY 540 ALDRDEV--GNSSHSFGQPLCPDANFTVQDNEDLPA-----WEPFLM 581
Db 505 AIDKDDPENGQOPIYSLTAEMANHNFTLQDNKMDTAIVLIRNRGFRQBOGSVFLPLPFI 564
QY 582 ASASSWHLWMPAERGN-----QPASQGSKSSLPCCGLPGAL--BSCQLPL 624

```

Db 565 VDSGS-----PSLSSTNTLTIRVCCDDADGIACTCAAEYILPAGLSGALIALIACVTL 620
QY 625 GIPALGIV 632
Db 621 LVPLVLIV 628

RESULT 9

cadherin-14 - human
C.Species: Homo sapiens (man)
C.Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C.Accession: G02678
R.Shibata, T.; Shimoyama, Y.; Gotch, M.; Hirschashi, S.
Submitted to the EMBL Data Library, May 1996
A.Reference number: H01584
A.Accession: G02678
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-790 <SHR>
A.Cross-References: UNIPROT:Q13634, EMBL:U59325, NID:q1398952, PIDN:AA02933.1, PID:q13
A.Superfamily: cadherin, cadherin repeat homology
P162-268/Domain: cadherin repeat homology <CDH>

Query Match	42.1%;	Score 1412.5;	DB 2;	Length 790;
Best Local Similarity	45.9%;	Pred. No. 4.4e-86;		

```

QY 41 ATRSSWNNQFFVIEVNAPEPVLIGLHSDVDEGECKTLLGEGAGTPEVIDEAGN 100
Db 50 RPKGWNWQFFVIEEHMGDPQYVGGKLHSDSDKDGSKVILLGEGAGTFLIDDTGG 109
QY 101 IHVKSJLDEREKAQYVLLAQAVDRASNRELPPESEFIIKQODINDNPEIPLGPHYATVP 160
Db 110 IHSTSLDREQKTHVYLAQALDRTNKFLPESEFIIKQODINDNAKFDGPFYIVHP 169
QY 161 EMSNVGTSVIOVTADPADDPYGNLSAKLYVVLGCLPFPSYDPQGVRIAPMNDREBTO 220
Db 170 EMSNDGTSVIOVTATDADDPYGNLSARVYSILQGQPFSDPKGVRIATAHNDREAR 229
QY 221 EEFLVIOAKMGHMGGLSGSTVTVVLSVDNPNPKFPOSLYQFSVETAGPGLTVGR 280
Db 230 EHSYVIOAKMAGVGGLSGSTTVNITLTVNDNPPRPQKHVQLYVPESAKOVSAVAK 289
QY 281 LRAQDPDLGDNALMAYSTLDEGSEAPSIITDLQRODILLVXRKLDRESGRSYFRVEA 340
Db 290 IKADADTGSNADMTYSITINDGKGFISITDKETREBILBKPKPLNTEKKKSYTLNIBG 349
QY 341 TNLIDPAPYLRRGPEFKDVA SVRVAVQDAPPEPAFTQAAVYHLPVENKAPGLVGOISAD 400
Db 350 ANTHIDPFHSHLGPCKOATMKIITGVDDVEPLFSPMYLAEVYENAKIGTGVTVLAQD 409
QY 401 LDSPASPRYSILPHSDPERCFSTOPEBGTHHTAAPLIDREARAMNLVLTALGWSMGP 460
Db 410 PDSTNSJVRYSINYNVEDDRFENIDANTGTRITKYVLDREETPMNITVLTASEI----- 463
QY 461 ERGWVFLVAEWSAPAPRPORSPVGSNAVIGIPQDSSAQSARVOVALQITLDENDNAPOLAE 520
Db 464 -----DNPDLSHTVYGRIVDVNDNPELARE 491
QY 521 YDTFVDSAAEQULQVIRALDRDEVGNSSHVSF-----QGPLGPANFTVQDNRLPVA-- 574
Db 492 YDILVENSKEGQVHTHSATDKODFPAGPRPNFLDRLELPVNP--NTTLKNDENNTYSI 549
QY 575 -----WFHPLMASASWMLHWPDAERGNOPASQKSSS-----PCGRLLPG 615
Db 550 LTRRRFRSRTVQDYYVLYLIMTSD-----GGIP-SLSSSSTLIRVCACER-DG 595
QY 616 ALPSCQLPLGIPALG-----IYLC 634
Db 596 RVRTCHAEAFLLSSAGSLGALIAIILC 622

```

RESULT 10

150178
 C:Species: Gallus gallus (chicken)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
 C:Accession: 150178
 R:Nakagawa, S.; Takeichi, M.
 Development 121, 1321-1332, 1995
 A:Title: Neutral crest cell-cell adhesion controlled by sequential and subpopulation-spec
 A:Reference number: 150178; MUID:95309115; PMID:7540531
 A:Accession: 150178
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-790 <NKS>
 A:Cross-references: UNIPROT:Q90762; GB:D42149; NID:G9667998; PIDN:BA07720.1; PID:G9667998
 C:Superfamily: cadherin; cadherin repeat homology
 F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 41.7%; Score 1400; DB 2; Length 790;
 Best Local Similarity 49.0%; Pred. No. 36-85;
 Matches 263; Conservative 109; Mismatches 121; Indels 44; Gaps 3;

Qy	39	LLRRRSMWNNQFVIEEYVAGPEPVLLIGKLSVDVDRGEGRKTLTGEGAGTVFIDEAT	98
Db	48	LSRKRSMWNNQFVIEEYVAGPEPVLLIGKLSVDVDRGEGRKTLTGEGAGTVFIDEAT	107
Qy	99	GNIVHTSLDREKKAQVLLAQAVDRASNPLEPSEPFITKGGDINDNPIPLGPHAT	158
Db	108	GDIATKLDREKKAQVLLAQAVDRASNPLEPSEPFITKGGDINDNPIPLGPHAT	167
Qy	159	VPEKSNVTSVITQVTAHADDDPSYGSNAKLVYVLDGLPFSVPDQGVVRAIPMDRE	218
Db	168	IPKMSVDTGVVQVTAHADDDPSYGSNAKLVYVLDGLPFSVPDQGVVRAIPMDRE	227
Qy	219	TQEFLLVIAQKMGGMGLSGSTVTVTLSDVNDNPKPQSLQVSVFVAGGTLV	278
Db	228	NREYQVIVIAQKMGGMGLSGSTVTVTLSDVNDNPKPQSLQVSVFVAGGTLV	287
Qy	279	GRLEAOPDLDGNALMAYSILDEGESEAFSISTDLQGRDLTVRKPLDFESORSYSFV	338
Db	288	GRLEAOPDLDGNALMAYSILDEGESEAFSISTDLQGRDLTVRKPLDFESORSYSFV	347
Qy	339	EATVTLIDPAVLRGPKDVASVAVQDAPPEPAFQAAYHLTVENKAPGLVQIQA	398
Db	348	EATVTLIDPAVLRGPKDVASVAVQDAPPEPAFQAAYHLTVENKAPGLVQIQA	407
Qy	399	ADLSPASPIRYSILPHSDPERCSIQPEEGTHTAPLDRARAHNLTVLTELGMGM	458
Db	408	QDPDAKNPVYKSYDRTDMRVNINSNGSIFTEKTLDRFTLLMNTVIAEL	463
Qy	459	GPERGWVLLVAEKSAAPAPQSPVGSVAVGIPQSSAQAARVQVAIQTLIDENNA	518
Db	464	-----NNPKQSSRVPEFIKVLVDVNDNAPEFA	489
Qy	519	EPYDFVCDAAAPGQLIOVIRALDRDEVGNSHVSFGGLGPA-----NFTVQDN	571
Db	490	MEYDFVCDAAAPGQLIOVIRALDRDEVGNSHVSFGGLGPA-----NFTVQDN	544

RESULT 11
 151638
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C:Accession: 151638; S53591
 R:Espebeth, A.; Johnson, E.; Kintner, C.
 Mol. Cell. Neurosci. 6, 199-212, 1995
 A:Title: Xenopus F-cadherin, a novel member of the cadherin family of cell adhesion mole
 A:Reference number: 151638; MUID:96039533; PMID:7496667
 A:Accession: 151638
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA

A:Residues: 1-790 <ESP>
 A:Cross-references: UNIPROT:Q91838; EMBL:X85330; NID:G854634; PIDN:CAA59679.1; PID:G854634
 C:Superfamily: cadherin; cadherin repeat homology
 F:161-267/Domain: cadherin repeat homology <CR2>

Query Match 41.4%; Score 1389.5; DB 2; Length 790;
 Best Local Similarity 45.9%; Pred. No. 1-58-84;
 Matches 282; Conservative 107; Mismatches 164; Indels 61; Gaps 9;

Qy	41	RTRRSMWNNQFVIEEYVAGPEPVLLIGKLSVDVDRGEGRKTLTGEGAGTVFIDEAT	100
Db	49	RLKRSMWNNQFVIEEYVAGPEPVLLIGKLSVDVDRGEGRKTLTGEGAGTVFIDEAT	108
Qy	101	IHTVSLDREKKAQVLLAQAVDRASNPLEPSEPFITKGGDINDNPIPLGPHAT	160
Db	109	IHTVSLDREKKAQVLLAQAVDRASNPLEPSEPFITKGGDINDNPIPLGPHAT	168
Qy	161	EMSNVTSVITQVTAHADDDPSYGSNAKLVYVLDGLPFSVPDQGVVRAIPMDRE	220
Db	169	EMSNVTSVITQVTAHADDDPSYGSNAKLVYVLDGLPFSVPDQGVVRAIPMDRE	228
Qy	221	EEFLVIAQKMGGMGLSGSTVTVTLSDVNDNPKPQSLQVSVFVAGGTLV	280
Db	229	DYEVITQAKMGGMGLSGSTVTVTLSDVNDNPKPQSLQVSVFVAGGTLV	288
Qy	281	LRADPDLGNALMAYSILDEGESEAFSISTDLQGRDLTVRKPLDFESORSYSFV	340
Db	289	VLAQDLDEGVNAEKNNILDEGESEAFSISTDLQGRDLTVRKPLDFESORSYSFV	348
Qy	341	TNTLIDPAVLRGPKDVASVAVQDAPPEPAFQAAYHLTVENKAPGLVQIQA	400
Db	349	SNALIEIFLWLGPRDTSVHTVEDVDEPVVGSFYPEVESENDIGITQIVAKD	408
Qy	401	LDSPASPIRYSILPHSDPERCSIQPEEGTHTAPLDRARAHNLTVLTELGMGM	460
Db	409	PDATNSVRYIIDSDDGRFYVDVTTGALMTARPIDREVSNNHTILAMEN	462
Qy	461	ERGWPVLLVAEKSAAPAPQSPVGSVAVGIPQSSAQAARVQVAIQTLIDENNA	520
Db	463	-----NNPAQIGVPTIKVLVDVNDNAPEFA	490
Qy	521	YDFVCDAAAPGQLIOVIRALDRDEVGNSHVSFGGLGPA-----NFTVQDN	576
Db	491	SETLMCAKADQQLIOVIRALDRDEVGNSHVSFGGLGPA-----NFTVQDN	548
Qy	577	--HPLMASASWLMWP--PAERGNQPAQSGKSSL--PCGRLPGALPSCQ----	623
Db	549	LTRRGFKQSQSTFYVPLILSDGNPNLSTGTTLTQVCSCK-DGDIWSCNAEPYLLP	607
Qy	624	LGI---PALGIVLC	634
Db	608	ISLSRGALITLTC	621

RESULT 12
 159372
 C:Species: Homo sapiens (man)
 C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
 C:Accession: 159372
 R:Seilig, S.; Bruno, S.; Scharf, J.M.; Wang, C.H.; Vitale, E.; Gilliam, T.C.; Kunkel, L.M.
 Proc. Natl. Acad. Sci. U.S.A. 92, 3707-3706, 1995
 A:Title: Expressed cadherin pseudogenes are localized to the critical region of the spli
 A:Reference number: 159372; MUID:95249541; PMID:7731968
 A:Accession: 159372
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
 A:Molecule type: mRNA
 A:Cross-references: UNIPROT:P55289; GB:L33477; NID:G793942; PIDN:AA848539.1; PID:G793942
 A:Gene: GDB:CDH12
 A:Cross-references: GDB:596324

A:Map position: 5p13-5p14
 C:Superfamily: cadherin; cadherin repeat homology
 C:Keywords: calcium binding; cell adhesion; duplication; transmembrane protein
 F:57-160/Domain: cadherin repeat homology <CR1>
 F:163-269/Domain: cadherin repeat homology <CR2>
 F:272-384/Domain: cadherin repeat homology <CR3>
 F:387-489/Domain: cadherin repeat homology <CR4>
 F:491-601/Domain: cadherin repeat homology <CR5>
 F:610-637/Domain: transmembrane #status predicted <TM>
 F:638-794/Domain: intracellular #status predicted <INT>

Query Match 40.8%; Score 1368.5; DB 2; Length 794;
 Best Local Similarity 44.4%; Pred. No. 3.8e-83;
 Matches 282; Conservative 114; Mismatches 154; Indels 65; Gaps 11;

```

QY 30 GSRHPGALLTRRSVMNQFVIEYAGPEVYLICKLHSDVDVRSRGRTKYLITGEAG 89
DB 44 GQRSH---FORVKKRWVMNQFVLEEMGSEPPQYVKLHSDLDKSGTAVYTLSDGAG 99
QY 90 TVFVDEATGNHTKSLDREKAQVYLAAVNRASNPPEPSEFIIINGQIINNPPI 149
DB 100 TVFTLDETTGDIHAIKSLDREKPPYTLRAQAVIETRKPLEPSEFIIKQVQINDNPK 159
QY 150 FPLGPRHATVEMSNVGTSTQVTAHADDPDSYGNASKLYTVLGLPFPSVDPQTGVR 209
DB 160 FLDDGYATVPEMSPVGAIVVQVAKADADDPYNSARVYSILQGGPYFSIDPKTVIR 219
QY 210 TATNMDRETOEFLVLAQADNGHNGLSGTTVYTLSDVNDNPKPKPOSIXQTSVY 269
DB 220 TATNMDRETOEFLVLAQADNGHNGLSGTTVYTLSDVNDNPKPKPOSIXQTSVY 279
QY 270 ETAGGTLVGRTRADPDLGNALMAYSILDGSESAFSTIDQGRDGLTVKRPDPE 329
DB 280 ESSPTGSAIGIRAVDPFGQNAIEKNTVPGDGNLFDIYTDIDDEGVIKLKKPDEF 339
QY 330 SQRYSFPEVATNTLIDPAYLRGPPKQVAVSVAAVODAPPPAFTAAYHLYPENKAP 389
DB 340 TKKATYFKVDASNLHLDRFHSAGPFGKQATATKISIVDVEPPFVSKPLTMEVYEDTPV 399
QY 390 GTLWQGSAAADLPASPIRYSILPHSDPERCFSTQPEEGTTHAAPLDEPARAHNLT 449
DB 400 GTTGAVTAQDLDGSSAVRYFLDKKSDGDSYFTIDKEGTTATNELIDESTIQVPSI 459
QY 450 LATELGMSWGERGVPLLVAEWSAPAPAPQSPVGSAGVIGIPDSSAQSAYVAIQTL 509
DB 460 IASKYS-----NPL-----TSKVNILINVL 481
QY 510 ENDNAPQALPEYDFVCSANPQGLQVIRALDRDEVGNSSHVFGQPLGPD-----NFT 565
DB 482 VNEPPEITSVETAVACENAKPGQITQVSAADLDSPAGQSFRL--LSEALIKRNPFT 539
QY 566 VQNRNDLPA-----WFHPLIMASASWLMHPAERGNQAPQCKSSSLP 609
DB 540 VRDRPNNTAGIETRRNGYSRQQLYFLPVVIEDSSY-----PYQ-----SSNTMTIR 588
QY 610 CGRL--PGALPSCQ-----LPLGTPA---LGIIVLC 634
DB 589 VQRCDSGDTILSCNVEAFLPVGISTGALIALILLC 623

```

RESULT 13

ITRUC5
 cadherin 5 precursor - human
 N:Alternate names: 7B4 antigen; cadherin, endothelial-specific; VE-cadherin
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1993 #sequence revision 13-Sep-1996 #text_change 09-Jul-2004
 C:Accession: S49893; S24305; A43418
 R:Brevario, F.; Cavada, L.; Corada, M.; Martin-Padura, I.; Gelay, J.; Introna, M.; Lamp
 submitted to the EMBL Data Library, June 1994
 A:Description: Molecular and functional properties of VE-cadherin (7B4/cadherin-5) a nov
 A:Reference number: S49893
 A:Accession: S49893
 A:Status: preliminary

A:Molecule type: mRNA
 A:Residues: 1-784

 A:Cross-references: UNIPROT:P3151; EMBL:X79961; NID:G599833; PIDN:CAA6306.1; PID:G5998
 R:Guzuki, S.; Sano, K.; Tanihara, H.
 Cell Regul. 2, 261-270, 1991
 A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t
 A:Reference number: S24305; MUID:91283540; PMID:2059658

A:Accession: S24305
 A:Molecule type: mRNA
 A:Residues: 5-516, '1', 518-784 <SUZ>
 A:Cross-references: EMBL:X59796; NID:G639976; PIDN:CAA42468.1; PID:G29593
 R:Lampugnani, M.G.; Resnati, M.; Rateri, M.; Pigott, R.; Piscane, A.; Hoven, G.; Ruco
 J. Cell Biol. 118, 1511-1522, 1992
 A:Title: A novel endothelial-specific membrane protein is a marker of cell-cell contact:
 A:Reference number: A43418; MUID:92394977; PMID:1522121

A:Accession: A43418
 A:Molecule type: protein
 A:Residues: 48-60, 'X', 62, 'X', 64, 108-116, 'X', 118-123, 237-238, 'X', 240, 'X', 242-252, 'X', 254.
 A:Experimental source: cultured endothelial cells
 A:Note: sequence extracted from NCBI backbone (NCBI:113040, NCBI:113045, NCBI:113047
 C:Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought t
 C:Genetics: GDB:CDHS

A:Gene: GDB:CDHS
 A:Cross-references: GDB:134230; OMIM:601120
 A:Map position: 16q22.1-16q22.1
 C:Superfamily: cadherin; cadherin repeat homology
 C:Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane pr
 F:1-25/Domain: signal sequence #status predicted <PRO>
 F:26-47/Domain: propeptide #status predicted <PRO>
 F:48-784/Product: cadherin 5 #status predicted <XMT>
 F:48-593/Domain: extracellular #status predicted <EXT>
 F:50-151/Domain: cadherin repeat homology <CR1>
 F:154-258/Domain: cadherin repeat homology <CR2>
 F:261-372/Domain: cadherin repeat homology <CR3>
 F:375-479/Domain: cadherin repeat homology <CR4>
 F:481-587/Domain: cadherin repeat homology <CR5>
 F:591-620/Domain: transmembrane #status predicted <TM>
 F:621-784/Domain: intracellular #status predicted <INT>
 F:726-753/Region: serine-rich
 F:61,112,157,362,442,523,535/Binding site: carboxylate (Asn) (covalent) #status predic

Query Match 28.0%; Score 940.5; DB 1; Length 784;
 Best Local Similarity 39.5%; Pred. No. 1.1e-54;
 Matches 227; Conservative 85; Mismatches 208; Indels 55; Gaps 12;

```

QY 6 RLTLAWLGWGMGRIAPAPARMAAGSRHPPG-----PALLRTRRSVMNQFVIEBY 57
DB 3 RLMLLATSGACGLLAVAVAAGA--NPAQRDTHSLPFRHQRKRWIMNQMHDEBK 60
QY 58 ACEPEPLIKLHSDVDVRSRGRTKYLITGEAGTVFVIDATGNHTKSLDREKAQVYL 117
DB 61 NTSLPFHVKIKISSVR--KNAKYLLKGYVAKVRVDAETDVAIERLDENISEYHL 118
QY 118 LAQAVNRASNPPEPSEFIIINGQIINNPPIFPFGPYATVPEMSNVGTSTQVTAHDA 177
DB 119 TATVYKQDGENLETSSFTIKYHVDNDWPFTHRLFPAASPESSAVGTSIVTAADA 178
QY 178 DDESYNSAKLYTVLGLPFPSVDPQTGVVTRTALPNMDRETOEFLVLAQADNGHNG 237
DB 179 DDETVGDHASVMYQILKGEYFAID--NSGRITITTSKSLDREKQARVEIVEARDAG--LR 236
QY 238 GLSGSTTVVTLSDVNDNPKPKPOSIXQTSVYETAGPGLVGRTRADPDLGNALMAYS 297
DB 237 GDSGTAIVTVTLQDINDNPPFTQIKYTVVPEDRVGVSGSLFPEDDDEQNRTKKS 296
QY 298 ILDEGSEAFSISTDLQSGDGLTVKRPDLDFESSQRSYFPEVATNTLIDPAYLRGPP 357
DB 297 ILRGYQDAFTLETNPAHNEGIIKPKKPLDYETIQYYSFIVETALPTIDLRYM--SPAPN 355
QY 358 VASVRVAVODAPPPAFTAAYHLYPEN--KAPGLTVGQISAADSPASPIRYSILPHS 416
DB 356 RAQVITNITVDDEPPLFQGPFIHFOLEKQKAP--LIGIVLAMPDPAASHSIGISIRTS 413

```

QY 417 DPECFSTIOPEEGTHTHTAPLDREARAHNLVLTATELGWSWGERGWLVAEMGAPA 476
 DB 414 DKGFPRV-TKKGITYNEKELDRREYVEMYLITAEAKL-----450
 QY 477 APPORSVGSVAVGIPDSSAQSVOVALIOTLDENDNAPOLAEYDTFVCDSPAAGQLIQ 536
 DB 451 -----DSTGTP--TGKESIVQVHIEVLDENDNAPEFAKPCPKVCENAVHGLVLI 498
 QY 537 VIRALDREVNSSHSVFCGLGPDANFTVQDNND 571
 DB 499 QISAIKDQI--TPRNKFRKFTLTENNFTLIDND 531

RESULT 14

R-cadherin precursor - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
 C:Accession: J04424
 R:Inuzuka, H.; Miyatani, S.; Takeichi, M.
 Neuron 7, 69-79, 1991
 A:Title: R-cadherin: a novel Ca2+-dependent cell-cell adhesion molecule expressed in the
 A:Reference number: J04424; MUID:91299341; PMID:11712604
 A:Accession: J04424

A:Molecule type: mRNA
 A:Residues: 1-913 <INU>

A:Cross-references: UNIPROT:P24503; GB:D14459; GB:D00849; NID:G222854; PIDN:BAA03356.1;
 A:Experimental source: retina

C:Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought to
 C:Keywords: calcium binding; cell adhesion; duplication; glycoprotein; retina; transmembr

F:127-166/Domain: signal sequence #status predicted <PRO>
 F:167-913/Product: R-cadherin #status predicted <EXT>

F:167-913/Domain: extracellular #status predicted <EXT>
 F:169-274/Domain: cadherin repeat #status predicted <CR1>

F:244-249/Region: cadherin binding #status predicted
 F:227-389/Domain: cadherin repeat homology <CR2>

F:392-504/Domain: cadherin repeat homology <CR3>
 F:507-612/Domain: cadherin repeat homology <CR4>

F:613-721/Domain: cadherin repeat homology <CR5>
 F:722-753/Domain: transmembrane #status predicted <TM>

F:754-913/Domain: intracellular #status predicted <INT>
 F:870-885/Region: serine-rich
 F:280,409,554,629,658,699/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.0%; Score 604; DB 1; Length 913;
 Best Local Similarity 31.7%; Pred. No. 3,5e-32;

Matches 195; Conservative 82; Mismatches 236; Indels 102; Gaps 23;

QY 4 LVRLILAM-----IGGWMCM-----GRLLAPR-----RAMGSR 32
 DB 97 LILVLTAMDPQTJGRMEALIVRFLVGEFLQHNHKKPKGRKSGPVDLAQQQSDTLPL--R 153
 QY 33 EH-PGPAALTRRSWMNQFVIEVAGPEPVILGKLSVDVDRGRTKYLITGEGAG-- 89
 DB 154 QHQAQKALFRQKRWVPIPIVNPENSGRPFQQLVIRISQKX-EHIRYSTIGVADDP 212
 QY 90 --TYFVIDEATGNIHTVKSIDREKAQYVLLAQAVDRASRPLPEPSEFIKQDINDP 147
 DB 213 PMEFSTIDPVSGRMYIVRPMDRERBRASYLRAHAVMNGKR-VEENIDYIYVIDNDR 271
 QY 148 PIFPLGYHATVPEPMVSVGTSVICVPAHDADDPYGSALVTVVTDGP-----PFSV 201
 DB 272 PEFINQVYNSVDEGSKRGTYVTVTRANDADSTIAN-GVRRIRIYOTPOSSQMFTI 330
 QY 202 DPQIGVVRPAI PNMDETQEEPLVIVIOAKMGHMG-GLSGSTTVTLSDVNDNPKFP 260
 DB 331 NSEIGDILVTAAGIDREKVOQYVIVIOATMEGNLNGJSTNATAIITVDVNDPPEPT 390
 QY 261 QSLVQFVETAGGTLVGRLRADQDPL--GDNALMAYSITLDEGESEASISIDQGRG 318
 DB 391 TSTYSGVEPNR-VEVVVAVLTVMDRDPQHSFPMNAIYRIISGDSGHFTIRIDPVYNEG 449

QY 319 LITVRKPLDFESQRSYRVEATINTLIDPAIIRG---PFQDVASVYVAVQDAPEPAFT 375
 DB 450 MVTIVKADVYENKRFMLTWVSN---QALASGIQMSFQSTAGTISTVDVNEAPFP 505
 QY 376 QAAVHLTPENKAPFOTLVGOISAADLDS-PASPIRYSILPSPDEPGRFSIQPEGTHTA 434
 DB 506 TMHKLIRIEGVPSTIVLTFSADVDPDRFQGAARYSL--SDPAMNINIANQGLTTA 563
 QY 435 APIDREARAHNLVLTATELGWSWGERGWLVAEMGAPAPQSPGSAVGTIQQDS 494
 DB 564 AVLDRSDYIKNNVYEA-----FLAANDGIPPA-----SGTGLIQ-- 599
 QY 495 SAQASRGVVAIOTLDENDNAPOLAEYDTFVCDSPAAGQLIQVIRALDREVNSSHSVS 554
 DB 600 -----IYLIDINNAPELL-PKEAQICER--PMLAVINTIADADIDPVGPFVF 646
 QY 555 QGPLCPDA--NFTV 566
 DB 647 ELPSVPSAVRKWIT 661

RESULT 15

IJMSCN
 N-cadherin precursor, neuronal - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
 C:Accession: A32759; A46163

R:Miyatani, S.; Shimamura, K.; Hatta, M.; Nagafuchi, A.; Nose, A.; Matsumaga, M.; Hatta,
 Science 245, 631-635, 1989
 A:Title: Neutral cadherin: role in selective cell-cell adhesion.
 A:Reference number: A32759; MUID:89346748; PMID:2762814
 A:Accession: A32759

A:Molecule type: mRNA
 A:Residues: 1-906 <MT>

A:Cross-references: UNIPROT:P15116; GB:M31131; NID:G192327; PIDN:AAA37353.1; PID:G3091225
 Proc. Natl. Acad. Sci. U.S.A. 86, 8443-8447, 1989

A:Title: Genomic structure and chromosomal mapping of the mouse N-cadherin gene.
 A:Reference number: A46163; MUID:92409532; PMID:11528849
 A:Accession: A46163

A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 839-906 <MT>
 A:Cross-references: GB:S45011; NID:G256010; PIDN:AAA23356.1; PID:G256011

A:Note: sequence extracted from NCBI backbone (NCBI:N113759, NCBI:P113760)
 C:Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought to
 C:Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane pro

F:127-127/Domain: signal sequence #status predicted <PRO>
 F:128-159/Domain: propeptide #status predicted <PRO>

F:160-906/Product: N-cadherin #status predicted <TM>
 F:162-267/Domain: extracellular #status predicted <EXT>

F:237-242/Region: cadherin binding #status predicted
 F:270-382/Domain: cadherin repeat homology <CR2>

F:385-497/Domain: cadherin repeat homology <CR3>
 F:500-605/Domain: cadherin repeat homology <CR4>

F:606-714/Domain: cadherin repeat homology <CR5>
 F:715-746/Domain: transmembrane #status predicted <TM>

F:747-906/Domain: intracellular #status predicted <INT>
 F:865-878/Region: serine-rich
 F:190,273,325,402,572,651,692/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.9%; Score 601; DB 1; Length 906;
 Best Local Similarity 33.9%; Pred. No. 5,5e-32;

Matches 190; Conservative 76; Mismatches 214; Indels 80; Gaps 21;

QY 33 EHPGPAALTRRSWMNQFVIEVAGPEPVILGKLSVDVDRGRTKYLITGEGAGT-- 90
 DB 149 KHSG-ALQROGRDQVPIPIVNPENSGRPFQQLVIRISQKXLS-LRYEVTGAGADQP 206
 QY 91 --VFVIDEATGNIHTVKSIDREKAQYVLLAQAVDRASRPLPEPSEFIKQDINDP 148

This Page Blank (uspto)

Db	181	SYGNSAKLVYTVLIDGLPFSSVDPQGVVRIAPIMNDETQEEFLVYIQADMGHMGGLS	240
Qy	241	GSTTVTVLISDVNDNPPKPFQSLYQSVETAGPCTVGLRAODPDLGNALMAVSIID	3000
Db	241	GSTTVTVLISDVNDNPPKPFQSLYQSVETAGPCTVGLRAODPDLGNALMAVSIID	3000
Qy	301	GESSEAFTSIIDLQGGDGLITRKXLDPESSORSYFVREANTLIDPAYLRGPFQDVA	360
Db	301	GESSEAFTSIIDLQGGDGLITRKXLDPESSORSYFVREANTLIDPAYLRGPFQDVA	360
Qy	361	VRVAVDADPEPPAFPTQAAVHLTVPENKAPGLTVQISADLDSPASIRYSILPHSDPER	420
Db	361	VRVAVDADPEPPAFPTQAAVHLTVPENKAPGLTVQISADLDSPASIRYSILPHSDPER	420
Qy	421	CFEIOEEEGTHTAAPLDREAAAMNLTVALTELGMNGPGRGVPVLVAENAPAAPQ	480
Db	421	CFEIOEEEGTHTAAPLDREAAAMNLTVALTELGMNGPGRGVPVLVAENAPAAPQ	480
Qy	481	RSVVGSAVGIPODSSAOSRVQVAIQTLDENDNAPOLAEPYDITVCSAPAGGLIVIRA	540
Db	481	RSVVGSAVGIPODSSAOSRVQVAIQTLDENDNAPOLAEPYDITVCSAPAGGLIVIRA	540
Qy	541	LDSDEVGNSHVSFOGPIGPPDANFVQDNRD-----LPA-----WF	576
Db	541	LDSDEVGNSHVSFOGPIGPPDANFVQDNRD-----LPA-----WF	576
Qy	577	HPILMASSSWLH-----WPPAEKRGQVPSAOG	603
Db	577	HPILMASSSWLH-----WPPAEKRGQVPSAOG	603
Qy	601	QPAIISTATVTVSVCRQCPDQSDVASCHPEBAHLSAAGSTG	640
Db	601	QPAIISTATVTVSVCRQCPDQSDVASCHPEBAHLSAAGSTG	640

RESULT 2

ID	06PFY6	PRELIMINARY:	PRT:	781 AA.
AC	06PFY6			
DT	05-JUL-2004	(TEMBLrel. 27, Created)		
DT	05-JUL-2004	(TEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(TEMBLrel. 27, Last annotation update)		
DE	Cadherin-1-like 24.			
GN	Name=Cdh24;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6; TISSUE=Brain;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Ustin T.B., Toshitsuki S., Carninci P., Prange S.,			
RA	Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijix S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchwood J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Gaimwood J., Schnutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzyniutek M.I., Skalska U., Smalins D.B., Schenker A., Schein J.E.,			
RA	Jones S.J., Marra M.A.,			
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RT	generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RP	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6; TISSUE=Brain;			
RA	Straussberg R.,			
RL	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.			


```

QY 481 RSPGASGVIGIPQDSSAQAARVOYA IOTLDENDNA POLAEPDFTVCDSAPGOLIOYIRA 540
DB 455 -----DSSAGSSRVQVAIOTLDENDNA POLAEPDFTVCDSAPGOLIOYIRA 502
QY 541 LDRDEGVNSSHVSFOGPGPDANFTVODNRDLPAWFFPLIMASASWLMHPAPER----- 595
DB 503 LDRDEVGNSSQVSLQGPVGPDPANFTVARDNRGSA---SLLPSPSPA---PPQAPYLIP 555
QY 596 -----GNQPAQSGSS-----SLPGRLPGALPSCQL-PLGIPA---LGYVLC 634
DB 556 IELMDWGPALSTATVTVSVCRGCRPDGSMASCMWEAOLSPGTGLTGALLAIVTC 610

RESULT 4
Q96LQ7 PRELIMINARY; PRT; 493 AA.
ID Q96LQ7
AC Q96LQ7;
DT 01-DEC-2001 (TRENBLREL 19, Created)
DT 01-DEC-2001 (TRENBLREL 19, Last sequence update)
DT 01-OCT-2003 (TRENBLREL 25, Last annotation update)
DE Hypothetical protein FLJ25193.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thyroid;
RA Niimaya K., Magatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Futuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kanahara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA Nagai K., Isogai T., Sugano S.;
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: Contains 4 cadherin domains.
CC
DR EMBL; AK057922; BAB7163.1; -.
DR HSSP; P12830; 1065.
DR Genew; HGNC:14265; CDH24.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro; IPR001216; Cadherin.
DR Pfam; PF00028; Cadherin_4.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA; 4.
DR PROSITE; PS00232; CADHERIN_1; 2.
DR PROSITE; PS00268; CADHERIN_2; 4.
DR KEGG; K04468; Calcium-binding.
KW Calcium; Calcium-binding.
SQ
SEQUENCE 493 AA; 53618 MW; 33F10DF63AF09C1E CRC64;

Query Match 71.1%; Score 2386; DB 2; Length 493;
Best Local Similarity 93.5%; Pred. No. 3.3e-140;
Matches 462; Conservative 2; Mismatches 8; Indels 22; Gaps 2;

```

```

DB 241 GSTTATVTLSDVNDNPPKPFQSLYQFSVETAGPGLVGRLRADDPDLGNALMAYSLTD 300
QY 301 GEGSAFISITDLQGRDLITVRKPLDESGRSYSFVREATNTLIDPAYLRGPFKVAS 360
DB 301 GEGSAFISITDLQGRDLITVRKPLDESGRSYSFVREATNTLIDPAYLRGPFKVAS 360
QY 361 VRVAQDAPPEPAPFOAAYHLTVPENKAPGLVQOISADUDSPASPIRYSILPHSPER 420
DB 361 VRVAQDAPPEPAPFOAAYHLTVPENKAPGLVQOISADUDSPASPIRYSILPHSPER 420
QY 421 CESIQPEGTHTTAFLDREARAHNLTVLATELG-----MSWGPER 462
DB 421 CESIQPEGTHTTAFLDREARAHNLTVLATELGEDSRAHKAASAPRSCPMWV----- 476
QY 463 GWVPLVAMNSAPA 476
DB 477 GWRVLTALAPSPA 490

RESULT 5
CDB HUMAN
ID CDB HUMAN STANDARD; PRT; 796 AA.
AC P55287; Q15065; Q15066; Q9U093; Q9U094;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSF-4).
GN Name=CDH11;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RA Tanihara H., Sano K., Helmarx R.L., St John T., Suzuki S.;
RA "Cloning of five human cadherins clarifies characteristic features of
RA cadherin extracellular domain and provides further evidence for two
RA structurally different types of cadherin.";
RA Cell Adhes. Commun. 2:15-26(1994).
RL [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Osteosarcoma;
RA MEDLINE=95073006; PubMed=7982033;
RA MEDLINE=94216322; PubMed=8163513;
RA Okazaki M., Takeshita S., Kawai S., Kikuno R., Teijimura A., Kudo A.,
RA Amann E.;
RA "Molecular cloning and characterization of OB-cadherin, a new member
RA of cadherin family expressed in osteoblasts.";
RA J. Biol. Chem. 269:12092-12098(1994).
RL [3]
RP SEQUENCE OF 269-796 FROM N.A. (ISOFORM 1).
RC TISSUE=Fetal brain;
RA MEDLINE=91283540; PubMed=2059658;
RA Suzuki S., Sano K., Tanihara H.;
RA "Diversity of the cadherin family: evidence for eight new cadherins in
RA nervous tissue.";
RA Cell Regul. 2:261-270(1991).
RL [4]
RP SEQUENCE OF 600-668 FROM N.A. (ISOFORMS 1 AND 2).
RC Kools P.F.J., Hogendorn P.C.W., Boyce J.V.M.G., Van Roy F.;
RA "Alternative cadherin-11 transcripts encoding truncated adhesion
RA molecules are detectable in both human cancer and normal cells.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DE They preferentially interact with themselves in a homophilic
DE manner in connecting cells; cadherins may thus contribute to the
DE sorting of heterogeneous cell types.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P55287-1; Sequence=Displayed;

```

```

CC      Name=2;
CC      IsoId=PS5287-2; Sequence=VSP_000640, VSP_000641;
CC      TISSUE SPECIFICITY: Expressed mainly in brain but also found in
CC      other tissues. Expressed in neuroblasts.
CC      -1- SIMILARITY: Contains 5 cadherin domains.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by, and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; J34056; AAA5622.1; -
DR      EMBL; D21254; BA04798.1; -
DR      EMBL; D21255; BA04799.1; -
DR      EMBL; AF060370; AAD27755.1; -
DR      EMBL; AF060369; AAD27755.1; JOINED.
DR      EMBL; AF060370; AAD27755.1; -
DR      EMBL; AF060369; AAD27755.1; JOINED.
DR      PIR; A38992; A38992.
DR      HSSP; P09803; 117W.
DR      Genew; HGNC:1750; CDH11.
DR      MIM; 600023; -
DR      GO; GO:0016021; C: integral to membrane; NAS.
DR      GO; GO:0007156; P: homophilic cell adhesion; NAS.
DR      GO; GO:0001503; P: ossification; NAS.
DR      InterPro; IPR002126; Cadherin_C.
DR      InterPro; IPR000233; Cadherin_C-term.
DR      Pfam; PF00028; Cadherin_5.
DR      Pfam; PF01049; Cadherin_C_1.
DR      PRINTS; PR00205; CADHERIN.
DR      SMART; SM00112; CA; 5.
DR      PROSITE; PS00232; CADHERIN_1; 3.
DR      PROSITE; PS00268; CADHERIN_2; 5.
KW      Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
KW      Repeat; Signal; Transmembrane.
FT      SIGNAL          1..22
FT      PROPEP          23..53
FT      CHAIN           54..796
FT      DOMAIN          54..617
FT      TRANSMEM        618..640
FT      DOMAIN          641..796
FT      DOMAIN          54..159
FT      DOMAIN          160..268
FT      DOMAIN          269..383
FT      DOMAIN          384..486
FT      DOMAIN          487..612
FT      CARBOHYD        455..455
FT      CARBOHYD        540..540
FT      VARPSPIC        632..693
FT      VIVITFTLRQKKEPLVFEEDVRENTITTYDEGGGEED
FT      TEADPIATLQNPDIINGTIFR -> GQSLMEPSPEDWR
FT      LLYLGFQMLPSYVKNRFLCLGVFLKPLVYVATESPT
FT      TLTSL (in isoform 2).
FT      /FTId=VSP_000640.
FT      /FTId=VSP_000640.
FT      /FTId=VSP_000640.
FT      VARSPLIC        694..796
FT      CONFLICT        271..272
FT      CONFLICT        275..275
FT      CONFLICT        340..340
FT      CONFLICT        373..373
FT      CONFLICT        471..471
FT      SEQUENCE        796 AA; 88049 MW; 2C67044C78ADB2E CRC64;
Query Match      47.8%; Score 1602; DB 1; Length 796;
Beet Local Similarity 50.4%; Pred. No. 3.9e-91;
Matches 323; Conservative 98; Mismatches 134; Indels 86; Gaps 10;

```

```

QY      64 LIGKLSVDYDGRGRTKYLITGEGAGTVEIDEATGNIHVTSKDREEXAQVLLAQAVD 123
       73 LVKRLHSDIDSDGDNKITLSGEGACTIFVIDKSGNIHATKIDREBAQVTLMAQAVD 132
QY      124 RASNRPLEPPESEFIITKQDINDNPPIFPIGPYHATVPEKSNVSTYIQTADHADDPSYG 183
       133 RDNRPLEPPESEFIIVAQDINDNPEFFLETHANVPESNVTGSIQVTAADADDPYTG 192
QY      184 NSAKIVYATLDGIPESVAPDQGVRTAIENNDREOEFLVIAQKMGHAGGSGST 243
       193 NSAKLVSTLEGPPIPSVAQTGITRTALPNDRKAKEYHYVIAQKMGHAGGSGST 252
QY      244 TVVTITLDVNDNPPKPEQSLYQFSVETAPGPTLVGRTRAQDPDLDGNALMAYSLDGGG 303
       253 KVTITLTDVNDNPPKPEQSLYQFSVETAPGPTLVGRTRAQDPDLDGNALMAYSLDGGG 312
QY      304 SEAFSISTLQGRDGLITRKPLDESQSYFRYEATNTLDPAYLRGPKDVASYV 363
       313 MESFEITDYEIQEGVTKKRPVDTEBERASYLKVEAAVHIDPKVISNGPKDYVYAKI 372
QY      364 AVQDAPEPPAFTQAAYHLTVPENKAFGLVGOISAADLDPASPTRYSTILPSDEPERCS 423
       373 SVEDADEPPMFLAPSVIHVGENAAAGIVGVAKDPDPAANSPIRYSIDRHTDDRPFT 432
QY      424 IQPEEGTITPAAPLDREAPAMNLYLATELGMSWGPBGRVPLVAEWSAPAAPQPSF 483
       433 INEDDPIKITKYLDEESTAMNITVFAEI ----- 463
QY      484 VGSAAVGIPDSSQAQRVOVAIQTLDENMDAPOLAEPYDFVCDG-----AARGLIQVIR 539
       464 -----HNHQEQVVAIRVLDVNDAKKPAAPGFTCEBQOTPLSNQPIVTS 514
QY      540 ALDRDEVGNSHVSFGP--LGPDAFTVQNRDIP-----WHPILM 581
       515 ADDKDDTANGPRIFSLPEIITHNPFTVDRNDVNAGVYARRGSPRQKQDLYLPIVI 574
QY      582 ASASSTLWHPAERGNQPSQKSSLP-CG-RLGALDSC 620
       575 -----SDGPIPPYSTNTYLTITKVGCDVAGALASC 604

```

RESULT 6

Q96CZ9 PRELIMINARY; PRT; 796 AA.

AC Q96CZ9; 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Cadherin 11, type 2, isoform 1 preproprotein.

GN Name=CDH11;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC NCBI_TaxId=9606;

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=22386257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Scheimen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Shapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz F.E.,

RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Hulton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,

RA Whitting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.U., Maiza M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL, BC013609; AAI13609.1; -.
 DR HSSP, P09803; I17W.
 DR GO, GO:0016020; C:membrane; IEA.
 DR GO, GO:0005509; F:calcium ion binding; IEA.
 DR GO, GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro, IPR002126; Cadherin.
 DR InterPro, IPR000333; Cadherin_C_term.
 DR InterPro, IPR001901; Sec6.
 DR Pfam, PF00028; Cadherin_5.
 DR Pfam, PF01049; Cadherin_C_1.
 DR PRINTS, PRO0205; CADHERIN.
 DR SMART, SM00112; CA; 5.
 DR PROSITE, PS00232; CADHERIN_1; 3.
 DR PROSITE, PS50268; CADHERIN_2; 5.
 DR PROSITE, PS01067; SECE_SEC6LG; UNKNOMN_1.
 DR KMW, KMW:Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 796 AA; 87979 MW; 8497F9B834F7547C CRC64;
 Query Match 47.7%; Score:1601; DB 2; Length 796;
 Best local similarity 50.4%; Pred. No. 4,5e-91;
 Matches 323; Conservative 98; Mismatches 134; Indels 86; Gaps 10;
 QY 17 CMGSLA-----APAR-----AMAGSRE--HPGALLRTRRSWVWQFVIEEYAGPEPY 63
 DB 13 CLGCLSHAPAPRRRGHLRPSFGHHEKGEQGLQRSXRGWVWQFVIEEYTPDPY 72
 QY 64 LIGLHSDVDRGERTYLLTGEGAGTVFVLDATGVIHTKSLDREKQVYLLAQVAD 123
 DB 73 LVGRLHSDIDSGDNKIKILSGEGAGTIVIDSSGNHATKILDRERQYTLMAQVAD 132
 QY 124 RASNRPLEPSEFEIKQDINDNPPIPLGPNATVBMNGVSVIQTADADPSYG 183
 DB 133 RDTNRPLEPSEFEIVKQDINDNPPELHETVHANVPSRNGVSVIQTADADPTYG 192
 QY 184 NSAKLVTVYDGLPFPSVDPTGVVTRATINMDRETEBEELVYIQADMGHNGISGST 243
 DB 193 NSAKLVYSILEGQYFVEAQTGIIRTLALNMDREAKEEYHVVIIQADMGHNGISGST 252
 QY 244 TVVTVLSPVNDNPKFPQSLYQFVSVEAGTIVGRILRAQDDPLGDNALMAVSIIDG 303
 DB 253 KVMITLIDVNDNPKFPQSVYQMSVSAVPGEEVGVKAKDDIGENGAVTINIVDGG 312
 QY 304 SEASISITDLOGRGLTVRKPLDFESQSYSPFVEVETNTLLIPAYIRRPFCVAVSV 363
 DB 313 MESEFITVDYETQGVIKLKPVDFFTKRAYSLKVEZANVHIDPKFISNPFKDTYTVK 372
 QY 364 AVQAPREPPATQAAHYLTVPENKAPGLVGOISADLDPPASPIRISIPHSPPRCS 423
 DB 373 AVEADDERPMTLASIYHEVOENAAAGTVGRVAKDPDANSPIRISIRHDDLRFT 432
 QY 424 IQPEEGTHTAPLIDREARAWENTLVATLGLWSWGERGVWPLLVNWSAPAPQRSD 483
 DB 433 INPDGFIKTKPKIDREETAINTVFAET----- 463
 QY 484 VGSAGVIRPOSSAASVVOVAIQTLDENNDAPQIARPYDTFVCS-----AAPGLQVIR 539
 DB 464 -----HRRHQBKPVAIKVLVDVNDAPKPAADYEGFTCSQDTKPLSNQPIVTTIS 514
 QY 540 ALRDDEVGNSHVSFGQRP--LGPDPANFTVDNRLDPA-----WFFPLLM 581

DB 515 ADDKODTANGPPIFSLPDEIITHNPFVRRNRNTAGVARRGCFGRQKODYLLPLVI 574
 QY 582 ASASSMLWPPAERGNQPSQKSSLP-CG-RUPGALPSC 620
 DB 575 -----SDGIRPMSSTNTLTIVKCCDVNGLLSC 604
 RESULT 7
 ID CADB MOUSE STANDARD; PRT; 796 AA.
 AC P5288;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSF-4).
 GN Name=Cdh11; Synonyms=Cad-11;
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95269886; PubMed=7750649;
 RA Hoffmann I.H., Baling R.;
 RT "Cloning and expression analysis of a novel mesodermally expressed
 RT cadherin."
 RL Dev. Biol. 169:337-346(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95269887; PubMed=7750650;
 RA Kimura Y., Matsunami H., Inoue T., Shimamura K., Uchida N., Ueno T.,
 RA Miyazaki T., Takeichi M.;
 RT "Cadherin-11 expressed in association with mesenchymal morphogenesis
 RT in the head, somite, and limb bud of early mouse embryos."
 RL Dev. Biol. 169:347-358(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Calvaria;
 RX MEDLINE=94216322; PubMed=8163513;
 RA Okazaki M., Takehita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,
 RA Amano E.;
 RT "Molecular cloning and characterization of OB-cadherin, a new member
 RT of cadherin family expressed in osteoblasts."
 RL J. Biol. Chem. 269:12092-12098(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=olfactory epithelium;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stalderon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.U., Ustin T.B., Tomshytski S., Canninci P., Prange C.,
 RA Raha S.S., Loughran N.A., Peters G.J., Adamson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.C., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Huily S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shvachenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Wyre R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Maiza M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP DEVELOPMENTAL STAGE.
 RC STRAIN=C57BL/6; TISSUE=Testis;
 RX MEDLINE=97033837; PubMed=8879495;

RA Munro S.B., Blaschuk O.W.;
 RT "A comprehensive survey of the cadherins expressed in the testes of
 RT fetal, immature, and adult mice utilizing the polymerase chain
 RT reaction";
 RL Biol. Reprod. 55:822-827(1996).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Selectively expressed in osteoblastic cell
 CC lines, precursor cell lines of osteoblasts, and primary
 CC osteoblastic cells from calvaria, as well as in lung, testis, and
 CC brain tissues at low levels.
 CC -1- DEVELOPMENTAL STAGE: In the testis, expression is highest in fetal
 CC gonad and decreases 8-fold in newborn.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See [http://www.ebi.ac.uk/announcements/](http://www.ebi.ac.uk/announcements)
 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL; X77557; CAAS4674.1; -;
 DR EMBL; D31963; BAA06730.1; -;
 DR EMBL; D21253; BAA04797.1; -;
 DR EMBL; BC046314; AAA46314.1; -;
 DR PIR; A53584; A53584;
 DR PIR; I48277; I48277;
 DR PIR; I49556; I49556;
 DR HSSP; P09803; I17W;
 DR MGSD; MGI:99217; Cdh11.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0005886; C:plasma membrane; IDA.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C_term.
 DR Pfam; PF00028; Cadherin_5;
 DR Pfam; PF01049; Cadherin_C_1.
 DR PRINTS; PR00205; CADHERIN.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 KM Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KM Transmembrane.
 FT SIGNAL 1 24 Potential.
 FT PROPEP 25 53 Potential.
 FT CHAIN 54 796 Cadherin-11.
 FT DOMAIN 54 617 Extracellular (Potential).
 FT TRANSMEM 618 640 Potential.
 FT DOMAIN 641 796 Cytoplasmic (Potential).
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.
 FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 612 Cadherin 5.
 FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 540 540 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 462 462 E -> D (in Ref. 1).
 FT CONFLICT 589 589 T -> L (in Ref. 2).
 FT CONFLICT 655 655 D -> N (in Ref. 2).
 FT CONFLICT 751 751 V -> M (in Ref. 1).
 FT CONFLICT 777 777 P -> Q (in Ref. 2).
 FT CONFLICT 782 782 L -> P (in Ref. 2).
 SQ SEQUENCE 796 AA; 88112 MW; 0D584D24641D529 CMC64;
 Query Match 47.6%; Score 1596; DB 1; Length 796;
 Best Local Similarity 50.7%; Pred. No. 9,1e-91;
 Matches 317; Conservative 97; Mismatches 127; Indels 84; Gaps 8;
 31 SREHP-----GPAALRTSRVWVNOFVIEEYAGEPVLIGLSDVVRSGRT 79

Db 29 SHLHPSFHGHEKKEGQVLRSKSGWVWVNOFVIEEYGPDPVLVGRLLHSDIGDGN 88
 QY KYLLTSEAGATFVDEATGNITHWKSIDPREKAQVYLLAQVADPASNRPPESEFTIK 139
 Db 89 KYLLSEAGATTFLVDDSGNTHAKTKLDRERAQYTLMAQVADDTNRPLPESEFTYK 148
 QY 140 GQDINDNPIPLGEPYHATVPEMSNVGTSVIGVTAHADDPDSYGNASAKLVYTVLDGLPE 199
 Db 149 VQDINDNPEFLHEITHAVPERSNVGTSVIGVTAHADDPDSYGNASAKLVYTVLDGLPE 208
 QY 200 SYDPQGVVTRTAPMMDRETOEFLVIAQKMGGMGLSGSTVTVTLSPVNDNPPKF 259
 Db 209 SEVAGQGLIRLALPNMDREKKEHVIVIAQKMGGMGLSGSTVTVTLSPVNDNPPKF 268
 QY 260 POSLYQFSVETAGPGLVGRLAQDPDLGDNALMAVSLDDESGEARSISTDLOGDGL 319
 Db 269 POSVQMSVSEAAVPGEEVGRVAKDPDIDGNGLVTVNIVDDGIELFEITTDVETQGV 328
 QY 320 LTRKRLDRESQRTSFRVETNTLIDPAYLRGGFKVAVSRVAVQAPPPATQAY 379
 Db 329 VTKRKRVDETRAVSLKLEAANVHIDPFISNGPKQTVYKISVEDADEPPMLASV 388
 QY 380 HTVPEKPAKGLVAGQISAAADLSDPASPIRSYIILPHSDPERCFSIQPEEGTHTAPLDR 439
 Db 389 IHEVGEMAAAGTVGRVHAKDPDANSPIRSYIDHTDLDRLFTINPEDGRFKTKPLDR 448
 QY 440 EAPAMNLTVALTELGSWNGPGRGVPLVIAEWSAPAPQPSVGSVAVGIPDSSAQS 499
 Db 449 EETAMINISVFAEEL-----NHRHOET 470
 QY 500 RYQVATQTLDENDNAQLAEPYDFVCDSSAP-----GQIQTVALDDEVGSSHVSPQ 555
 Db 471 KQVALRVLDVNDNAPKFAPEGFTCSCHFKALSNQPIVVSADDDQDTNNGRFTFS 530
 QY 556 GP--LGPDAFTVODNRDLPA-----WFPPLMASASSWILHMPAERGN 597
 Db 531 LPPEIMHNFVTRDNRDTAGVYARGGFSRQKQDFYLPVI-----SDGSI 579
 QY 598 QPASQCKSSLP--CG-RLPGLPSC 620
 Db 580 PPMSTNTLTIRKCGDVNALLSC 604
 RESULT 8
 ID 08CT06 PRELIMINARY; PRT; 796 AA.
 AC 08CT06;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length
 DE enriched library, clone:C530015F15 product:cadherin 11, full insert
 DE sequence.
 GN Name=Cdh11;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa;
 OC Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_Taxid=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=spinal cord;
 RC MEDLINE=92279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=spinal cord;
 RC MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RA The FANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Komno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630 (2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Komno H., Akiyama J., Nishi K., Kikunai T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto S., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwake S., Inoue K., Togawa Y., Irawa M., Ohara E., Wataniki M.,
 RA Okazaki Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai U.,
 RA Kozaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771 (2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RA Adachi U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kaech H., Kawai J., Kojima Y., Kondo S., Komno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ono M., Ohato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sero H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL; AK049652; BAC3860.1; -.
 DR HSSP; P09803; 117W.
 DR MGD; MGI:99217; Cdh11.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0005886; C:plasma membrane; IDA.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR00233; Cadherin_C-term.
 DR Pfam; PF01049; Cadherin_5; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 KW Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 KW SEQUENCE 796 AA; 88126 MW; 71963374B2E1B529 CRC64;
 SO Query Match 47.6%; Score 1595.5; DB 2; Length 796;
 Best Local Similarity 51.6%; Pred. No. 9.8e-91;
 Matches 314; Conservative 97; Mismatches 125; Indels 73; Gaps 7;
 QY 36 GPALLRRRWVWVNOFVIEBYAGPEPVILGKLHSDVDRGEGTFTKLLTGEGAGTVFVID 95
 DB 45 GQVLRKSRGWVWVNOFVIEBYAGPEPVILGRLHSDIDSDGNIKYLLSGEGAGTVFVID 104

QY 96 EATGNHVTSLDREKAQVYLLAQVDRASNRELPSEFIIKGODINDNPFIPLGPY 155
 DB 105 DKSNGIHATKTLDRERQAQYLLMAQVDRDNRLEPSEFIVKQDINDPPEFLHEIY 164
 QY 156 HATVPEMNGSVQVTAHNDADPSVGNASKVYTVLDGPFPSVDPQGVATAPM 215
 DB 165 HANVPERSNVGTVQVATSPADDPPTVGNASKVYSLDGPFVSEVAGTITLAPM 224
 QY 216 DRETOEBFLVYIAQDMGNGHGLSGTFTVTLSDVNDNPKPQSLYQSVVETAGQC 275
 DB 225 DREAEEHVYIAQDMGNGHGLSGTFTVTLSDVNDNPKPQSVQSVSEAAVPG 284
 QY 276 TLVGRLLAQDPLDGNALMAVSLIDGESSEAFSLTDLQGDGLYTRKPLDPSQSSYS 335
 DB 285 BEVGRVAKADPDIGENGVLTVNIVDGDIELEFITTYYEQDGVKKKPVDFETKAYS 344
 QY 336 FREVATNPLIDPAYARRPFDQVAVRAVADAEPAFTQAHLTVPENKAGTVYQ 395
 DB 345 LKIEAANHIDPKFTSNPFQDTYTKISVADAEPEMFLAPSTIHWQENAAAGTVGR 404
 QY 396 ISADLDSPASPIRYSILPHSDPERCSIOPEEGTHTAPLDREARAHNLYLATELG 455
 DB 405 VYAKDPDANSPIRYSIDRHTDLRPFINDEDFIKTKPLDREETAMNLSVPAEI- 463
 QY 456 MSWGERGWVPLVLAEMGAPAPAPQSPVSGAVGIPQDSSAQASRVQVAIOTLDENNPAP 515
 DB 464 -----HNHQETKVAIRVLDVNDNP 486
 QY 516 QLAEPYDFVCDAAPE---GQLIQVIRALDRDEVGNSSHVSFGCP--LQPDANFTVDN 569
 DB 487 KFAAPYEGFICSDHPKALSNQPIVTSADQDDDTANGPFFIFLPEIMHNPFFTVRN 546
 QY 570 RDLPA-----WFHPLMASASSLHMPAERGQNPASQGSGLP-CG- 611
 DB 547 RDNTGVYARRGGSSRQKQDFYLLPIYI-----SDGILPMSSTNTLTIKVCGC 595
 QY 612 RLPGALPSC 620
 DB 596 DYNGLALSC 604
 RESULT 9
 ID 093264 PRELIMINARY; PRT; 794 AA.
 AC 093264;
 DT 01-NOV-1998 (TRENBLrel. 08. Created)
 DT 01-NOV-1998 (TRENBLrel. 09. Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26. Last annotation update)
 DE Cadherin precursor.
 GN Name: Xcad-11;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_Taxid=8355;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Zygote;
 RX MEDLINE=98202517; PubMed=9533956;
 RA Hadelball B., Borchers A., Wedlich D.;
 RT "Xenopus cadherin-11 (Xcadherin-11) expression requires the Wg/Wnt
 RT signal."
 RL Mech. Dev. 72:101-113 (1998).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL; AF002983; AAC28073.1; -.
 DR HSSP; P09803; 117W.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; P:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.

DR InterPro: IPR000233; Cadherin_C_term.
 DR Pfam: PF00028; Cadherin_5.
 DR Pfam: PF01049; Cadherin_C_1.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SM00112; CA; 5.
 DR PROSITE: PS00232; CADHERIN 1; 3.
 DR PROSITE: PS0268; CADHERIN 2; 5.
 DR Calcium; Calcium-binding; Cell adhesion; Signal; Transmembrane.
 FT SIGNAL 1 53 potential.
 FT CHAIN 54 794 cadherin.
 SO SEQUENCE 794 AA; 88302 MW; 7221AD4CEFA719DB CRC64;
 Query Match 47.2%; Score 1582.5; DB 2; Length 794;
 Best Local Similarity 50.4%; Pred. No. 6,36-90;
 Matches 310; Conservative 97; Mismatches 133; Indels 75; Gaps 5;
 QY 36 GPALLRTRRSWVWVNOQFVIEEYAGPEPVILGKLSVDVDRGGRKTKYLLTGEGATVVID 95
 DB 45 GQVLRHSKRGVWVNOQFVIEEYTPDPVLVGRHSVDVSGDWKIKYLLSGGATITVID 104
 QY 96 EATGNHVTKSLDREKKAQVYLLAQAVDRASNRPLEPSEETIKGODINDNPPIFFLPY 155
 DB 105 DKSNGHAKTKLDRERKQYTLMAQVDRETNKELEPSEETIVKQDINDNPPEFLHENY 164
 QY 156 HATVPENSVNGTSVYQVTAHDADDPBSYNSAKLYTVLDGLPFRSVDPQGVVTAIPNM 215
 DB 165 HANVPENSVNGTSVYQVTAHDADDPBSYNSAKLYTVLDGLPFRSVDPQGVVTAIPNM 224
 QY 216 DRETQEEFLVVIQAKDMGGMGSLSGSTTVTVLSDVNDNPKPKPQSLYQSVVETAGPG 275
 DB 225 DRAKEEYHVVVIOAKDMGGMGSLSGSTTKVITLTDVNDNPKPKPQSLYQSVVETAGPG 284
 QY 276 TLVGRLLRAQDDPLDGNALMAYSLIDEGSEAFSISTDLQGRDGLLVTRKPLDPESQSYS 335
 DB 285 EEVGRIRKAKDPDIGNGLIKYRILEGDAEWEFTADVTQEGVAKLKVDVETKKEYS 344
 QY 336 FRVATNTLIDPVLTRGSPFQVAVSVYAVQADAPPEPFAQAAHLVPEKKAAGTLVQ 395
 DB 345 MKVEAVNVHIDPFRFSRQPDYATVTKISVEDPEPFLERSYILVEYENASBDTVVGR 404
 QY 396 ISAADLDSPPASPIRYSILPHSDPERCFSTQPEEGTHTAFLDREARAHNLVLTATLG 455
 DB 405 VHADPDPAKSPIRYSIDRHDTLDRFSINPEDVAKTKKLDREESPMHNISITATEV- 463
 QY 456 WSWGPERGWPVLVAEMSAAPAAPPQRBSVSAVGIPODSSAQASRVOYALITLDENNAP 515
 DB 464 -----HNRLHETRVPAALKVDKDNAP 486
 QY 516 QLABRYDTFVCDASAPGQLIQVIRALDRDEVGNSSHVSGPQ---LGGDANFTQDNRDL 572
 DB 487 EFAPRYEAFVCEMNAFINOEFILITRAVDCDITANGIRFRFSPPETVAPNPFITIDKDN 546
 QY 573 PA-----WFHPLMASASWLMWPPAER-----GNOPASQ 602
 DB 547 TASIRVGRGVFSRQKQDLYLVIVISDGS---PPMSTNTLTSVRICSCNSDGSQSCN 602
 QY 603 GKSSSLPCGRLPGL 617
 DB 603 AEPQSLNGLSTGAL 617
 RESULT 10
 CADA_CHICK STANDARD; PRT; 792 AA.
 AC 093319
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 05-JUL-2004 (Rel. 44; Last annotation update)
 DE Cadherin-11 precursor.
 DE Name=CDH11;
 GN Gallus gallus (Chicken).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

CC Gallus.
 CC NCBI_TaxID=9031;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=White Leghorn;
 CC RA Wei J., Dong X.R., Topouzis S., Zimmer W.E., Broders F., Thierry J.P.,
 CC RA Koteliarsky V., Vajesky M.W.;
 CC RT Molecular cloning of chick cadherin 11 and its expression during
 CC RT smooth muscle differentiation and formation of the tunica media.";
 CC RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: AF053342; AAC3675.1; -.
 CC DR HESP; P09803; 117W.
 CC DR InterPro: IPR002126; Cadherin.
 CC DR InterPro: IPR000233; Cadherin_C_term.
 CC DR Pfam: PF00028; Cadherin_5.
 CC DR Pfam: PF01049; Cadherin_C_1.
 CC DR PRINTS: PR00205; CADHERIN.
 CC DR SMART: SM00112; CA; 5.
 CC DR PROSITE: PS00232; CADHERIN 1; 3.
 CC DR PROSITE: PS0268; CADHERIN 2; 5.
 CC DR Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 CC KW Transmembrane.
 CC FT SIGNAL 1 22
 CC FT PROPEP 23 53 potential.
 CC FT CHAIN 54 792 Cadherin-11.
 CC FT DOMAIN 54 613 Extracellular (Potential).
 CC FT TRANSMEM 614 634 Cytoplasmic (Potential).
 CC FT DOMAIN 635 792
 CC FT DOMAIN 54 159 Cadherin 1.
 CC FT DOMAIN 160 268 Cadherin 2.
 CC FT DOMAIN 269 383 Cadherin 3.
 CC FT DOMAIN 384 486 Cadherin 4.
 CC FT DOMAIN 487 608 Cadherin 5.
 CC FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
 CC FT CARBOHYD 536 536 N-linked (GlcNAc...) (Potential).
 CC FT CARBOHYD 594 594 N-linked (GlcNAc...) (Potential).
 CC FT SEQUENCE 792 AA; 87572 MW; 3B3486C6866731AB CRC64;
 Query Match 46.5%; Score 1558; DB 1; Length 792;
 Best Local Similarity 55.0%; Pred. No. 2,1e-88;
 Matches 296; Conservative 86; Mismatches 116; Indels 40; Gaps 2;
 QY 36 GPALLRTRRSWVWVNOQFVIEEYAGPEPVILGKLSVDVDRGGRKTKYLLTGEGATVVID 95
 DB 45 GQVLRHSKRGVWVNOQFVIEEYTPDPVLVGRHSVDVSGDWKIKYLLSGGATITVID 104
 QY 96 EATGNHVTKSLDREKKAQVYLLAQAVDRASNRPLEPSEETIKGODINDNPPIFFLPY 155
 DB 105 DKSNGHAKTKLDRERKQYTLMAQVDRETNKELEPSEETIVKQDINDNPPEFLHENY 164
 QY 156 HATVPENSVNGTSVYQVTAHDADDPBSYNSAKLYTVLDGLPFRSVDPQGVVTAIPNM 215
 DB 165 HANVPENSVNGTSVYQVTAHDADDPBSYNSAKLYTVLDGLPFRSVDPQGVVTAIPNM 224
 QY 216 DRETQEEFLVVIQAKDMGGMGSLSGSTTVTVLSDVNDNPKPKPQSLYQSVVETAGPG 275
 DB 225 DRAKEEYHVVVIOAKDMGGMGSLSGSTTKVITLTDVNDNPKPKPQSLYQSVVETAGPG 284

QY 276 TLVGRRAQDPDLDGNALMAYSIIDGSGSEAFSISTDLQQRDGLTLVRKPLDFESQSRYS 335
 DB 285 EGVGVKXAKDPDIDENGLVAYSIIDGDMFELTTDYETQEGVVKLKLDEETKXYS 344
 QY 336 FRVETWTLIDPAVLRGPFCDVASVRVADAPPEPPAQAHLVLPENKAPGLTYGQ 395
 DB 345 LKVERANVHIDPKXISNGPFCDTYKITYVEDADEPVPFLKPSITFEVQNAASGTVGK 404
 QY 396 ISAADLDSAPSPIRYSILPHSDPERCSIOPEEGTITTAAPLDREARAWNLTVLATELG 455
 DB 405 VHAQDPDANSAIRYSIDRHDTLERYFTINADGNIKTIKALBREETAMNISVPAVEV- 463
 QY 456 WSWPGRGVWPLVLAEMSAPAAPQSRPVSAGVIRPDDSSAQSRVQVATQITDENMDAP 515
 DB 464 -----HKQHQEKVPAIKVADVNDNA 486
 QY 516 QLAPEYDTFVCDSPAGQLICVIRALPDREVGSSHSVFOGP--LGPANFTVQDRD 571
 DB 487 KFAAAYEAFAVCENARNSQGFITISADKXDSANGPRIFLPPRIINPRFSLRDRD 544
 RESULT 11
 Q8C449 PRELIMINARY; PRT; 716 AA.
 ID Q8C449;
 AC Q8C449;
 DT 01-MAR-2003 (Tremblrel. 23. Created)
 DT 01-MAR-2003 (Tremblrel. 23. Last sequence update)
 DT 01-OCT-2004 (Tremblrel. 28. Last annotation update)
 DE Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched
 DE library, clone:6530002D14 product:cadherin 8, full insert sequence
 DE (Cdh8 protein).
 GN Name=Cdh8;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High efficiency full-length cDNA cloning";
 RL Mech. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA The FANTOM Consortium;
 RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA Adachi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashitume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kaigawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohashi N., Okazaki Y.,
 RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RT Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Klausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.W., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heif F.,
 RA Datchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,
 RA Krzywinski M.I., Skalske U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RA Strausberg R.;
 RT Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 DR EMBL, AK083092; BAC38758.1; -;
 DR EMBL, BC057581; AAH57581.1; -;
 DR HSSP, P15116; INCT.
 DR MGD, MGI:107434; Cdh8.
 DR GO, GO:0016020; C:membrane; IEA.
 DR GO, GO:0005509; P:calcium ion binding; IEA.
 DR GO, GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro, IPR002126; Cadherin.
 DR InterPro, IPR00233; Cadherin_C term.
 DR Pfam, PF00028; Cadherin_5.
 DR Pfam, PF01049; Cadherin_C_1.
 DR PRINTS, PR00205; CADHERIN.
 DR PROSITE, PS00232; CADHERIN.
 DR PROSITE, PS0268; CADHERIN_2; 5.
 DR Calcutin, Calcium-binding; Cell adhesion; Transmembrane.
 KW SEQUENCE 716 AA; 79145 MW; 976FSPD845P938BD CRC64;
 Query Match 45.8%; Score 1536.5; DB 2; Length 716;

Best Local Similarity 48.1%, Pred. No. 4e-87;
Matches 301; Conservative 109; Mismatches 135; Indels 81; Gaps 9;

QY 39 LLRTSRWVWVNFVIEEYAGEPEVILIGKLSHDVDRGEGRTKYLITGEGATVFIIDENAT 98
DB 56 LSRSGKGVWVWVNFVIEEYAGEPEVILIGKLSHDVDRGEGRTKYLITGEGATVFIIDENAT 115
QY 99 GNHYTKSLDREKAKQVYLLAQAVDASNRPLEPSEFIIKQDINDNPFPPLGPYHAT 158
DB 116 GDHAKRLDREKAEVYLLAQAVDASNRPLEPSEFIIKQDINDNPFPPLGPYHAT 175
QY 159 VPMSNVGTSVIQTATADADPSYNSAKLYVTLGDLPPFSVPDQTVATAPNDRE 218
DB 176 VPMSILGTSTVNTATADADPSYNSAKLYVTLGDLPPFSVPDQTVATAPNDRE 235
QY 219 TQSEFLVVIQAKMGHMGSLGSGTIVTLLSDVNDNPKPQSLYQFSVETAGPGLV 278
DB 236 AKSEYLVVVIQAKMGHMGSLGSGTIVTLLSDVNDNPKPQSLYQFSVETAGPGLV 295
QY 279 GRLLAQDPLGDMNLMAYSILDGSGSEAFSITDLOGRDGLTVRKPLDFESQSYSPRY 338
DB 296 GRVKNDDQIGENAGSYDIIIDGDTALFEITSDAQDGVIRKRPDLDFETKSYTLKV 355
QY 339 EATNTLIDPAYLRGPFQDVASVAVAVQDAPEPAFTQAAHYLTVPENKAPGLVQGIS 398
DB 356 EAAHIDHIDPRFSRGPFDOTATVKIVEDADEPVPFSPTVLLVHENAALNSVIGQVTA 415
QY 399 ADLDSAPPIRYSILPHSDPERCESIOPEEGTHTAAPLDREBARAHNLTVALTELGWSM 458
DB 416 RDPDITSSPFRSIDRHTDLERQFINADGKITLAPLDRELSVWHNTITIAIEI 471
QY 459 GPERGWVPLVAEWSAPAPQPSVGSAGVIFODSSAQSRYOVAIQTLDENDAPOLA 518
DB 472 -----RHSQISRPVPAIKVLDVNDAPDEFA 497
QY 519 EPYDTFVCDASAPGQILQVIRALDRDEVGNSSHVSFOGFLGPD-----ANFTVQDNRD 571
DB 498 SEYEAFICENKGFQGVITQVSAKMDPKNGHF--FLYSLLPEWVNNPFIKKEDNSL 555
QY 572 -----LPAWFPPLMASASWLMHPPARGNQPSAQKSSSL-PCG-RLPGA 616
DB 556 SILAKHNGFRKQKQEVYLLPIVI-----SDSGNPPLSSTITLIRVCGCSDGV 604
QY 617 LPSCQ-----LPLGI--PALGIYLC 634
DB 605 VQSCNVEAYVLPILGSMGALIIAIIAC 630

RESULT 12
AAH57581 PRELIMINARY; PRT; 716 AA.

ID AAH57581; TISSUE=Brain;
AC AAH57581; PubMed=12477932;
RX MEDLINE=22388257; PubMed=12477932;
RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klavener R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buecaw K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wang S.I., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Mullany S.J.,
RA Raha S.S., Loguailano N.A., Peters G.J., Abramson R.D., Pringle S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maier M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Struhsberg R.,
RL Submitted (SEP-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC057581; AAH57581.1;
SQ SEQUENCE 716 AA; 79145 MW; 976FF5D845F938BD CRC64;

Query Match 45.8%; Score 1536.5; DB 2; Length 716;

Best Local Similarity 48.1%, Pred. No. 4e-87;
Matches 301; Conservative 109; Mismatches 135; Indels 81; Gaps 9;

QY 39 LLRTSRWVWVNFVIEEYAGEPEVILIGKLSHDVDRGEGRTKYLITGEGATVFIIDENAT 98
DB 56 LSRSGKGVWVWVNFVIEEYAGEPEVILIGKLSHDVDRGEGRTKYLITGEGATVFIIDENAT 115
QY 99 GNHYTKSLDREKAKQVYLLAQAVDASNRPLEPSEFIIKQDINDNPFPPLGPYHAT 158
DB 116 GDHAKRLDREKAEVYLLAQAVDASNRPLEPSEFIIKQDINDNPFPPLGPYHAT 175
QY 159 VPMSNVGTSVIQTATADADPSYNSAKLYVTLGDLPPFSVPDQTVATAPNDRE 218
DB 176 VPMSILGTSTVNTATADADPSYNSAKLYVTLGDLPPFSVPDQTVATAPNDRE 235
QY 219 TQSEFLVVIQAKMGHMGSLGSGTIVTLLSDVNDNPKPQSLYQFSVETAGPGLV 278
DB 236 AKSEYLVVVIQAKMGHMGSLGSGTIVTLLSDVNDNPKPQSLYQFSVETAGPGLV 295
QY 279 GRLLAQDPLGDMNLMAYSILDGSGSEAFSITDLOGRDGLTVRKPLDFESQSYSPRY 338
DB 296 GRVKNDDQIGENAGSYDIIIDGDTALFEITSDAQDGVIRKRPDLDFETKSYTLKV 355
QY 339 EATNTLIDPAYLRGPFQDVASVAVAVQDAPEPAFTQAAHYLTVPENKAPGLVQGIS 398
DB 356 EAAHIDHIDPRFSRGPFDOTATVKIVEDADEPVPFSPTVLLVHENAALNSVIGQVTA 415
QY 399 ADLDSAPPIRYSILPHSDPERCESIOPEEGTHTAAPLDREBARAHNLTVALTELGWSM 458
DB 416 RDPDITSSPFRSIDRHTDLERQFINADGKITLAPLDRELSVWHNTITIAIEI 471
QY 459 GPERGWVPLVAEWSAPAPQPSVGSAGVIFODSSAQSRYOVAIQTLDENDAPOLA 518
DB 472 -----RHSQISRPVPAIKVLDVNDAPDEFA 497
QY 519 EPYDTFVCDASAPGQILQVIRALDRDEVGNSSHVSFOGFLGPD-----ANFTVQDNRD 571
DB 498 SEYEAFICENKGFQGVITQVSAKMDPKNGHF--FLYSLLPEWVNNPFIKKEDNSL 555
QY 572 -----LPAWFPPLMASASWLMHPPARGNQPSAQKSSSL-PCG-RLPGA 616
DB 556 SILAKHNGFRKQKQEVYLLPIVI-----SDSGNPPLSSTITLIRVCGCSDGV 604
QY 617 LPSCQ-----LPLGI--PALGIYLC 634
DB 605 VQSCNVEAYVLPILGSMGALIIAIIAC 630

RESULT 13
CADD_HUMAN STANDARD; PRT; 799 AA.
ID CADD_HUMAN
AC P55286; Q9UBB2;
DT 01-OCT-1996 (Rel. 34, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-8 precursor.
 CN Name=CDH8;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=10861224;
 RA Shimoyama Y., Teujimoto G., Kitaajima M., Natori M.;
 RT "Identification of three human type-II classic cadherins and frequent heterophilic interactions between different subclasses of type-II classic cadherins.";
 RL Biochem. J. 349:159-167 (2000).
 RN [2]
 RP SEQUENCE OF 7-799 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95073006; PubMed=7982033;
 RA Tanihara H., Sano K., Helmark R.L., St John T., Suzuki S.;
 RT "Cloning of five human cadherins clarifies characteristic features of cadherin extracellular domain and provides further evidence for two structurally different types of cadherin.";
 RL Cell Adhes. Commun. 2:15-26 (1994).
 RN [3]
 RP SEQUENCE OF 294-799 FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=91283540; PubMed=2059659;
 RA Suzuki S., Sano K., Tanihara H.;
 RT "Diversity of the cadherin family: evidence for eight new cadherins in nervous tissue.";
 RL Regul. 2:261-270 (1991).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins. They preferentially interact with themselves in a homophilic manner in connecting cells; cadherins may thus contribute to the sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Mainly expressed in brain. Found in certain nerve cell lines, such as retinoblasts, glioma cells and neuroblasts.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB035305; BA87419.1; -
 DR EMBL; U34060; AAA35628.1; ALT_INT.
 DR HSSP; P09803; 117W.
 DR Genew; HGNC:1767; CDH8.
 DR MIM; 603008; -
 DR GO; GO:0007155; P:cell adhesion; TAS.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin_C; 1.
 DR PRINTS; PR0205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00233; CADHERIN_1; 3.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 KW Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal; Transmembrane.
 KM TISSUE=Brain.
 FT SIGNAL 1 29 Potential.
 FT PROPEP 30 61 Potential.
 FT CHAIN 62 621 Cadherin-8.
 FT DOMAIN 62 621 Extracellular (Potential).
 FT TRANSEM 622 642 Potential.
 FT DOMAIN 643 799 Cytoplasmic (Potential).

FT DOMAIN 62 167 Cadherin 1.
 FT DOMAIN 168 276 Cadherin 2.
 FT DOMAIN 277 391 Cadherin 3.
 FT DOMAIN 392 494 Cadherin 4.
 FT DOMAIN 495 616 Cadherin 5.
 FT CARBOHYD 33 33 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 57 57 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 188 188 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 473 473 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 544 544 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 355 355 V -> D (in Ref. 2 and 3).
 FT CONFLICT 647 647 H -> HQ (in Ref. 2 and 3).
 SQ SEQUENCE 799 AA; 88253 MM; 9811986039C6A0A CRC64;
 Query Match 45.8%; Score 1536.5; DB 1; Length 799;
 Best Local Similarity 47.9%; Pred. No. 4.6e-87;
 Matches 300; Conservative 111; Mismatches 194; Indels 81; Gaps 9;
 QY 39 ILRTRRSVWVWVQPFVIEBYAGPEPVYIGKLSVDVDSRGRTKYLITGEGATVFVIDEAT 98
 DB 56 LNRKRGVWVWVQPFVIEBYAGPEPVYIGKLSVDVDSRGRTKYLITGEGATVFVIDEAT 115
 QY 99 GNHHTKSLDPEERKQVYLAQAVDPRASNRLEPPESEITKGODINNPPIFPGPHAT 158
 DB 116 GDHAIKRLDREERKAEVYLAQAVDPRASNRLEPPESEITKGODINNPPIFPGPHAT 175
 QY 159 VPEMSVGTSVIQTADHDADDPYSGNSAKLYVTYLDGLPFSVPQGTAVRTAIPNDRE 218
 DB 176 VPEMSIGLSTVNTVATDADDPYSGNSAKLYVTYLDGLPFSVPQGTAVRTAIPNDRE 235
 QY 219 TOEPLVYIQAQKNGHNGGLSSSTVYVTLSDVNDNPPKPPQSLYQPSVETKPGETLV 278
 DB 236 AKEEVLVYIQAQKNGHNGGLSSSTVYVTLSDVNDNPPKPPQSLYQPSVETKPGETLV 295
 QY 279 GLRQADPDLDNLMAYSLIDGEGSEAFSTDLQGRDGLTVRKPLDFESQSYGFRV 338
 DB 296 GRVANDPDIDENNAQSYDIIIDGGTALFELTSQAQDGIIRKRLDDETKSYLKV 355
 QY 339 EATNTLIDPAYLRGPFQDVASVRVAVODAPPAFTQAAVHLTVENKAPGLVGOISA 398
 DB 356 EAAVNHIDPRFGSGPFQDTATVKIWEDEDPVFSPLYLLEHENAALNSVIGQVTA 415
 QY 399 ADLSPASPIRYSILPHSDPERCSIQPEESTITTAPLDREARAWNTLVLAETELGMSW 458
 DB 416 RDPDTSSPIRYSILPHSDPERCSIQPEESTITTAPLDREARAWNTLVLAETELGMSW 471
 QY 459 GPERGWVPLVAEWSAPAPAPQSPVSAVGIPODSSAQASRVQVAIQTIDENDAPOLA 518
 DB 472 -----RNHSQISRVVAIKVLDVNDNADEFA 497
 QY 519 EPIYDFVCDAAAPQGLIQTIVATLDRDEVGNSHVSFOGPIGPD-----ANFVQDNRD--- 571
 DB 498 SEYEFPLCENGRPQVQIVTASAMKDDPKRGHY--FYSLPDEVVNNPNFPIKKNEDNSL 555
 QY 572 -----LPAMFPLMASASSWILMPAERGNOPASQKSSSL-PCG-RUPGA 616
 DB 556 SIANKHGNFKQKQEVILPILI-----SDSGNPPLSTSLTLTRVCGCSNDGV 604
 QY 617 LPSCQ-----LPGLI---PALGIYLC 634
 DB 605 VQSCNVEAVYVPLIGLSWGLAIYAIAC 630
 RESULT 14
 QY Q8BRK4 PRELIMINARY; PRT; 754 AA.
 AC Q8BRK4;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830083f13 product:cadherin 8, full insert

sequence.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RX MEDLINE=99279253; PubMed=10349366;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 403:685-690(2001).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RA The FANTOM Consortium,
 RT the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Katsuna T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RA Adachi T., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Futuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kachi H., Kawati Y., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura Y.,
 RA Nihei K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Saeki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL; AK044046; BAC31751.1; -.
 DR HSP; F51516; INCU.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:000509; F:calcium ion binding; IEA.

DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF000233; Cadherin_C_term.
 DR Pfam; PF00028; Cadherin_5.
 DR Pfam; PF01049; Cadherin_C_1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SW00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 KW Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 754 AA; 89624 MW; 149C3C70D3F21568 CRC64;
 Query Match 45.7%; Score 1532.5; DB 2; Length 754;
 Best Local Similarity 47.9%; Pred. No. 7.6e-87;
 Matches 300; Conservative 110; Mismatches 135; Indels 81; Gaps 9;
 QY 39 LILRRSWTWNQPFVIEEYAGPEPVILGKLSVDVDRGSEGRKYLLTGEGAGTVFYDEAT 98
 Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 115
 56 LSRKRGWYWNQPFVIEEYAGPEPVILGKLSVDVDRGSEGRKYLLTGEGAGTVFYDEAT 115
 QY 99 GNHVTYSLDREKQAVLLAQVDRASNPLEPSEFTIKQDINDNPITPLGPHAT 158
 Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 175
 116 GDTHAKRLDREKQAVYLLAQVDRASNPLEPSEFTIKQDINDNPITPLGPHAT 175
 QY 159 VPEMSVWGSVYQVTHADDDPSYNSAKLVYTVLDGLPEFVDPQGVYVTAIPYMDSE 218
 Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 235
 176 VPEMSVWGSVYQVTHADDDPSYNSAKLVYTVLDGLPEFVDPQGVYVTAIPYMDSE 235
 QY 219 TOEPLVVIQAKMGMGGLSGSTVTVTLSDVNDNPKPPOSIVQSFVETAGPILV 278
 Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 295
 236 AKSEYLVVIAQKMGHSGSLGTTTLTVLTDVNDNPKPPOSIVQSFVETAGPILV 295
 QY 279 GRIRADDPDLGNALMAYSLIDEGSEASISTDLOGRGGLTVKRPDLFESQSRISFV 338
 Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 355
 296 GRVAKDDQIGENAGSSYDIDGGTALFEITSDAQAGVIRLRKPLDFETKSYTLV 355
 QY 339 EATNTLIDAVYLRGCFKDVASVAVVADAPPEPAFTCAHYLTVENKAPGTLVQISA 398
 Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 415
 356 EANNITIDRFSSRGFKTATYKIVYEDADEPVPVSSSTYLLVHEMNAALSVIQVYA 415
 QY 399 ADIDSPASPIRYSILHSPERCFSTQPEEGTHTAPLDRAPAMHNTVLTATELGSW 458
 Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 471
 416 RDEDITSSIRFSDHTLDEROFINADGGKITLATPDRSLSVNHTITITATEL---- 471
 QY 459 GPERGWVPLLVAKMSAPAPRQSPVGSVAGIPDSSAASVQVAYIQLDENDNAPOLA 518
 Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 535
 472 -----RHSQISKVPVPAIKVLVDNDNAPOLA 535
 QY 519 EPHYTVCDASAPGQLIQVIRALDRDEVGNSSHVSFOGLPDP-----ANFTVQDND 571
 Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 588
 498 SEYEAFLENGKRGVITVSAMDKDPKNGHF--FLYSLLEPMVNNPFTIKKNDNL 588
 QY 572 -----LPMHPLMASASSWLHPPAERGQNPASQGSSSL-FCG-RLPRA 616
 Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 633
 556 SIIAKENGNNRQKQEVLLPIVY-----SDSGNPVUSSTITLTVRGCGSNDGV 604
 QY 617 LPSCQ-----LPLGI--PALGIIVLC 634
 Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 651
 605 VQSCNVEAVYPLIGLSMGLINILAC 630
 RESULT 15
 CAD8 RAT STANDARD; PRT; 799 AA.
 ID CAD8 RAT
 AC 054800; 054801;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-8 precursor.
 GN Name=Cdh8;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCB1_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain;
RX MEDLINE=98190518; PubMed=3521872;
RA Kido M., Obata S., Tanihara H., Rochelle J.M., Seldin M.F.,
RT Taketani S., Suzuki S.T.;
RL "Molecular properties and chromosomal location of cadherin-8.";
CC Genomics 48:186-194(1998).
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O54800-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O54800-2; Sequence=VSP_000638, VSP_000639;
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
CC or send an email to license@ebi.ac.uk).
CC -----
CC DR EMBL; AB010436; BAA24452.1; -;
CC EMBL; AB010437; BAA24453.1; -;
CC HSSP; P09803; 117W.
DR RGD; 69286; Cdh8.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR002333; Cadherin_C_term.
DR Pfam; PF00028; Cadherin_5.
DR Pfam; PF01049; Cadherin_C_1.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA_5.
DR PROSITE; PS00232; CADHERIN_1; 3.
DR PROSITE; PS0268; CADHERIN_2; 5.
KW Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 61 Cadherin-8.
FT CHAIN 62 799 Extracellular (Potential).
FT DOMAIN 62 621 Potential.
FT TRANSMEM 622 642 Cytoplasmic (Potential).
FT DOMAIN 643 799 Potential.
FT DOMAIN 168 167 Cadherin 1.
FT DOMAIN 168 276 Cadherin 2.
FT DOMAIN 277 391 Cadherin 3.
FT DOMAIN 392 494 Cadherin 4.
FT DOMAIN 495 616 Cadherin 5.
FT CARBOHYD 188 188 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 473 473 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 544 544 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 514 532 IGVASAMDDDPKXGHFL -> NISMLILNFFVNCFLV
FT N (in isoform 2).
FT FTId=VSP_000638.
FT VARSPLIC 533 799 Missing (in isoform 2).
FT FTId=VSP_000639.
SQ SEQUENCE 799 AA; 88332 MW; F01D145A80966CB6 CRC64;
Query March 45.6%; Score 1530.5; DB 1; Length 799;
Best Local Similarity 47.9%; Pred. No. 1.1e-86;
Matches 300; Conservative 110; Mismatches 135; Indels 81; Gaps 9;
QY 39 LRTTRSVWVWQFVIEBAPPEVLIGKLSVDVREGGRTKYLITGEGAGTVFVIDEAT 98
DB 56 LNRKRGVWVWQFVIEBAPPEVLIGKLSVDVREGGRTKYLITGEGAGTVFVIDEAT 98
115

QY 99 GNHYTKSLDREKAQVYLLAQAADVDRASNRPLEPSEFIIKGQDINDNPPIPLPGYHAT 158
DB 116 GDHAIKRLDREKAEVYLLTAQAVDMETNKLPEPSEFIIKVGQDINDNPPIPLPGYHAT 175
QY 159 VPENANVTSTVQTAAHADDPVGNKAKLYVTYLDGPFPSVDPQGVARTALPNMDRE 218
DB 176 VPENMILSTVNTVNTADDPVGNKAKLYVSLLEGQVPSIPEFTALITLALPNMDRE 235
QY 219 TQEEFLVYIQAQDMGSHGSGSTTVTVTLSDVNDNPPKPSQSLYQSVVETAGPGLV 278
DB 226 AKBEVLVYIQAQDMGSHGSGSTTVTVTLSDVNDNPPKPSQSLYQSVVETAGPGLV 295
QY 279 GRLAQPDPDGNALMAVSIIDGESSEAFSISTDLQGRDGLITRKPLDEPQSQSYSPRV 338
DB 296 GVKAKNDQDIENMAOSSYDIIDGGTALFEITSDAQADGVITRKPLDEPQSYSPRV 355
QY 339 EATNTLIDPAYLRGPFQDVASVRVAVODAPPEPAFTQAAVHLYTPENKAPGTLVGOISA 398
DB 356 EATNTLIDPAYLRGPFQDVASVRVAVODAPPEPAFTQAAVHLYTPENKAPGTLVGOISA 415
QY 399 ADLSPASPIRYSIIPHSDFPCTSIQPEBGTHTAPLDRERAMHNLVTLATELQSW 458
DB 416 RPPDITSSPIRFSIDRHTDLEROFNINADDDKITLAPLDELSTVWHNISITATEI 471
QY 459 GPERGVPLVLAEMSAAPAPQRPVGSVAVGIPDDSSAQASRYOVAIQTLDENAPOLA 518
DB 472 -----RHSQISRVVYALKVDVNDNAPERA 497
QY 519 EBYDTFVDSAPAGQLIGVIRALDRDEVGNSSHVSFOGFLGPD-----ANFTVQDNR 571
DB 498 SEYEAFLCENKPGQVITVASAMDKDPKGNH--FLYSLLPEWNNPNFTIKKQNDNL 555
QY 572 -----LPAMFHPILMASASSMHWPAAERGNQPAQSGKSSSL-PCG-RLPGA 616
DB 556 SLIAGHGFNNQKQEVYLLPIVI-----SDSGNPPLSSTLTITIKVCGCSNDGV 604
QY 617 LPSCQ-----PLGI---PALGIYLC 634
DB 605 VQSCNVEPVYPIGSMGALTAIILAC 630

Search completed: December 8, 2004, 10:24:33
Job time : 257.926 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 10:13:18 ; Search time 649.891 Seconds
(without alignments)
349.544 Million cell updates/sec

Title: US-09-788-051-4
Perfect score: 3354
Sequence: 1 MNGIVRLILAWIGWGMGR.....LPSCQLPLGIPALGIVLCAS 636

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3354	100.0	636	US-09-788-051-4	Sequence 4, App1
2	3259	97.2	620	US-09-788-051-7	Sequence 7, App1
3	2746.5	81.9	781	US-09-860-868-2	Sequence 2, App1
4	2746.5	81.9	781	US-10-245-752-98	Sequence 98, App1
5	2746.5	81.9	781	US-10-245-859-98	Sequence 98, App1
6	2746.5	81.9	781	US-10-245-103-98	Sequence 98, App1
7	2746.5	81.9	781	US-10-245-107-98	Sequence 98, App1
8	2746.5	81.9	781	US-10-245-143-98	Sequence 98, App1
9	2746.5	81.9	781	US-10-245-771-98	Sequence 98, App1
10	2746.5	81.9	781	US-10-245-851-98	Sequence 98, App1
11	2746.5	81.9	781	US-10-245-883-98	Sequence 98, App1
12	2746.5	81.9	781	US-10-237-535-98	Sequence 98, App1
13	2746.5	81.9	781	US-10-238-163-98	Sequence 98, App1

14	2746.5	81.9	781	US-10-238-283-98	Sequence 98, App1
15	2746.5	81.9	781	US-10-238-370-98	Sequence 98, App1
16	2746.5	81.9	781	US-10-245-055-98	Sequence 98, App1
17	2746.5	81.9	781	US-10-245-147-98	Sequence 98, App1
18	2746.5	81.9	781	US-10-245-730-98	Sequence 98, App1
19	2746.5	81.9	781	US-10-245-739-98	Sequence 98, App1
20	2746.5	81.9	781	US-10-246-210-98	Sequence 98, App1
21	2746.5	81.9	781	US-10-239-196-98	Sequence 98, App1
22	2746.5	81.9	781	US-10-243-024-98	Sequence 98, App1
23	2746.5	81.9	781	US-10-243-409-98	Sequence 98, App1
24	2746.5	81.9	781	US-10-245-621-98	Sequence 98, App1
25	2746.5	81.9	781	US-10-245-880-98	Sequence 98, App1
26	2746.5	81.9	781	US-10-245-033-98	Sequence 98, App1
27	2746.5	81.9	781	US-10-243-095-98	Sequence 98, App1
28	2746.5	81.9	781	US-10-245-185-98	Sequence 98, App1
29	2746.5	81.9	781	US-10-245-427-98	Sequence 98, App1
30	2746.5	81.9	781	US-10-245-473-98	Sequence 98, App1
31	2746.5	81.9	781	US-10-245-770-98	Sequence 98, App1
32	2746.5	81.9	781	US-10-245-877-98	Sequence 98, App1
33	2746.5	81.9	781	US-10-246-976-98	Sequence 98, App1
34	2746.5	81.9	781	US-10-243-320-98	Sequence 98, App1
35	2746.5	81.9	781	US-10-162-435-13	Sequence 13, App1
36	2746.5	81.9	781	US-10-242-743-98	Sequence 98, App1
37	2746.5	81.9	781	US-10-242-845-98	Sequence 98, App1
38	2746.5	81.9	781	US-10-237-636-98	Sequence 98, App1
39	2746.5	81.9	781	US-10-238-345-98	Sequence 98, App1
40	2746.5	81.9	781	US-10-238-346-98	Sequence 98, App1
41	2746.5	81.9	781	US-10-238-411-98	Sequence 98, App1
42	2746.5	81.9	781	US-10-243-124-98	Sequence 98, App1
43	2746.5	81.9	781	US-10-243-425-98	Sequence 98, App1
44	2746.5	81.9	781	US-10-243-446-98	Sequence 98, App1
45	2746.5	81.9	781	US-10-245-874-98	Sequence 98, App1

ALIGNMENTS

RESULT 1
US-09-788-051-4
Sequence 4, Application US/09788051
Publication No. US2003014491A1
GENERAL INFORMATION:
APPLICANT: Codbole, Shubhada D
APPLICANT: Kuo, Chiaoyun
APPLICANT: Atterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Dymarc, Rodolfe T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES A
FILE REFERENCE: HYS-39
CURRENT APPLICATION NUMBER: US/09/788,051
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 636
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-4
Query Match 100.0%; Score 3354; DB 10; Length 636;
Best Local Similarity 100.0%; Pred. No. 9.1e-242;
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGIVRLILAWIGWGMGRILAPARAMGRHRHPPALLRTSRVWVWVFFIEEYAGP 60

```

Db      1  MMGLVRLLLAMLGCMGCKRLAARAMASREHPGALLTRRSWNNQPFVIEEYACG 60
Qy      61  EPLVIGKLHSVDNREGRTKLLTGEAGTVFIDEATGNIHVTKSLDREKAQYVLLAQ 120
Db      61  EPLVIGKLHSVDNREGRTKLLTGEAGTVFIDEATGNIHVTKSLDREKAQYVLLAQ 120
Qy      121  AVDRASNRPLEPSEFFIKGQDINDNPIFPLGPHATVPEMSVNGSVIQTVAHDDDP 180
Db      121  AVDRASNRPLEPSEFFIKGQDINDNPIFPLGPHATVPEMSVNGSVIQTVAHDDDP 180
Qy      181  SYGNSAKLVTVLDGLPEFSDPQGVYRTAIPMDRETOEELVVIQAADMGGHMGSL 240
Db      181  SYGNSAKLVTVLDGLPEFSDPQGVYRTAIPMDRETOEELVVIQAADMGGHMGSL 240
Qy      241  GSTTATLSDVNNPPKFPQSLYQFSVETAGGTLVGRRAQDPLGDMALMAYSIID 300
Db      241  GSTTATLSDVNNPPKFPQSLYQFSVETAGGTLVGRRAQDPLGDMALMAYSIID 300
Qy      301  GEGSEAFSISTDLQGRDGLTVRKPLDPEQSRYSFVEATNTLIDPAYLRGPFQVVS 360
Db      301  GEGSEAFSISTDLQGRDGLTVRKPLDPEQSRYSFVEATNTLIDPAYLRGPFQVVS 360
Qy      361  VRVAVQADAPPPATQAAYHITVBNKAPGTLVQISADLDSBPASIRYSILPHSDPER 420
Db      361  VRVAVQADAPPPATQAAYHITVBNKAPGTLVQISADLDSBPASIRYSILPHSDPER 420
Qy      421  CFSIQPEEGTHTAAPPDREARAHNTLVATELGWNGPERGVPLTVEMGAPAPAPQ 480
Db      421  CFSIQPEEGTHTAAPPDREARAHNTLVATELGWNGPERGVPLTVEMGAPAPAPQ 480
Qy      481  RSPVGAAGTIPQSSAASRVQVAIQTLDENNDAPQLAEPYDTFVCDSPAAPQGLIYIRA 540
Db      481  RSPVGAAGTIPQSSAASRVQVAIQTLDENNDAPQLAEPYDTFVCDSPAAPQGLIYIRA 540
Qy      541  LDRREVGNSSHVSPQGLPGDANFTVQDNNDLPAMFHPILMASASSMLHPPAERGNQPA 600
Db      541  LDRREVGNSSHVSPQGLPGDANFTVQDNNDLPAMFHPILMASASSMLHPPAERGNQPA 600
Qy      601  SQGKSSLPQGRPLPGALPSCQLPLGIPALGIVLCAS 636
Db      601  SQGKSSLPQGRPLPGALPSCQLPLGIPALGIVLCAS 636

```

RESULT 2

```

US-09-788-051-7
; Sequence 7, Application US/09788051
; Publication No. US20030144491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Atterburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dmanac, Radoje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN
; FILE REFERENCE: HVS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 620
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-788-051-7

```

```

Query Match      97.2%; Score 3259; DB 10; Length 620;
Best Local Similarity 100.0%; Pred. No. 1,1e-234;
Matches 620; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      17  CMGRLAAPARAMASREHPGALLTRRSWNNQPFVIEEYAGEPVLIGLHSDVDNREG 76
Db      1  CMGRLAAPARAMASREHPGALLTRRSWNNQPFVIEEYAGEPVLIGLHSDVDNREG 60
Qy      61  EPLVIGKLHSVDNREGRTKLLTGEAGTVFIDEATGNIHVTKSLDREKAQYVLLAQ 120
Db      61  EPLVIGKLHSVDNREGRTKLLTGEAGTVFIDEATGNIHVTKSLDREKAQYVLLAQ 120
Qy      121  AVDRASNRPLEPSEFFIKGQDINDNPIFPLGPHATVPEMSVNGSVIQTVAHDDDP 180
Db      121  AVDRASNRPLEPSEFFIKGQDINDNPIFPLGPHATVPEMSVNGSVIQTVAHDDDP 180
Qy      181  SYGNSAKLVTVLDGLPEFSDPQGVYRTAIPMDRETOEELVVIQAADMGGHMGSL 240
Db      181  SYGNSAKLVTVLDGLPEFSDPQGVYRTAIPMDRETOEELVVIQAADMGGHMGSL 240
Qy      241  GSTTATLSDVNNPPKFPQSLYQFSVETAGGTLVGRRAQDPLGDMALMAYSIID 300
Db      241  GSTTATLSDVNNPPKFPQSLYQFSVETAGGTLVGRRAQDPLGDMALMAYSIID 300
Qy      301  GEGSEAFSISTDLQGRDGLTVRKPLDPEQSRYSFVEATNTLIDPAYLRGPFQVVS 360
Db      301  GEGSEAFSISTDLQGRDGLTVRKPLDPEQSRYSFVEATNTLIDPAYLRGPFQVVS 360
Qy      361  VRVAVQADAPPPATQAAYHITVBNKAPGTLVQISADLDSBPASIRYSILPHSDPER 420
Db      361  VRVAVQADAPPPATQAAYHITVBNKAPGTLVQISADLDSBPASIRYSILPHSDPER 420
Qy      421  CFSIQPEEGTHTAAPPDREARAHNTLVATELGWNGPERGVPLTVEMGAPAPAPQ 480
Db      421  CFSIQPEEGTHTAAPPDREARAHNTLVATELGWNGPERGVPLTVEMGAPAPAPQ 480
Qy      481  RSPVGAAGTIPQSSAASRVQVAIQTLDENNDAPQLAEPYDTFVCDSPAAPQGLIYIRA 540
Db      481  RSPVGAAGTIPQSSAASRVQVAIQTLDENNDAPQLAEPYDTFVCDSPAAPQGLIYIRA 540
Qy      541  LDRREVGNSSHVSPQGLPGDANFTVQDNNDLPAMFHPILMASASSMLHPPAERGNQPA 600
Db      541  LDRREVGNSSHVSPQGLPGDANFTVQDNNDLPAMFHPILMASASSMLHPPAERGNQPA 600
Qy      601  SQGKSSLPQGRPLPGALPSCQLPLGIPALGIVLCAS 636
Db      601  SQGKSSLPQGRPLPGALPSCQLPLGIPALGIVLCAS 636

```

RESULT 3

```

US-09-860-868-2
; Sequence 2, Application US/09860868
; Patent No. US20020076757A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A. J.
; TITLE OF INVENTION: MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-050001
; CURRENT APPLICATION NUMBER: US/09/860,868
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 60/205,674
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 781
; TYPE: PR
; ORGANISM: Homo Sapiens
US-09-860-868-2

Query Match      81.3%; Score 2746.5; DB 9; Length 781;
Best Local Similarity 84.8%; Pred. No. 3e-196;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

```

```

QY      1 MMGLVRLLLAMVIGSMGCMGRLLAAPARAWAGSRHEHGPALLTRRSWVMNQFVIEEYAGP 60
Db      1 MMGLVRLLLAMVIGSMGCMGRLLAAPARAWAGSRHEHGPALLTRRSWVMNQFVIEEYAGP 60
QY      61 EPLVIGKLSHSDVDGEGRTKYLITGEGAGTVFIDEATGNIHVTKSLDREKKAQYVLLAQ 120
Db      61 EPLVIGKLSHSDVDGEGRTKYLITGEGAGTVFIDEATGNIHVTKSLDREKKAQYVLLAQ 120
QY      121 AVDASNRPLEPPEEFIIKQDINDNPIFPLGPHATVPMMSVGTSVQVTAHADDP 180
Db      121 AVDASNRPLEPPEEFIIKQDINDNPIFPLGPHATVPMMSVGTSVQVTAHADDP 180
QY      181 SYGNSAKLVYTVLDGLPEFSVDPQTGVVRTAIPNMDRETOEEFLVVIQAKDMGGMGLS 240
Db      181 SYGNSAKLVYTVLDGLPEFSVDPQTGVVRTAIPNMDRETOEEFLVVIQAKDMGGMGLS 240
QY      241 GSTTVTVTLSDVNDNPKFPQSLYQFSVETAGPGLVGRRAODPDLDGNALMAYSLD 300
Db      241 GSTTVTVTLSDVNDNPKFPQSLYQFSVETAGPGLVGRRAODPDLDGNALMAYSLD 300
QY      301 GEGSEAFSISTDLQGRDGLTVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFKDVAS 360
Db      301 GEGSEAFSISTDLQGRDGLTVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFKDVAS 360
QY      361 VRVAVQADPEPPATQAAVHLTVPEKAPGTLVGCISADLDSASPIRYSILPHSDPER 420
Db      361 VRVAVQADPEPPATQAAVHLTVPEKAPGTLVGCISADLDSASPIRYSILPHSDPER 420
QY      421 CFSIQPEEGTHTAALDREARAHNLTVLATELGMSWGPGRGWPLVAEWSAPAAPQ 480
Db      421 CFSIQPEEGTHTAALDREARAHNLTVLATELGMSWGPGRGWPLVAEWSAPAAPQ 480
QY      481 RSPVGSAGVIGIPQDSSAQSARVQVAIQTLDENNDNAPQALAEPYDTFVCDSSAAGLIQVIRA 540
Db      481 RSPVGSAGVIGIPQDSSAQSARVQVAIQTLDENNDNAPQALAEPYDTFVCDSSAAGLIQVIRA 540
QY      541 LDRDEVGNSSHVSGQPLGPDANFTVQDNRD-----LPA-----WF 576
Db      541 LDRDEVGNSSHVSGQPLGPDANFTVQDNRD-----LPA-----WF 576
QY      577 HPLMASASWLH-----WPAERGNQASQG 603
Db      577 HPLMASASWLH-----WPAERGNQASQG 603

RESULT 4
US-10-245-752-98
; Sequence 98, Application US/10245752
; Publication No. US20030064473A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephen, Jean-Phillippe
; APPLICANT: Matembe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C66
; CURRENT FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046

```

```

; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-752-98

```

```

Query Match      81.9%; Score 2746.5; DB 14; Length 781;
Best Local Similarity 84.8%; Pred. No. 36-196;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

```

```

QY      1 MMGLVRLLLAMVIGSMGCMGRLLAAPARAWAGSRHEHGPALLTRRSWVMNQFVIEEYAGP 60
Db      1 MMGLVRLLLAMVIGSMGCMGRLLAAPARAWAGSRHEHGPALLTRRSWVMNQFVIEEYAGP 60
QY      61 EPLVIGKLSHSDVDGEGRTKYLITGEGAGTVFIDEATGNIHVTKSLDREKKAQYVLLAQ 120
Db      61 EPLVIGKLSHSDVDGEGRTKYLITGEGAGTVFIDEATGNIHVTKSLDREKKAQYVLLAQ 120
QY      121 AVDASNRPLEPPEEFIIKQDINDNPIFPLGPHATVPMMSVGTSVQVTAHADDP 180
Db      121 AVDASNRPLEPPEEFIIKQDINDNPIFPLGPHATVPMMSVGTSVQVTAHADDP 180
QY      181 SYGNSAKLVYTVLDGLPEFSVDPQTGVVRTAIPNMDRETOEEFLVVIQAKDMGGMGLS 240
Db      181 SYGNSAKLVYTVLDGLPEFSVDPQTGVVRTAIPNMDRETOEEFLVVIQAKDMGGMGLS 240
QY      241 GSTTVTVTLSDVNDNPKFPQSLYQFSVETAGPGLVGRRAODPDLDGNALMAYSLD 300
Db      241 GSTTVTVTLSDVNDNPKFPQSLYQFSVETAGPGLVGRRAODPDLDGNALMAYSLD 300
QY      301 GEGSEAFSISTDLQGRDGLTVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFKDVAS 360
Db      301 GEGSEAFSISTDLQGRDGLTVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFKDVAS 360
QY      361 VRVAVQADPEPPATQAAVHLTVPEKAPGTLVGCISADLDSASPIRYSILPHSDPER 420
Db      361 VRVAVQADPEPPATQAAVHLTVPEKAPGTLVGCISADLDSASPIRYSILPHSDPER 420
QY      421 CFSIQPEEGTHTAALDREARAHNLTVLATELGMSWGPGRGWPLVAEWSAPAAPQ 480
Db      421 CFSIQPEEGTHTAALDREARAHNLTVLATELGMSWGPGRGWPLVAEWSAPAAPQ 480
QY      481 RSPVGSAGVIGIPQDSSAQSARVQVAIQTLDENNDNAPQALAEPYDTFVCDSSAAGLIQVIRA 540
Db      481 RSPVGSAGVIGIPQDSSAQSARVQVAIQTLDENNDNAPQALAEPYDTFVCDSSAAGLIQVIRA 540
QY      541 LDRDEVGNSSHVSGQPLGPDANFTVQDNRD-----LPA-----WF 576
Db      541 LDRDEVGNSSHVSGQPLGPDANFTVQDNRD-----LPA-----WF 576
QY      577 HPLMASASWLH-----WPAERGNQASQG 603
Db      577 HPLMASASWLH-----WPAERGNQASQG 603

RESULT 5

```



```
US-10-245-859-98
; Sequence 98, Application US/10245859
; Publication No. US2003064474A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Matambe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C12
; CURRENT FILING DATE: 2002-09-16
; PRIOR FILING DATE: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR FILING DATE: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/066478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-859-98

Query Match      81.9%; Score 2746.5; DB 14; Length 781;
Best Local Similarity 84.8%; Pred. No. 3e-196;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MMGLVRLLLMVLGWMGCMGRLLAARAWAGSRHHPGALLRTSRVWVNOFFVIEYAP 60
DB 1 MMGLVRLLLMVLGWMGCMGRLLAARAWAGSRHHPGALLRTSRVWVNOFFVIEYAP 60
QY 61 EPLLIGLHSDVDGRGRTYLLTGEGAGTVFVIDEATGNIHVTKSLDSEKQAYLLAQ 120
DB 61 EPLLIGLHSDVDGRGRTYLLTGEGAGTVFVIDEATGNIHVTKSLDSEKQAYLLAQ 120
QY 121 AVPRASRPLEPPEEFLLKQDINDNPFIFPLGPYATVPEMNVGTSVIQVTAHADDP 180
DB 121 AVPRASRPLEPPEEFLLKQDINDNPFIFPLGPYATVPEMNVGTSVIQVTAHADDP 180
QY 181 SYGSAALVYTVLDGLFFSVDPQTGVRTAIPNMDRETOBEFLVVIQAKDMGHVGLS 240
DB 181 SYGSAALVYTVLDGLFFSVDPQTGVRTAIPNMDRETOBEFLVVIQAKDMGHVGLS 240
QY 241 GSTTVYTVLSDVNDNPKFPQSLYQSFVETAGPGLVGLRAQDDPLGDNALMAYSIID 300
DB 241 GSTTVYTVLSDVNDNPKFPQSLYQSFVETAGPGLVGLRAQDDPLGDNALMAYSIID 300
```

```
QY 301 GEGSEAFSISTDLQGRDGLTVRKLPDESGRSYSFRVEATNTLLIDPAYLRGPFKVAS 360
DB 301 GEGSEAFSISTDLQGRDGLTVRKLPDESGRSYSFRVEATNTLLIDPAYLRGPFKVAS 360
QY 361 VRVAQDAPEPPAFQQAAYHVLTVBENKAPGLTVQGISADLDSASPIRYSILHSPER 420
DB 361 VRVAQDAPEPPAFQQAAYHVLTVBENKAPGLTVQGISADLDSASPIRYSILHSPER 420
QY 421 CFSIQPEEGTHTTAAPLDREARAHNLTVLATELGWSGPERGWPLLVAEWSAPAAPQ 480
DB 421 CFSIQPEEGTHTTAAPLDREARAHNLTVLATELGWSGPERGWPLLVAEWSAPAAPQ 480
QY 481 RSPVGSANGIRQDSSAQAARSQVAIQTLIDENDNAPQLAEPYDTVCDSAPGQIQYIRA 540
DB 481 RSPVGSANGIRQDSSAQAARSQVAIQTLIDENDNAPQLAEPYDTVCDSAPGQIQYIRA 540
QY 541 LDRDEVGSSHYVSFCGPGPDANFTVQDNRD-----LPA-----WF 576
DB 541 LDRDEVGSSHYVSFCGPGPDANFTVQDNRGASLILFSPRAPPRHAPYIVTELDWG 562
QY 577 HPLMASASSWLH-----WPAERGNQPASQ 603
DB 577 HPLMASASSWLH-----WPAERGNQPASQ 603
QY 583 QPALSTATVTVSVCRCPDGSVASCWFEALHLSAGLSTG 602
DB 583 QPALSTATVTVSVCRCPDGSVASCWFEALHLSAGLSTG 602

RESULT 6
US-10-245-103-98
; Sequence 98, Application US/10245103
; Publication No. US2003068778A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Matambe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C12
; CURRENT FILING DATE: 2002-09-17
; PRIOR FILING DATE: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
```

Wed Dec 8 11:46:29 2004

us-09-788-051-4.rapb

Page 5

US-10-245-103-98

Query Match 81.9%; Score 2746.5; DB 14; Length 781;
Best Local Similarity 84.8%; Pred. No. 36-196;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MMGLVRLILAMLGWCMGRLAARAPAMAGSREHPGALLRTRRSWMNQFVIEEYAGP 60
DB 1 MMGLVRLILAMLGWCMGRLAARAPAMAGSREHPGALLRTRRSWMNQFVIEEYAGP 60
QY 61 EPLVIGKLSHDVDRGEGRTKYLITGEGAGTVFIDEATGNHVTSLDREBAQYVLLAQ 120
DB 61 EPLVIGKLSHDVDRGEGRTKYLITGEGAGTVFIDEATGNHVTSLDREBAQYVLLAQ 120
QY 121 AVDRASNRPLEPPESEFIKGGDINDNPIPLGPGYHATVPEMSNVGTSVIQVTAHDADP 180
DB 121 AVDRASNRPLEPPESEFIKGGDINDNPIPLGPGYHATVPEMSNVGTSVIQVTAHDADP 180
QY 181 SYGNSAKLVYTVLDGLPFPSVDPQTGVVRAIPNMDRETOEEFLVVIQAKDMGSHGGLS 240
DB 181 SYGNSAKLVYTVLDGLPFPSVDPQTGVVRAIPNMDRETOEEFLVVIQAKDMGSHGGLS 240
QY 241 GSTTVTVTLSDVNNPPKFPQSLYQFSVETAGPGLVGRADPDLGNALMAYSLID 300
DB 241 GSTTVTVTLSDVNNPPKFPQSLYQFSVETAGPGLVGRADPDLGNALMAYSLID 300
QY 301 GEGSEAFSISTDLQGRDGLITVRKPLDPESQSYSPFEATNTLIDPAYLRGPFKDVAS 360
DB 301 GEGSEAFSISTDLQGRDGLITVRKPLDPESQSYSPFEATNTLIDPAYLRGPFKDVAS 360
QY 361 VRVAVODAPPEPPAFTOAAVHITVPEKAPGTLVQGISADLDSAPISIRYSILPHSDPER 420
DB 361 VRVAVODAPPEPPAFTOAAVHITVPEKAPGTLVQGISADLDSAPISIRYSILPHSDPER 420
QY 421 CFSIOPEEGTIHTAFLDREARAHNLTVLATELGWSWGPGRGWVPLVAEWSAPAPQ 480
DB 421 CFSIOPEEGTIHTAFLDREARAHNLTVLATELGWSWGPGRGWVPLVAEWSAPAPQ 480
QY 481 RSPVGSAGVIGPODSSAQASRVQVAIQTLDENDNAPQALAEPYDTFVCDSPAAGQLIQVIRA 540
DB 481 RSPVGSAGVIGPODSSAQASRVQVAIQTLDENDNAPQALAEPYDTFVCDSPAAGQLIQVIRA 540
QY 541 LDRDEVGNSSHVSFOGPIGPDANFTVQDNRD-----LPA-----WF 576
DB 541 LDRDEVGNSSHVSFOGPIGPDANFTVQDNRD-----LPA-----WF 576
QY 577 HPLMASASSWLH-----WPAERGNQAPASOG 603
DB 577 HPLMASASSWLH-----WPAERGNQAPASOG 603

RESULT 7
US-10-245-107-98
Sequence 98, Application US/10245107
Publication No. US2003006879A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Bacon, Dan
APPLICANT: Filvarsoff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watande, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C71
CURRENT APPLICATION NUMBER: US/10/245,107
CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See file Wrapper or PALM.
SEO ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-107-98

Query Match 81.9%; Score 2746.5; DB 14; Length 781;
Best Local Similarity 84.8%; Pred. No. 36-196;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MMGLVRLILAMLGWCMGRLAARAPAMAGSREHPGALLRTRRSWMNQFVIEEYAGP 60
DB 1 MMGLVRLILAMLGWCMGRLAARAPAMAGSREHPGALLRTRRSWMNQFVIEEYAGP 60
QY 61 EPLVIGKLSHDVDRGEGRTKYLITGEGAGTVFIDEATGNHVTSLDREBAQYVLLAQ 120
DB 61 EPLVIGKLSHDVDRGEGRTKYLITGEGAGTVFIDEATGNHVTSLDREBAQYVLLAQ 120
QY 121 AVDRASNRPLEPPESEFIKGGDINDNPIPLGPGYHATVPEMSNVGTSVIQVTAHDADP 180
DB 121 AVDRASNRPLEPPESEFIKGGDINDNPIPLGPGYHATVPEMSNVGTSVIQVTAHDADP 180
QY 181 SYGNSAKLVYTVLDGLPFPSVDPQTGVVRAIPNMDRETOEEFLVVIQAKDMGSHGGLS 240
DB 181 SYGNSAKLVYTVLDGLPFPSVDPQTGVVRAIPNMDRETOEEFLVVIQAKDMGSHGGLS 240
QY 241 GSTTVTVTLSDVNNPPKFPQSLYQFSVETAGPGLVGRADPDLGNALMAYSLID 300
DB 241 GSTTVTVTLSDVNNPPKFPQSLYQFSVETAGPGLVGRADPDLGNALMAYSLID 300
QY 301 GEGSEAFSISTDLQGRDGLITVRKPLDPESQSYSPFEATNTLIDPAYLRGPFKDVAS 360
DB 301 GEGSEAFSISTDLQGRDGLITVRKPLDPESQSYSPFEATNTLIDPAYLRGPFKDVAS 360
QY 361 VRVAVODAPPEPPAFTOAAVHITVPEKAPGTLVQGISADLDSAPISIRYSILPHSDPER 420
DB 361 VRVAVODAPPEPPAFTOAAVHITVPEKAPGTLVQGISADLDSAPISIRYSILPHSDPER 420
QY 421 CFSIOPEEGTIHTAFLDREARAHNLTVLATELGWSWGPGRGWVPLVAEWSAPAPQ 480
DB 421 CFSIOPEEGTIHTAFLDREARAHNLTVLATELGWSWGPGRGWVPLVAEWSAPAPQ 480
QY 481 RSPVGSAGVIGPODSSAQASRVQVAIQTLDENDNAPQALAEPYDTFVCDSPAAGQLIQVIRA 540
DB 481 RSPVGSAGVIGPODSSAQASRVQVAIQTLDENDNAPQALAEPYDTFVCDSPAAGQLIQVIRA 540
QY 541 LDRDEVGNSSHVSFOGPIGPDANFTVQDNRD-----LPA-----WF 576
DB 541 LDRDEVGNSSHVSFOGPIGPDANFTVQDNRD-----LPA-----WF 576
QY 577 HPLMASASSWLH-----WPAERGNQAPASOG 603
DB 577 HPLMASASSWLH-----WPAERGNQAPASOG 603

Db 563 QPALSTATVTVSVCRQCPDGSVASCPPEAHLASAAGLSTG 602

RESULT 8

US-10-245-143-98

Sequence 98, Application US/10245143

Publication No. US20030068780A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Baton, Dan

APPLICANT: Filvaroff, Ellen

APPLICANT: Goddard, Audrey

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe

APPLICANT: Wacande, Colin

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

APPLICANT: Fong, Sherman

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3630R1C90

CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 10/197942

PRIOR FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/059114

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/063046

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/065027

PRIOR FILING DATE: 1997-11-10

PRIOR APPLICATION NUMBER: 60/079689

PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/086478

PRIOR FILING DATE: 1998-05-22

PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/089801

PRIOR FILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: 60/090557

PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090689

PRIOR FILING DATE: 1998-06-25

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 116

SEQ ID NO 98

LENGTH: 781

TYPE: PRT

ORGANISM: Homo Sapien

US-10-245-143-98

Query Match 81.9%; Score 2746.5; DB 14; Length 781;

Best Local Similarity 84.8%; Pred. No. 3e-196;

Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MGGVIRLLLLAMLGWGMGSLAARPARMAGSREHPGPAIRTRRSWMMQFVIEBYAP 60

Db 1 MGGVIRLLLLAMLGWGMGSLAARPARMAGSREHPGPAIRTRRSWMMQFVIEBYAP 60

QY 61 EPLVIGLHSDVDVGRGERTKYLLTGEAGVTFVIDATGNIHTKSLDREERAAQVYLLAQ 120

Db 61 EPLVIGLHSDVDVGRGERTKYLLTGEAGVTFVIDATGNIHTKSLDREERAAQVYLLAQ 120

QY 121 AVDRASRPLPPESEFIIKQDINDNPFIFPLGPHYATVPKMSNVGTSVYQVTAHDADP 180

Db 121 AVDRASRPLPPESEFIIKQDINDNPFIFPLGPHYATVPKMSNVGTSVYQVTAHDADP 180

QY 181 SYGNASALVYTVLDGLPFSSVDPTQGVRRALPMNRREFQSEELVYIOAKMGNGHGGIS 240

Db 181 SYGNASALVYTVLDGLPFSSVDPTQGVRRALPMNRREFQSEELVYIOAKMGNGHGGIS 240

QY 241 GSTTIVTLSDVNDNPKFPQSLYQFSVETAGFGLVGRIRADDPDLGDNALMAYSILD 300

Db 241 GSTTIVTLSDVNDNPKFPQSLYQFSVETAGFGLVGRIRADDPDLGDNALMAYSILD 300

QY 301 GEGSEAFSISTDLQSDGLTVRKPLDRESGRSFVEATNTLIDPAYLRGPFKQVAS 360

Db 301 GEGSEAFSISTDLQSDGLTVRKPLDRESGRSFVEATNTLIDPAYLRGPFKQVAS 360

QY 361 VRVAVQDAPPEPPAFTQAAVHLTVPENKAPGTLVQGISAADIDSPASPIRYSILHSDPER 420

Db 361 VRVAVQDAPPEPPAFTQAAVHLTVPENKAPGTLVQGISAADIDSPASPIRYSILHSDPER 420

QY 421 CESTOPEEGTHTTAPLDRERAMHNLTVALTELGWNGPGRGVPLLVWMSAPAPQ 480

Db 421 CESTOPEEGTHTTAPLDRERAMHNLTVALTELGWNGPGRGVPLLVWMSAPAPQ 480

QY 481 RSPVSAVGIPDSSAQSRVQVAIQTLDENDNAPOLAEPYDTFCDSAPAGQLIOYIRA 540

Db 481 RSPVSAVGIPDSSAQSRVQVAIQTLDENDNAPOLAEPYDTFCDSAPAGQLIOYIRA 540

QY 455 -----DSSAQSRVQVAIQTLDENDNAPOLAEPYDTFCDSAPAGQLIOYIRA 502

Db 455 -----DSSAQSRVQVAIQTLDENDNAPOLAEPYDTFCDSAPAGQLIOYIRA 502

QY 541 LDRDEVGNSSHYSGPGLPDPANTVQDNRP-----LPA-----WF 576

Db 541 LDRDEVGNSSHYSGPGLPDPANTVQDNRP-----LPA-----WF 576

QY 503 LDRDEVGNSSHYSGPGLPDPANTVQDNRPDGSASLLPSPAPPRHAPYLPIELMDWG 562

Db 503 LDRDEVGNSSHYSGPGLPDPANTVQDNRPDGSASLLPSPAPPRHAPYLPIELMDWG 562

QY 577 HPLMASASWLM-----WPAERGRQPASOG 603

Db 577 HPLMASASWLM-----WPAERGRQPASOG 603

Db 563 QPALSTATVTVSVCRQCPDGSVASCPPEAHLASAAGLSTG 602

RESULT 9

US-10-245-771-98

Sequence 98, Application US/10245771

Publication No. US20030068781A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Baton, Dan

APPLICANT: Filvaroff, Ellen

APPLICANT: Goddard, Audrey

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe

APPLICANT: Wacande, Colin

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

APPLICANT: Fong, Sherman

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3630R1C98

CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 10/197942

PRIOR FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/059114

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/063046

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/065027

PRIOR FILING DATE: 1997-11-10

PRIOR APPLICATION NUMBER: 60/079689

PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/086478

PRIOR FILING DATE: 1998-05-22

PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/089801

PRIOR FILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: 60/090557

PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090689

PRIOR FILING DATE: 1998-06-25

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 116
 SEQ ID NO 98
 LENGTH: 781
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-245-771-98

Query Match 81.9%; Score 2746.5; DB 14; Length 781;
 Best Local Similarity 84.8%; Pred. No. 3e-196;
 Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

```

QY 1 MMGLVRLLLAMLGWGMCMGRLAAPARAWAGSREHPALLRTRRWVWNOQFVIEEYAGP 60
DB 1 MMGLVRLLLAMLGWGMCMGRLAAPARAWAGSREHPALLRTRRWVWNOQFVIEEYAGP 60
QY 61 EPLVIGKHSVDVDRGEGRTKYLITGEGAGTVFIDEATGNHVTSLDREKAOYVLLAQ 120
DB 61 EPLVIGKHSVDVDRGEGRTKYLITGEGAGTVFIDEATGNHVTSLDREKAOYVLLAQ 120
QY 121 AVDRASNRPLEPPESEFIKQODINDNPIFPLGPHATVPMSVVGTSVIQVTAHDADDP 180
DB 121 AVDRASNRPLEPPESEFIKQODINDNPIFPLGPHATVPMSVVGTSVIQVTAHDADDP 180
QY 181 SYGNSAKLVYTVLDGLPFPSVDPQGVVRTAI PMNDRETOEFLVVIQAKDMGGMGGLS 240
DB 181 SYGNSAKLVYTVLDGLPFPSVDPQGVVRTAI PMNDRETOEFLVVIQAKDMGGMGGLS 240
QY 241 GSTTVTVTLSDVNDNPKFPQSLYQFSVETAGPGLVGRLAQDPDLGNALMAYSLTD 300
DB 241 GSTTVTVTLSDVNDNPKFPQSLYQFSVETAGPGLVGRLAQDPDLGNALMAYSLTD 300
QY 301 GEGSEAFSISTDLQSGDGLITVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFKDVAS 360
DB 301 GEGSEAFSISTDLQSGDGLITVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFKDVAS 360
QY 361 VRVAVQDAPEPPAFTQAAYHLTVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPER 420
DB 361 VRVAVQDAPEPPAFTQAAYHLTVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPER 420
QY 421 CFSIQPEEGTHTTAAPLDREARAHNLTIVLATELGWSWGERGWPLLVAEWSAPAPAPQ 480
DB 421 CFSIQPEEGTHTTAAPLDREARAHNLTIVLATELGWSWGERGWPLLVAEWSAPAPAPQ 480
QY 481 RSPVGSAGVIGIPQDSSAQASRVQVAIQTLIDENDNAPQALAPYDTFVCDSPAAGQLIQVIRA 540
DB 481 RSPVGSAGVIGIPQDSSAQASRVQVAIQTLIDENDNAPQALAPYDTFVCDSPAAGQLIQVIRA 540
QY 545 -----DSSAQASRVQVAIQTLIDENDNAPQALAPYDTFVCDSPAAGQLIQVIRA 502
DB 545 -----DSSAQASRVQVAIQTLIDENDNAPQALAPYDTFVCDSPAAGQLIQVIRA 502
QY 541 LDRPEVGNSSHYVSQGLGPDANFTVQGNRD-----LPA-----NF 576
DB 541 LDRPEVGNSSHYVSQGLGPDANFTVQGNRD-----LPA-----NF 576
QY 577 HPLMASASWLH-----WPPAERGNQAPASQ 603
DB 577 HPLMASASWLH-----WPPAERGNQAPASQ 603
QY 563 QPALSTATVTVSVCRQCPDGSVASCWPEAHLSAAGLSTG 602
DB 563 QPALSTATVTVSVCRQCPDGSVASCWPEAHLSAAGLSTG 602

```

RESULT 10

US-10-245-851-98
 Sequence 98, Application US/10245851
 Publication No. US20030068782A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin
 APPLICANT: Bacon, Dan
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, V. Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Smith, Victoria
 APPLICANT: Stephan, Jean-Philippe
 APPLICANT: Matembe, Colin
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 APPLICANT: Fong, Sherman

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ACIDS ENCODING THE SAME
 FILE REFERENCE: P3630RIC93
 CURRENT APPLICATION NUMBER: US/10/245,851
 CURRENT FILING DATE: 2002-09-16
 PRIOR APPLICATION NUMBER: 10/197942
 PRIOR FILING DATE: 2002-07-19
 PRIOR APPLICATION NUMBER: 60/059114
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/063046
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/065027
 PRIOR FILING DATE: 1997-11-10
 PRIOR APPLICATION NUMBER: 60/079689
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/086478
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090689
 PRIOR FILING DATE: 1998-06-25
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 116
 SEQ ID NO 98
 LENGTH: 781
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-245-851-98

Query Match 81.9%; Score 2746.5; DB 14; Length 781;
 Best Local Similarity 84.8%; Pred. No. 3e-196;
 Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

```

QY 1 MMGLVRLLLAMLGWGMCMGRLAAPARAWAGSREHPALLRTRRWVWNOQFVIEEYAGP 60
DB 1 MMGLVRLLLAMLGWGMCMGRLAAPARAWAGSREHPALLRTRRWVWNOQFVIEEYAGP 60
QY 61 EPLVIGKHSVDVDRGEGRTKYLITGEGAGTVFIDEATGNHVTSLDREKAOYVLLAQ 120
DB 61 EPLVIGKHSVDVDRGEGRTKYLITGEGAGTVFIDEATGNHVTSLDREKAOYVLLAQ 120
QY 121 AVDRASNRPLEPPESEFIKQODINDNPIFPLGPHATVPMSVVGTSVIQVTAHDADDP 180
DB 121 AVDRASNRPLEPPESEFIKQODINDNPIFPLGPHATVPMSVVGTSVIQVTAHDADDP 180
QY 181 SYGNSAKLVYTVLDGLPFPSVDPQGVVRTAI PMNDRETOEFLVVIQAKDMGGMGGLS 240
DB 181 SYGNSAKLVYTVLDGLPFPSVDPQGVVRTAI PMNDRETOEFLVVIQAKDMGGMGGLS 240
QY 241 GSTTVTVTLSDVNDNPKFPQSLYQFSVETAGPGLVGRLAQDPDLGNALMAYSLTD 300
DB 241 GSTTVTVTLSDVNDNPKFPQSLYQFSVETAGPGLVGRLAQDPDLGNALMAYSLTD 300
QY 301 GEGSEAFSISTDLQSGDGLITVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFKDVAS 360
DB 301 GEGSEAFSISTDLQSGDGLITVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFKDVAS 360
QY 361 VRVAVQDAPEPPAFTQAAYHLTVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPER 420
DB 361 VRVAVQDAPEPPAFTQAAYHLTVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPER 420
QY 421 CFSIQPEEGTHTTAAPLDREARAHNLTIVLATELGWSWGERGWPLLVAEWSAPAPAPQ 480
DB 421 CFSIQPEEGTHTTAAPLDREARAHNLTIVLATELGWSWGERGWPLLVAEWSAPAPAPQ 480
QY 481 RSPVGSAGVIGIPQDSSAQASRVQVAIQTLIDENDNAPQALAPYDTFVCDSPAAGQLIQVIRA 540
DB 481 RSPVGSAGVIGIPQDSSAQASRVQVAIQTLIDENDNAPQALAPYDTFVCDSPAAGQLIQVIRA 540
QY 455 -----DSSAQASRVQVAIQTLIDENDNAPQALAPYDTFVCDSPAAGQLIQVIRA 502
DB 455 -----DSSAQASRVQVAIQTLIDENDNAPQALAPYDTFVCDSPAAGQLIQVIRA 502

```

QY 541 LDRDEVNSSHVSGFGLGPDANFTVQDNRD-----LPA-----WF 576
DB 503 LDRDEVGNSSHVSGFGLGPDANFTVQDNRDGASALLPSPAPRPAPVPIELMDWG 562
QY 577 HPLMASASSWLH-----WPPARGNQPSAQ 603
DB 563 QPALSSTATVTVSVRCQPDGVSASCPWEAHLASAAGLSTG 602

RESULT 11

US-10-245-883-98
; Sequence 98, Application US/10245883
; Publication No. US20030068783A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C70
; CURRENT APPLICATION NUMBER: US/10/245, 883
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-883-98

Query Match 81.9%; Score 2746.5; DB 14; Length 781;
Best Local Similarity 84.8%; Pred. No. 36-196;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MMGLVRLLLAWLGGWGMCGRLAARARAGSREHPGALRTSRSMWNOFVIEBYAGP 60
DB 1 MMGLVRLLLAWLGGWGMCGRLAARARAGSREHPGALRTSRSMWNOFVIEBYAGP 60
QY 61 EPLVIGKLSHSDVDRGEGRTKYLTLGEGAGTVFVIDEATGNIHTKSLDREKKAQYVLLAQ 120
DB 61 EPLVIGKLSHSDVDRGEGRTKYLTLGEGAGTVFVIDEATGNIHTKSLDREKKAQYVLLAQ 120
QY 121 AVDASNRPLPPEPSEFIKKODINDNPEIFPLGPHATVPEMNGSVQVTAHADDP 180

DB 121 AVDASNRPLPPEPSEFIKKODINDNPEIFPLGPHATVPEMNGSVQVTAHADDP 180
QY 181 SYGNASAKYTVYVLDGLPFFSVDPQGTGVRTAIIPMDDETOEEFLVYLQAKDMGGHMGSL 240
DB 181 SYGNASAKYTVYVLDGLPFFSVDPQGTGVRTAIIPMDDETOEEFLVYLQAKDMGGHMGSL 240
QY 241 GSTTVTLVLSVDNPNPPEFQSLYQSVETAGGTLVGRRAADPDPLGDMALAAVSLD 300
DB 241 GSTTVTLVLSVDNPNPPEFQSLYQSVETAGGTLVGRRAADPDPLGDMALAAVSLD 300
QY 301 GEGSEAFSISTDLOCRDGLTVRKPLDPESQSRYSFRVEATNTLIDPAYLRGPFKVAS 360
DB 301 GEGSEAFSISTDLOCRDGLTVRKPLDPESQSRYSFRVEATNTLIDPAYLRGPFKVAS 360
QY 361 VRNAVQDAPPEPPAFQAAVYHLLVPEBKAPGLVQOIAADSDSASIRISILHSDPER 420
DB 361 VRNAVQDAPPEPPAFQAAVYHLLVPEBKAPGLVQOIAADSDSASIRISILHSDPER 420
QY 421 CFSIQPEEGTHTTAAPLDRERANHLTVLATBELGMSGMPERGVPVLLVWKSAPAAPQ 480
DB 421 CFSIQPEEGTHTTAAPLDRERANHLTVLATBELGMSGMPERGVPVLLVWKSAPAAPQ 480
QY 481 RSPVGSAGVIGIPQDSQAQSRVQVAIOTLDEBNDNAPOLAEPYDFVCDSPAAGQLOVIRA 540
DB 481 RSPVGSAGVIGIPQDSQAQSRVQVAIOTLDEBNDNAPOLAEPYDFVCDSPAAGQLOVIRA 540
QY 541 LDRDEVNSSHVSGFGLGPDANFTVQDNRD-----LPA-----WF 576
DB 503 LDRDEVGNSSHVSGFGLGPDANFTVQDNRDGASALLPSPAPRPAPVPIELMDWG 562
QY 577 HPLMASASSWLH-----WPPARGNQPSAQ 603
DB 563 QPALSSTATVTVSVRCQPDGVSASCPWEAHLASAAGLSTG 602

RESULT 12

US-10-237-535-98
; Sequence 98, Application US/10237535
; Publication No. US20030073188A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C3
; CURRENT APPLICATION NUMBER: US/10/237, 535
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18

Wed Dec 8 11:46:29 2004

us-09-788-051-4.rapb

Page 9

```

PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090699
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091358
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/106932
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/115554
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119342
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/123957
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123972
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: 60/127372
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/131271
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/133459
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/135725
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135729
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135750
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/138385
PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: 60/140653
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144732
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144790
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145228
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146843
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/148188
PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/148513
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/149327
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149395
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/150114
PRIOR FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: 60/151700
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/151734
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/170262
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/177118
PRIOR FILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: 60/179851

PRIOR FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 60/180921
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: 60/187202
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/198587
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 60/199614
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 60/206330
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206368
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/209832
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 60/218371
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/222695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/229896
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/230621
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/232887
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/235147
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/261878
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/261910
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/261939
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/262150
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/264395
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/266421
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/267623
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/274399
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/280982
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/282129
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/282199
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/290589
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 60/180997
PRIOR FILING DATE: 1998-11-19
PRIOR APPLICATION NUMBER: 60/267213
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 60/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 60/403297
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 60/423741
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: 60/709238
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/802706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/872035
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/924419
PRIOR FILING DATE: 2001-08-06
```

;; PRIOR APPLICATION NUMBER: 09/927796
;; PRIOR FILING DATE: 2001-08-09
;; PRIOR APPLICATION NUMBER: 09/929404
;; PRIOR FILING DATE: 2001-08-13
;; PRIOR APPLICATION NUMBER: 09/931836
;; PRIOR FILING DATE: 2001-08-16
;; PRIOR APPLICATION NUMBER: 09/941992
;; PRIOR FILING DATE: 2001-08-28
;; PRIOR APPLICATION NUMBER: 09/946374
;; PRIOR FILING DATE: 2001-09-04
;; PRIOR APPLICATION NUMBER: 10/001054
;; PRIOR FILING DATE: 2001-11-30
;; PRIOR APPLICATION NUMBER: 10/052586
;; PRIOR FILING DATE: 2002-01-15
;; PRIOR APPLICATION NUMBER: 10/081056
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: 10/119480
;; PRIOR FILING DATE: 2002-04-09

Query Match 81.9%; Score 2746.5; DB 14; Length 781;
Best Local Similarity 84.8%; Pred. No. 3e-196;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

Qy 1 MWGLVRLILAWLGWGMGRLADAPAMAGSREHGPALLIRTSWVWNOFVIEEYAGP 60
Db 1 MWGLVRLILAWLGWGMGRLADAPAMAGSREHGPALLIRTSWVWNOFVIEEYAGP 60
Qy 61 EPLVIGKLSVDNDEGEKTKYLITGEGATVVIDEATGNINHTKSLDREKQYVLLAQ 120
Db 61 EPLVIGKLSVDNDEGEKTKYLITGEGATVVIDEATGNINHTKSLDREKQYVLLAQ 120
Qy 121 AVDRASNRPLEPSEFIIKQDINDNPPIPLGPHATVEMSVNGSVIQTVAHDADDP 180
Db 121 AVDRASNRPLEPSEFIIKQDINDNPPIPLGPHATVEMSVNGSVIQTVAHDADDP 180
Qy 181 SYGSATKLVTVLDGLTFPSVDPTGVRTAIPMDETGEELVVIQADMGHNGGLS 240
Db 181 SYGSATKLVTVLDGLTFPSVDPTGVRTAIPMDETGEELVVIQADMGHNGGLS 240
Qy 241 GSTVTVTLSPVNDNPKFPQSLYQFSVETAGCGTLVGLRAODPLGDMALMAYSLD 300
Db 241 GSTVTVTLSPVNDNPKFPQSLYQFSVETAGCGTLVGLRAODPLGDMALMAYSLD 300
Qy 301 GEGEAPISITDLOGRGLLTVKKPLDPEQSISYFPAVTNTLIDPAYRRGPFDVVS 360
Db 301 GEGEAPISITDLOGRGLLTVKKPLDPEQSISYFPAVTNTLIDPAYRRGPFDVVS 360
Qy 361 VRVAVODAPPEPATQAAHLTVPENKAPGTLVGQISAADLDSPASIRYSILPHSDPER 420
Db 361 VRVAVODAPPEPATQAAHLTVPENKAPGTLVGQISAADLDSPASIRYSILPHSDPER 420
Qy 421 CFSIQPEEGTHTAPLDRKARAHNTLVATLGLMSWGERGMVPLLVAEMGAPAAPQ 480
Db 421 CFSIQPEEGTHTAPLDRKARAHNTLVATLGLMSWGERGMVPLLVAEMGAPAAPQ 480
Qy 481 RSPFGSANGIPQSSAASRVQVAILDNDNAPOLAEHYDTFVCSAPQGLIQVIRA 540
Db 481 RSPFGSANGIPQSSAASRVQVAILDNDNAPOLAEHYDTFVCSAPQGLIQVIRA 540
Qy 455 -----DSSAASRVQVAILDNDNAPOLAEHYDTFVCSAPQGLIQVIRA 502
Db 455 -----DSSAASRVQVAILDNDNAPOLAEHYDTFVCSAPQGLIQVIRA 502
Qy 541 LDRDEVANGSSHSFQGLGPDANFTVQDNRD-----LPA-----WF 576
Db 541 LDRDEVANGSSHSFQGLGPDANFTVQDNRD-----LPA-----WF 576
Qy 503 LDRDEVANGSSHSFQGLGPDANFTVQDNRDGSASLLPFRPAPRHAPLVYIELMDWG 562
Db 503 LDRDEVANGSSHSFQGLGPDANFTVQDNRDGSASLLPFRPAPRHAPLVYIELMDWG 562
Qy 577 HPLMASASSWLH-----WPPAREGNQRPASQ 603
Db 577 HPLMASASSWLH-----WPPAREGNQRPASQ 603
Qy 563 QPALSTATVTVSVCRQPDGVSACWPEAHLAAGLSTG 602
Db 563 QPALSTATVTVSVCRQPDGVSACWPEAHLAAGLSTG 602

RESULT 13
US-10-238-183-98
; Sequence 98, Application US/10238183
; Publication No. US20030073189A1
; GENERAL INFORMATION:

;; APPLICANT: Baker, Kevin
;; APPLICANT: Baton, Dan
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin
;; APPLICANT: Smith, Victoria
;; APPLICANT: Stephan, Jean-Philippe
;; APPLICANT: Watanabe, Colin
;; APPLICANT: Wood, William
;; APPLICANT: Zhang, Zemin
;; APPLICANT: Fong, Sherman
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P3630R.C11
;; CURRENT FILING DATE: 2002-09-09
;; PRIOR APPLICATION NUMBER: 10/179942
;; PRIOR FILING DATE: 2002-07-18
;; PRIOR APPLICATION NUMBER: 60/059114
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/063046
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/065027
;; PRIOR FILING DATE: 1997-11-10
;; PRIOR APPLICATION NUMBER: 60/079689
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/086478
;; PRIOR FILING DATE: 1998-05-22
;; PRIOR APPLICATION NUMBER: 60/087607
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/089801
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090689
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/091358
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/099803
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/106932
;; PRIOR FILING DATE: 1998-11-03
;; PRIOR APPLICATION NUMBER: 60/115554
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/119342
;; PRIOR FILING DATE: 1999-02-09
;; PRIOR APPLICATION NUMBER: 60/123957
;; PRIOR FILING DATE: 1999-03-12
;; PRIOR APPLICATION NUMBER: 60/123972
;; PRIOR FILING DATE: 1999-03-11
;; PRIOR APPLICATION NUMBER: 60/127372
;; PRIOR FILING DATE: 1999-04-01
;; PRIOR APPLICATION NUMBER: 60/131271
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/133459
;; PRIOR FILING DATE: 1999-05-11
;; PRIOR APPLICATION NUMBER: 60/135725
;; PRIOR FILING DATE: 1999-05-25
;; PRIOR APPLICATION NUMBER: 60/135729
;; PRIOR FILING DATE: 1999-05-25
;; PRIOR APPLICATION NUMBER: 60/135750
;; PRIOR FILING DATE: 1999-05-25
;; PRIOR APPLICATION NUMBER: 60/138385
;; PRIOR FILING DATE: 1999-06-09
;; PRIOR APPLICATION NUMBER: 60/140653
;; PRIOR FILING DATE: 1999-06-22
;; PRIOR APPLICATION NUMBER: 60/141037
;; PRIOR FILING DATE: 1999-06-23
;; PRIOR APPLICATION NUMBER: 60/144732
;; PRIOR FILING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144790
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145228
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146843
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/148188
PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/148513
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/149327
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149395
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/150114
PRIOR FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: 60/151700
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/151734
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/170262
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/171118
PRIOR FILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: 60/179851
PRIOR FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 60/180921
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: 60/187202
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/198587
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 60/199614
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 60/206330
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206368
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/209832
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 60/218371
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/222695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/229896
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/230621
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/232887
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/235147
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/261878
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/261910
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/261939
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/262150
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/264395
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/266421
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/267623

PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/274399
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/280982
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/282129
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/282199
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/290589
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 09/180997
PRIOR FILING DATE: 1998-11-19
PRIOR APPLICATION NUMBER: 09/267213
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 09/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/403297
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 09/423741
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: 09/709238
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 09/802706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 09/872035
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/924419
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/927796
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/929404
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 09/931836
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 09/941892
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 09/946374
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 10/001054
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 10/081056
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: 10/119480
PRIOR FILING DATE: 2002-04-09

Query Match 81.9%; Score 2746.5; DB 14; Length 781;
Best Local Similarity 84.8%; Pred. No. 36-196; Indels 75; Gaps 4;
Matches 543; Conservative 5; Mismatches 17;

QY 1 MMGLVRLIAMIWGCMGRLAAPARAWGSEHPEPALIRRRSWMNQFVIEBYACP 60
1 MMGLVRLIAMIWGCMGRLAAPARAWGSEHPEPALIRRRSWMNQFVIEBYACP 60
Db 1 MMGLVRLIAMIWGCMGRLAAPARAWGSEHPEPALIRRRSWMNQFVIEBYACP 60
QY 61 EPLVLIKLSHDVDRGGRTRKYLITLGGAGTVFVIDEATGNHVTSLDDEEKAQVYLLAQ 120
61 EPLVLIKLSHDVDRGGRTRKYLITLGGAGTVFVIDEATGNHVTSLDDEEKAQVYLLAQ 120
Db 61 EPLVLIKLSHDVDRGGRTRKYLITLGGAGTVFVIDEATGNHVTSLDDEEKAQVYLLAQ 120
QY 121 AVDRASNRPLPEPSEFIKQDINDNPPIPLGPHYATVPENSVGTSVIQTADADDP 180
121 AVDRASNRPLPEPSEFIKQDINDNPPIPLGPHYATVPENSVGTSVIQTADADDP 180
Db 121 AVDRASNRPLPEPSEFIKQDINDNPPIPLGPHYATVPENSVGTSVIQTADADDP 180
QY 181 SVGNKAKLYVTLDGPFPSVDQGTGVTATLPMNDETEQEEFLVIAQKMGHGGLS 240
181 SVGNKAKLYVTLDGPFPSVDQGTGVTATLPMNDETEQEEFLVIAQKMGHGGLS 240
Db 181 SVGNKAKLYVTLDGPFPSVDQGTGVTATLPMNDETEQEEFLVIAQKMGHGGLS 240
QY 241 GSTTVVTLSDVNDNPKPEQSLYQFSVETAGPGLVGRILRAODPDLDGNALMAYSIID 300
241 GSTTVVTLSDVNDNPKPEQSLYQFSVETAGPGLVGRILRAODPDLDGNALMAYSIID 300

```

Db 241 GSTTAVTILSDVNDNPKFPOSILYQFSVETAGGTIVGLRAODPDLGNALMAYSILD 300
Qy 301 GEGSEAFSISTDLQGRDGLTVRRKPLDFESQSYSPFEVATNTLIDPAVLRGPFKDVAS 360
Db 301 GEGSEAFSISTDLQGRDGLTVRRKPLDFESQSYSPFEVATNTLIDPAVLRGPFKDVAS 360
Qy 361 VRVAVQDAPPEPPAFTQAAVHLTVPENKAPGTLVGQISAADLSPASPIRYSILPHSDPER 420
Db 361 VRVAVQDAPPEPPAFTQAAVHLTVPENKAPGTLVGQISAADLSPASPIRYSILPHSDPER 420
Qy 421 CFSIQPEEGTHTAAPLDREARAHNLTVALTELGMWGPERGVPLVAVMSAPAPQ 480
Db 421 CFSIQPEEGTHTAAPLDREARAHNLTVALTELGMWGPERGVPLVAVMSAPAPQ 480
Qy 481 RSPVGSAGVIRQDSSAQASRVQVAIQTLDENDNAPQIAEPYDFVCDSPAAGLIQVIRA 540
Db 481 RSPVGSAGVIRQDSSAQASRVQVAIQTLDENDNAPQIAEPYDFVCDSPAAGLIQVIRA 540
Qy 455 -----DSSAQASRVQVAIQTLDENDNAPQIAEPYDFVCDSPAAGLIQVIRA 502
Db 455 -----DSSAQASRVQVAIQTLDENDNAPQIAEPYDFVCDSPAAGLIQVIRA 502
Qy 541 LDRDEVGNSSHVSFGPLGPDANFTVQDNRD-----LPA-----WF 576
Db 541 LDRDEVGNSSHVSFGPLGPDANFTVQDNRD-----LPA-----WF 576
Qy 503 LDRDEVGNSSHVSFGPLGPDANFTVQDNRDGASALLPSRPAPRRAPVLPVIELMDWG 562
Db 503 LDRDEVGNSSHVSFGPLGPDANFTVQDNRDGASALLPSRPAPRRAPVLPVIELMDWG 562
Qy 577 HPLMASASWLH-----WPPARGNQOPASQG 603
Db 577 HPLMASASWLH-----WPPARGNQOPASQG 603
Qy 563 QPALSSTAVTVSVRCQPDGASVASCWPEALHLSAAGLSTG 602
Db 563 QPALSSTAVTVSVRCQPDGASVASCWPEALHLSAAGLSTG 602

RESULT 14
US-10-238-283-98
; Sequence 98, Application US/10238283
; Publication No. US20030073190A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C15
; CURRENT APPLICATION NUMBER: US/10/238, 283
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98

```

```

; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-238-283-98
Query Match
Best Local Similarity 81.9%; Score 2746.5; DB 14; Length 781;
Matches 543; Conservative 5; Pred. No. 3e-196; Mismatches 17; Indels 75; Gaps 4;

Qy 1 MMGLVRLILANLGGCMGRILAPARAWAGSRHPPALLLTRSWMNQOFVLEETAGP 60
Db 1 MMGLVRLILANLGGCMGRILAPARAWAGSRHPPALLLTRSWMNQOFVLEETAGP 60
Qy 61 EPLLIGKLSHSDVDRGGRKYLITGEGAGTVFIDEATGNHVTXSLDREKQAYVLLAQ 120
Db 61 EPLLIGKLSHSDVDRGGRKYLITGEGAGTVFIDEATGNHVTXSLDREKQAYVLLAQ 120
Qy 121 AYDRASNPPLPPSPFFITKQDINDNPIPLGSGYATVPMSVNGSVIQTTHADDP 180
Db 121 AYDRASNPPLPPSPFFITKQDINDNPIPLGSGYATVPMSVNGSVIQTTHADDP 180
Qy 181 SYGNSAKLVYTVLDELFFSVDPQTVYRTAIPNMDSETOBEPLVVIQAKDMGSMGLS 240
Db 181 SYGNSAKLVYTVLDELFFSVDPQTVYRTAIPNMDSETOBEPLVVIQAKDMGSMGLS 240
Qy 241 GSTTAVTILSDVNDNPKFPOSILYQFSVETAGGTIVGLRAODPDLGNALMAYSILD 300
Db 241 GSTTAVTILSDVNDNPKFPOSILYQFSVETAGGTIVGLRAODPDLGNALMAYSILD 300
Qy 301 GEGSEAFSISTDLQGRDGLTVRRKPLDFESQSYSPFEVATNTLIDPAVLRGPFKDVAS 360
Db 301 GEGSEAFSISTDLQGRDGLTVRRKPLDFESQSYSPFEVATNTLIDPAVLRGPFKDVAS 360
Qy 361 VRVAVQDAPPEPPAFTQAAVHLTVPENKAPGTLVGQISAADLSPASPIRYSILPHSDPER 420
Db 361 VRVAVQDAPPEPPAFTQAAVHLTVPENKAPGTLVGQISAADLSPASPIRYSILPHSDPER 420
Qy 421 CFSIQPEEGTHTAAPLDREARAHNLTVALTELGMWGPERGVPLVAVMSAPAPQ 480
Db 421 CFSIQPEEGTHTAAPLDREARAHNLTVALTELGMWGPERGVPLVAVMSAPAPQ 480
Qy 481 RSPVGSAGVIRQDSSAQASRVQVAIQTLDENDNAPQIAEPYDFVCDSPAAGLIQVIRA 540
Db 481 RSPVGSAGVIRQDSSAQASRVQVAIQTLDENDNAPQIAEPYDFVCDSPAAGLIQVIRA 540
Qy 455 -----DSSAQASRVQVAIQTLDENDNAPQIAEPYDFVCDSPAAGLIQVIRA 502
Db 455 -----DSSAQASRVQVAIQTLDENDNAPQIAEPYDFVCDSPAAGLIQVIRA 502
Qy 541 LDRDEVGNSSHVSFGPLGPDANFTVQDNRD-----LPA-----WF 576
Db 541 LDRDEVGNSSHVSFGPLGPDANFTVQDNRD-----LPA-----WF 576
Qy 503 LDRDEVGNSSHVSFGPLGPDANFTVQDNRDGASALLPSRPAPRRAPVLPVIELMDWG 562
Db 503 LDRDEVGNSSHVSFGPLGPDANFTVQDNRDGASALLPSRPAPRRAPVLPVIELMDWG 562
Qy 577 HPLMASASWLH-----WPPARGNQOPASQG 603
Db 577 HPLMASASWLH-----WPPARGNQOPASQG 603
Qy 563 QPALSSTAVTVSVRCQPDGASVASCWPEALHLSAAGLSTG 602
Db 563 QPALSSTAVTVSVRCQPDGASVASCWPEALHLSAAGLSTG 602

RESULT 15
US-10-238-370-98
; Sequence 98, Application US/10238370
; Publication No. US20030073191A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME

```

FILE REFERENCE: P3630R1C10
CURRENT APPLICATION NUMBER: US/10/238,370
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining prior application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-238-370-98

Query Match 81.9%; Score 2746.5; DB 14; Length 781;
Best Local Similarity 84.8%; Pred. No. 3e-196;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MMGLVRLLLAWLGGWCMGRLLAAPARAWAGSRHHPALLTRRSWVWVNFVIEEYAGP 60
DB 1 MMGLVRLLLAWLGGWCMGRLLAAPARAWAGSRHHPALLTRRSWVWVNFVIEEYAGP 60
QY 61 EPLVIGKLSHSDVDREGEKTKYLLTGEGAGTVFVIDEATGNTHVTKSLDREKAQYVLLAQ 120
DB 61 EPLVIGKLSHSDVDREGEKTKYLLTGEGAGTVFVIDEATGNTHVTKSLDREKAQYVLLAQ 120
QY 121 AVDRASNRPLEPPSEFFIKGODINDNPIPLPGPHATVPMSNVGTSVIQVTAHDDP 180
DB 121 AVDRASNRPLEPPSEFFIKGODINDNPIPLPGPHATVPMSNVGTSVIQVTAHDDP 180
QY 181 SYGNSAKLVYTVLDGLPFPSVDPQTGVVTAIPMDRETOEEPLVVIQAKMGHMGGLS 240
DB 181 SYGNSAKLVYTVLDGLPFPSVDPQTGVVTAIPMDRETOEEPLVVIQAKMGHMGGLS 240
QY 241 GSTTVTVLSDVNNPKKFPQSLQSVETAGPGLVGRLAQDPDLGDNALMAYSLD 300
DB 241 GSTTVTVLSDVNNPKKFPQSLQSVETAGPGLVGRLAQDPDLGDNALMAYSLD 300
QY 301 GEGSEAFSISTDLQGRDGLTVRKPLDFESORSYSFVEATNTLIDPAYLRGPFKDVAS 360
DB 301 GEGSEAFSISTDLQGRDGLTVRKPLDFESORSYSFVEATNTLIDPAYLRGPFKDVAS 360
QY 361 VRVAVQDAPEPPAFQAAVHLTVPENKAPGTLVGOISADLDSAPSPRYSILPHSDPER 420
DB 361 VRVAVQDAPEPPAFQAAVHLTVPENKAPGTLVGOISADLDSAPSPRYSILPHSDPER 420
QY 421 CFSIOPEEGTHTAAPLDREARAWNLTVLATELGMSWGPGRGWPLLVAEWSAPAAPQ 480
DB 421 CFSIOPEEGTHTAAPLDREARAWNLTVLATELGMSWGPGRGWPLLVAEWSAPAAPQ 480
QY 481 RSPVGSANGIPODSASQASRVQVAICTLDENDNAPQLAEPYDTFVCDGAPGQLIVIRA 540
DB 481 RSPVGSANGIPODSASQASRVQVAICTLDENDNAPQLAEPYDTFVCDGAPGQLIVIRA 540
QY 541 LDRDEVGNSSHVSFGPLGPDANFTVQDNRDGSASILLPSRPAPRHAAYLVPIELMDWG 562
DB 541 LDRDEVGNSSHVSFGPLGPDANFTVQDNRDGSASILLPSRPAPRHAAYLVPIELMDWG 562

Db 503 LDRDEVGNSSHVSFGPLGPDANFTVQDNRDGSASILLPSRPAPRHAAYLVPIELMDWG 562
QY 577 HPLMASASSWLH-----WPPAERGNDPASOG 603
Db 563 QPALSTATVTVSVCCQCPDGSVASGCPBAHLASAGLSTG 602

Search completed: December 8, 2004, 11:34:26
Job time : 651.891 secs

This Page Blank (usp)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 75.8394 Seconds
(without alignments)
556.152 Million cell updates/sec

Title: US-09-788-051-4

Perfect score: 3354
Sequence: 1 MWGLVRLILMLGWMGCMGR.....LPSCQLPLGIPALGIVLCAS 636

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1607	47.9	693	2	US-08-738-349-6
2	1607	47.9	693	4	US-09-918-457-55
3	1607	47.9	796	2	US-08-738-349-4
4	1602	47.8	796	1	US-08-188-228-58
5	1602	47.8	796	1	US-08-332-643-52
6	1602	47.8	796	1	US-08-332-643-58
7	1602	47.8	796	4	US-09-654-328-2
8	1596	47.6	796	2	US-08-738-349-2
9	1530.5	45.6	799	1	US-08-188-228-42
10	1530.5	45.6	799	1	US-08-332-638-42
11	1529.5	45.6	793	1	US-08-188-228-54
12	1529.5	45.6	793	1	US-08-332-643-48
13	1529.5	45.6	793	1	US-08-332-638-54
14	1493	44.5	615	2	US-08-738-349-12
15	1468	43.8	532	1	US-08-188-228-44
16	1468	43.8	532	1	US-08-332-638-44
17	1365.5	40.7	794	1	US-08-188-228-60
18	1365.5	40.7	794	1	US-08-332-643-54
19	1365.5	40.7	794	1	US-08-332-638-60
20	1136.5	33.9	653	1	US-08-188-228-46
21	1136.5	33.9	653	1	US-08-332-638-46
22	938.5	28.0	780	1	US-08-188-228-50
23	938.5	28.0	780	1	US-08-332-643-44
24	938.5	28.0	780	1	US-08-332-638-50
25	596	17.8	906	4	US-09-417-039-11
26	591	17.6	913	2	US-08-474-067-6
27	591	17.6	913	2	US-08-474-068A-6

28	591	17.6	913	2	US-08-472-481-5	Sequence 5, Appli
29	586	17.5	837	2	US-08-474-067-7	Sequence 7, Appli
30	586	17.5	837	2	US-08-474-068A-7	Sequence 7, Appli
31	586	17.5	837	2	US-08-472-481-6	Sequence 6, Appli
32	580.5	17.3	555	2	US-08-453-702A-98	Sequence 98, Appli
33	576	17.2	556	1	US-07-998-003A-98	Sequence 98, Appli
34	576	17.2	556	1	US-08-453-274B-98	Sequence 98, Appli
35	576	17.2	556	1	US-08-453-695A-98	Sequence 98, Appli
36	576	17.2	556	1	US-08-268-161A-98	Sequence 98, Appli
37	576	17.2	556	3	US-09-099-639-98	Sequence 98, Appli
38	574.5	17.1	712	2	US-08-474-067-2	Sequence 2, Appli
39	574.5	17.1	712	2	US-08-474-067-5	Sequence 2, Appli
40	574.5	17.1	712	2	US-08-474-068A-2	Sequence 2, Appli
41	574.5	17.1	712	2	US-08-472-481-5	Sequence 5, Appli
42	574.5	17.1	712	2	US-08-472-481-2	Sequence 2, Appli
43	574.5	17.1	717	2	US-08-474-067-4	Sequence 4, Appli
44	574.5	17.1	717	2	US-08-474-068A-4	Sequence 4, Appli
45	574.5	17.1	717	2	US-08-472-481-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-738-349-6
Sequence 6, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amann, Egon
TITLE OF INVENTION: Bone-Related Cadherin-like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 693 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-6

Query Match 47.9%; Score 1607; DB 2; Length 693;
Best Local Similarity 50.5%; Pred. No. 1.9e-134;
Matches 324; Conservative 98; Mismatches 133; Indels 86; Gaps 10;

17 CMGSLA-----APAR-----AMAGSRB--HPCGALLRTRRSVWVNOFVIEEYAGEPEV 63
13 CIGMICHSHAPRERGHRLRPSFGHHEKGEQGVLRKSKRGWVNOFVIEEYTGDDPV 72
64 LIGKLSHVDNDEGRTKYLITGEGAGTVFIDEATGNHTKSLDREKKAQYVLLAQAVID 123
73 LVGLHSDIDSGDGNIKYILSGEAGTIFVDDSGNHAHTKTLIDREERAOYTLMAQAVD 132
124 RASNPRLPPEPSEFIKQDINDNPPILPGPYHATVEMSNVGTSVIQTVAHDADDPSTG 183
133 RDTNRPLPPEPSEFIKQDINDNPPILPGPYHATVEMSNVGTSVIQTVAHDADDPSTG 192
184 NSAKLVYTVLDGLPFPSVDPOQTVGVRATIPMDRETOEFLVVIQAQDMGSHMGSLGST 243
193 NSAKLVYTVLDGLPFPSVDPOQTVGVRATIPMDRETOEFLVVIQAQDMGSHMGSLGST 252
244 TVTVLSDVNDNPPKPFQSLVQFVSVEVETAGGTLVGRADDPDGLGNALMAYSLIDGEG 303
253 KVTITLTVDNDNPPKPFQSLVQFVSVEVETAGGTLVGRADDPDGLGNALMAYSLIDGEG 312
304 SEAFSISTDLOGRDLTVRKPLDFESQRSYFVEATNTLIDPAVLRGPFKDVASVRY 363
313 MESFEITTDYETQEGVILKPKVPDFETKRAVSLKVEANVHIDPKFISNGPFKDTVTYKI 372
364 AVQDAPPEPAPTQAAYHLTVPENKAPGTLVQISAADLDPASPIRISILPHSDPERCS 423
373 AVEADEPMPMLASYSIHEVENAAGTVGVRHAKDPDANSPIRISIDRHDTDLDRFT 432
424 IOPEGTHITAPLDREARAWHNTLVATELGWSWGERGVVPLVAEMSAAPAPQSRP 483
433 INPDGFIKTTPKLDRETAHLNITVPAEL----- 463
484 VGSAGVIGPOSSAQSRYOVAIOTLDENDNAPOLAEYDTFVCD-----AAPGLIQVIR 539
464 -----HNRHBEAKVPVAIRVLDVNDNAPKPAAYEGFICSDQTKPLSNQPIYIS 514
540 ALDRDEVGNSSHVSFGCP--LGPDAFTVQDNRLPA-----WFHPLLM 581
515 ADDKDDTANGRRPFIPLPEIHHNPFTVRDNRNNTAGVYARRGFSRQKODLYLPIVI 574
582 ASASSWLMHPPAERGNOPASQKSSLP-CG-RLPGALPSC 620
575 -----SDGIRPPMSSTNTLTITKVCQDVNGALLSC 604

Db

RESULT 2
US-09-919-497-55
/ Sequence 55, Application US/09919497
/ Patent No. 6773883
/ GENERAL INFORMATION:
/ APPLICANT: Muller, George I.
/ TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
/ FILE REFERENCE: B0801/7225
/ CURRENT APPLICATION NUMBER: US/09/919,497
/ PRIOR FILING DATE: 2001-07-31
/ PRIOR APPLICATION NUMBER: US 60/221,735
/ NUMBER OF SEQ ID NOS: 100
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 55
/ LENGTH: 693
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-919-497-55

Query Match 47.9%; Score 1607; DB 4; Length 693;
Best Local Similarity 50.5%; Pred. No. 1.9e-134;
Matches 324; Conservative 98; Mismatches 133; Indels 86; Gaps 10;

QY 17 CMGSLA-----APAR-----AMAGSRB--HPCGALLRTRRSVWVNOFVIEEYAGEPEV 63
DB 13 CIGMICHSHAPRERGHRLRPSFGHHEKGEQGVLRKSKRGWVNOFVIEEYTGDDPV 72
QY 64 LIGKLSHVDNDEGRTKYLITGEGAGTVFIDEATGNHTKSLDREKKAQYVLLAQAVID 123
DB 73 LVGLHSDIDSGDGNIKYILSGEAGTIFVDDSGNHAHTKTLIDREERAOYTLMAQAVD 132
QY 124 RASNPRLPPEPSEFIKQDINDNPPILPGPYHATVEMSNVGTSVIQTVAHDADDPSTG 183
DB 133 RDTNRPLPPEPSEFIKQDINDNPPILPGPYHATVEMSNVGTSVIQTVAHDADDPSTG 192
QY 184 NSAKLVYTVLDGLPFPSVDPOQTVGVRATIPMDRETOEFLVVIQAQDMGSHMGSLGST 243
DB 193 NSAKLVYTVLDGLPFPSVDPOQTVGVRATIPMDRETOEFLVVIQAQDMGSHMGSLGST 252
QY 244 TVTVLSDVNDNPPKPFQSLVQFVSVEVETAGGTLVGRADDPDGLGNALMAYSLIDGEG 303
DB 253 KVTITLTVDNDNPPKPFQSLVQFVSVEVETAGGTLVGRADDPDGLGNALMAYSLIDGEG 312
QY 304 SEAFSISTDLOGRDLTVRKPLDFESQRSYFVEATNTLIDPAVLRGPFKDVASVRY 363
DB 313 MESFEITTDYETQEGVILKPKVPDFETKRAVSLKVEANVHIDPKFISNGPFKDTVTYKI 372
QY 364 AVQDAPPEPAPTQAAYHLTVPENKAPGTLVQISAADLDPASPIRISILPHSDPERCS 423
DB 373 AVEADEPMPMLASYSIHEVENAAGTVGVRHAKDPDANSPIRISIDRHDTDLDRFT 432
QY 424 IOPEGTHITAPLDREARAWHNTLVATELGWSWGERGVVPLVAEMSAAPAPQSRP 483
DB 433 INPDGFIKTTPKLDRETAHLNITVPAEL----- 463
QY 484 VGSAGVIGPOSSAQSRYOVAIOTLDENDNAPOLAEYDTFVCD-----AAPGLIQVIR 539
DB 464 -----HNRHBEAKVPVAIRVLDVNDNAPKPAAYEGFICSDQTKPLSNQPIYIS 514
QY 540 ALDRDEVGNSSHVSFGCP--LGPDAFTVQDNRLPA-----WFHPLLM 581
DB 515 ADDKDDTANGRRPFIPLPEIHHNPFTVRDNRNNTAGVYARRGFSRQKODLYLPIVI 574
QY 582 ASASSWLMHPPAERGNOPASQKSSLP-CG-RLPGALPSC 620
DB 575 -----SDGIRPPMSSTNTLTITKVCQDVNGALLSC 604

Db

RESULT 3
US-08-738-349-4
/ Sequence 4, Application US/08738349
/ Patent No. 5869638
/ GENERAL INFORMATION:
/ APPLICANT: Takeshita, Sunao
/ APPLICANT: Okazaki, Makoto
/ APPLICANT: Kawai, Shinji
/ APPLICANT: Tsujimura, Asumi
/ APPLICANT: Amami, Egon
/ TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
/ TITLE OF INVENTION: Process for Its Production
/ NUMBER OF SEQUENCES: 12
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
/ ADDRESS: 1300 I Street, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/738,349

Wed Dec 8 11:46:29 2004

us-09-788-051-4.rai

Page 3

FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.123--00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-4

Query Match 47.9%; Score 1607; DB 2; Length 796;
Best Local Similarity 50.5%; Pred. No. 2,4e-134;
Matches 324; Conservative 98; Mismatches 133; Indels 86; Gaps 10;

17 CMGRLA-----APAR-----AMAGSRE--HGPALLRTRRSWVWVNFVIEEYAGPEPV 63
13 CLGMLCHSHAFAPRRRGLRPSFHGHEKKEGVQLORSKRGWVWVNFVIEEYAGPEPV 72
64 LIGLHSHVDSGEGRKTYLLTGAGATVVIDEATGNIHVTSLSDEEKAQVYLLAQAYD 123
73 LVGRHSHDIDSGDNKIKYLLSGGAGTIFVIDKSGNIAHATKIDREERAAQVYLLAQAYD 132
124 RASNRPLEPPEPSEPIIKGODINDNPPIFPLGPHATVPENSVGTSVIQTAAHDADPSYG 183
133 RDTNRPLEPPEPSEPIIKGODINDNPPIFPLGPHATVPENSVGTSVIQTAAHDADPSYG 192
184 NSAKLYTVVLDGLPFPSVDPQTGVVTRTIPMDRETOEFLVYIOAKDMGSHGSLGTT 243
193 NSAKLYTVVLDGLPFPSVDPQTGVVTRTIPMDRETOEFLVYIOAKDMGSHGSLGTT 252
244 TVVTLSDVNDNPPKPEPPOSIVYFVETAGPGLVGRLRADDPDLGDNALMAVSIIDGEG 303
253 KVTITLTDVNDNPPKPEPPOSIVYFVETAGPGLVGRLRADDPDLGDNALMAVSIIDGEG 312
304 SEAFSISTDLQGRDGLTVRKPLDFESQRSYSFRVEATNTLIDPAYLRGPFKDVASVRY 363
313 MESFEITTDVETOEGVILKAKKPVDFETKRAVSLKYEANVHIDPFISNGPFKDVTVYVKI 372
364 AVQDAPEPPAFTQAAYHLTVPENKAPGLVGOISAADLSPASPIRYSIILHSPERCS 423
373 AVEDEDEPMTLAPSYIHVEQENAAAGTVGRVNAKDDAANSPIRYSIDHTDLDRTFT 432
424 IOPEEGTITHTAALDREKRAMHNTLVLATELGMSWGPGRVPLLVAMSPAAPPOKSP 483
433 INPEEGFIKTKRPLDREFTAMNITVFAAEI----- 463
464 VGSANGITPODSSAQSRVQVALQITLDNDNAPQALAPYDFTVYCS---AAPGOLIQVIR 539
464 HNEHQAKVPAVALRVLDVNDNAKFAAPYEGFICSDQTKPLSNDFITIS 514
540 ALDREVGNSSHVSEFGP--LGPDAFTVQDNRLDPA-----MFHPLLM 581
515 ADDKODTANGRRFISLPEIILHNPNFTYRDNRDNTAGVYARAGGFSROKQDLYLLPIVI 574
582 ASASSWLMHPAERGNQAPASQGSLLP--CG--RLTGALPSC 620
575 -----SDGGIPEWSSNTNLTILIKVCGDGVNALLSC 604

RESULT 4
US-08-188-228-58

Sequence 58, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray &
ADDRESSER: Borum
STREET: 6300 Seare Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-58

Query Match 47.8%; Score 1602; DB 1; Length 796;
Best Local Similarity 50.4%; Pred. No. 6,6e-134;
Matches 323; Conservative 98; Mismatches 134; Indels 86; Gaps 10;

17 CMGRLA-----APAR-----AMAGSRE--HGPALLRTRRSWVWVNFVIEEYAGPEPV 63
13 CLGMLCHSHAFAPRRRGLRPSFHGHEKKEGVQLORSKRGWVWVNFVIEEYAGPEPV 72
64 LIGLHSHVDSGEGRKTYLLTGAGATVVIDEATGNIHVTSLSDEEKAQVYLLAQAYD 123
73 LVGRHSHDIDSGDNKIKYLLSGGAGTIFVIDKSGNIAHATKIDREERAAQVYLLAQAYD 132
124 RASNRPLEPPEPSEPIIKGODINDNPPIFPLGPHATVPENSVGTSVIQTAAHDADPSYG 183
133 RDTNRPLEPPEPSEPIIKGODINDNPPIFPLGPHATVPENSVGTSVIQTAAHDADPSYG 192
184 NSAKLYTVVLDGLPFPSVDPQTGVVTRTIPMDRETOEFLVYIOAKDMGSHGSLGTT 243
193 NSAKLYTVVLDGLPFPSVDPQTGVVTRTIPMDRETOEFLVYIOAKDMGSHGSLGTT 252
244 TVVTLSDVNDNPPKPEPPOSIVYFVETAGPGLVGRLRADDPDLGDNALMAVSIIDGEG 303
253 KVTITLTDVNDNPPKPEPPOSIVYFVETAGPGLVGRLRADDPDLGDNALMAVSIIDGEG 312
304 SEAFSISTDLQGRDGLTVRKPLDFESQRSYSFRVEATNTLIDPAYLRGPFKDVASVRY 363
313 MESFEITTDVETOEGVILKAKKPVDFETKRAVSLKYEANVHIDPFISNGPFKDVTVYVKI 372

QY 364 AVQDAPPEPFAFQAAYH/LTVPENKAPGTLVQGISAADLSPASPIRYSILPHSDPERCFS 423
 DB 373 SVEDADEPMPFLAPSYIHVEQENAAAGTVGVRAKDPDANSPIRISIDHTDLDFFT 432
 QY 424 IQPEEGTHTAPLDREARAHNLTVLATELGMSGMBRGVPLVAEMSAAPAPORSP 463
 DB 433 INPDEGFIKTPLDRETAHLNITVFAAEI----- 463
 QY 464 VGSAGVIGQDSSAQSRYOVAIQTLDENDNAPQLAEYDFVCDSD---AAPQLQIVIR 539
 DB 464 -----HNHQAQVPAIRVLDVNDNAKFAAPYEGFICSDQTKPLSNQPIVITIS 514
 QY 540 ALDRDEVNSSHVSGQP--LGPDAFTVQDNRDLPA-----WFFPLM 561
 DB 515 ADDKDDTANGPRFIFSLPEPIIHNPFTVRDNDNTAGVYARRGFSROKODLYLPIVI 574
 QY 582 ASASSMLHMPAERGNQASQKSSSLP-CG-RLPGALPSC 620
 DB 575 -----SDGIPPMSSNTNLTITKVCQCDVNGALLSC 604

RESULT 5
 US-08-332-643-52
 ; Sequence 52, Application US/08332643
 ; Patent No. 5639634
 ; GENERAL INFORMATION:
 ; APPLICANT: Suzuki, Shintaro
 ; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; STREET: Two First National Plaza, 20 South Clark
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60603
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/332,643
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/872,643
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5639634 and, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 27866/30795
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 346-5750
 ; TELEFAX: (312) 984-9740
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 52:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 796 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-332-643-52

QY Query Match 47.8%; Score 1602; DB 1; Length 796;
 Best Local Similarity 50.4%; Pred. No.6.6e-134;
 Matches 323; Conservative 96; Mismatches 134; Indels 86; Gaps 10;
 OY 17 CMGRLA-----APAR-----AWAGSRE--HPCGALLTRRSWVWVQFVIEIYAGPEPV 63
 DB 13 CLGMLGSHAFADERGRHLRPSFHGHHEKKEGQVLRGSKRGVWVWQFVIEIYAGPEPV 72

QY 64 LIQKLSHSDVRGEGRTKYLITGEGAGTVFIDEATGNLHVTSLIDREKAQVYLAAQAVD 123
 DB 73 LVGRHLSDDLSDGINKITILSGAGTIFVLDSSGNLHAKTKLIDREBAQTLLMAQAVD 132
 QY 124 RASNPPLPEPSSFIKQDINDNPEIPLGQPHATVPEMSVGVSVIQTADADDPESYG 183
 DB 133 RDTNPLPEPSEFIVKQDINDNPEPLHETVHANVPEPSNVGTSVIVQTSADDDPYTG 192
 QY 184 NSAKIVYTVLDGLPEPVSVDPOGVVTRTAIPMNDPEQTEFLVJVOAKMGHMGGLSGST 243
 DB 193 NSAKIVYSLBQPIFVSVAQGTGIRTLPLMNDRAKEHYVVOAKMGHMGGLSGST 252
 QY 244 TVTVTLSDVNDNPKPKPQSLYQFSVETAGETLVGRLAQDPDLDGNALMAYSILDGEG 303
 DB 253 KVTITLTVDNDNPKFPQRLYQMSVSEAAYGEEGRVKAQDPDIDGNGVTVNIVQDGS 312
 QY 304 SEAFSISDLDGRDGLTVRKPLDPESQGSYSFRVEANLITIDAYLRGFFKVAAYRV 363
 DB 313 MESFEITTDYETQEBGVILKKRVFETERAYSLKVEANVAHIDPKFISNGPFDVTYKI 372
 QY 364 AVQDAPPEPFAFQAAYH/LTVPENKAPGTLVQGISAADLSPASPIRYSILPHSDPERCFS 423
 DB 373 SVEDADEPMPFLAPSYIHVEQENAAAGTVGVRAKDPDANSPIRISIDHTDLDFFT 432
 QY 424 IQPEEGTHTAPLDREARAHNLTVLATELGMSGMBRGVPLVAEMSAAPAPORSP 463
 DB 433 INPDEGFIKTPLDRETAHLNITVFAAEI----- 463
 QY 464 VGSAGVIGQDSSAQSRYOVAIQTLDENDNAPQLAEYDFVCDSD---AAPQLQIVIR 539
 DB 464 -----HNHQAQVPAIRVLDVNDNAKFAAPYEGFICSDQTKPLSNQPIVITIS 514
 QY 540 ALDRDEVNSSHVSGQP--LGPDAFTVQDNRDLPA-----WFFPLM 561
 DB 515 ADDKDDTANGPRFIFSLPEPIIHNPFTVRDNDNTAGVYARRGFSROKODLYLPIVI 574
 QY 582 ASASSMLHMPAERGNQASQKSSSLP-CG-RLPGALPSC 620
 DB 575 -----SDGIPPMSSNTNLTITKVCQCDVNGALLSC 604

RESULT 6
 US-08-332-638-58
 ; Sequence 58, Application US/08332638
 ; Patent No. 5646250
 ; GENERAL INFORMATION:
 ; APPLICANT: Suzuki, Shintaro
 ; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
 ; NUMBER OF SEQUENCES: 62
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; STREET: 6300 Sears Tower, 233 S. Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/332,638
 ; FILING DATE: 01-NOV-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/872,643
 ; FILING DATE: 17 APR 1992
 ; APPLICATION NUMBER: US/08/049,460
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:

```

1      NAME: No. 5646250and, Greet
2      REGISTRATION NUMBER: 35,100
3      REFERENCE/DOCKET NUMBER: 3
4      TELECOMMUNICATION INFORMATION
5      TELEPHONE: (312) 474-6300
6      TELEFAX: (312) 474-0448
7      TELEX: 25-3886
8      INFORMATION FOR SEQ ID NO: 58:
9      SEQUENCE CHARACTERISTICS:
10     LENGTH: 796 amino acids
11     TYPE: amino acid
12     TOPOLOGY: linear
13     MOLECULE TYPE: protein
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
101
```

Query Match	47.8%	Score 1602	DB 1	Length 796
Best Local Similarity	50.4%	Pred	No. 5.6e-134	
Matches 323, Conservative	38	Mismatches	134	Indels 86
		Gaps	10	

```

Cy 1 CMRLA-----AAR-----AMAGRE--HBPPLLTRBSMWNQCFVIEEVAAGEPV 63
Db 13 CLGMLCHSAFAFERRGHLRPSFHGHEKXKGOVLQSKRGWVNOQFVIEETGSDPV 72
Cy 64 LIGHLSVDVRGEGRTKYLITGEAGTVFIDATGNHVTKSLDREKAQVYLLAOVD 123
Db 73 LVGLHSDIDISGGDNKTYLISGGAOTIFVIDDKSGNHATKTLDRERAAQVTLMAAVD 132
Cy 124 RASNRLEPSESEFIIGODINDNPFLEPQPHATVPSEMSNGTSVIVTMAHDDPSYG 183
Db 133 RDNTRLEPSESEFIIVAYQDINDNPEFLHETTHAVPESNGTSIVLQVTSADDDPYG 192
Cy 184 NSAKLVTVVDGLPFFSVDPOGVARTAIENNDRETQEEFLVYIQAKYMGHGGSGST 243
Db 193 NSAKLVYSILEGPPYFSEVAQGTIIRTALENNDREKKEHYHVALQAKMGHGGSGST 253
Cy 244 TVVTVLSDVDNNDPKKPPQSLQYFSSVETIAGFGLVGRRAQDPDLDGDMALMAYSILDQEG 303
Db 253 KVTITLTDVNDNPPKPPQRLQMSVEBAVPGEVGRVAKADPDIGENGLVTYNIIVDQD 312
Cy 304 SEAFSISTDLQSGDGLTVRKPLPDSQSSYFRRZEAATNTLIDPAXLYARGPFXVASRV 366
Db 313 MESEIITDYTEDEGVATLKKPVPDETERAYSIKYEAAVNHIDEPFISNGPKQTVYKI 372
Cy 364 AVQDAPERPAPFTQAAHYLTVPENKAGITLVQIISAULDSPASPITYSLPHSDPERFS 422
Db 373 SVEDADERPFWLAPSYIHEQENAAAGTVAGRVHADPPAANSPIRYSIDHTLDRFFT 432
Cy 424 IOPEEGITHFAALPDEBARAHNLTVLATLELOKMSWGRKGVPLLVAMSAAPAPQOSP 483
Db 433 INPBDGIKTKTKPLDRBETMLNITYFAAI-----466
Cy 484 VGSALVGIPODSSAQASHVOYAIQTDENDNAPOLAEPYDTFYCDS---AAPQOLIQYR 533
Db 464 -----NHRHOEACVPVALRVLDVNDNAPKFAFAPYEGFICESDQTKP,SNQPIVTIS 514
Cy 540 ALPDEVGNSSHVSFCQF--LGDANFYQVODNRDLJA-----WPHPLM 587
Db 515 ADDKDPIANPFRFISLPEIINHNPYIVRDNDRNTAGVYARGGFSQKODIYLLPIVI 574
Cy 582 ASASSWILHPEAPERGNOPASQGSSSLP--CG-RLPALPSC 620
Db 575 -----SDGILPMSSTNTLITIKYCGDVNGALLSC 604

```

```

? FILE REFERENCE: B080177167/ENR/MAT
? CURRENT APPLICATION NUMBER: US/09/654,328
? CURRENT FILING DATE: 2000-09-01
? PRIOR APPLICATION NUMBER: US 60/152,456
? PRIOR FILING DATE: 1999-09-03
? PRIOR APPLICATION NUMBER: US 60/153,490
? PRIOR FILING DATE: 1999-09-13
? NUMBER OF SEQ ID NOS: 12
? SOFTWARE: FastSeq for Windows Version 3.
? SEQ ID NO 2
? LENGTH: 796
? TYPE: prt
? ORGANISM: Homo Sapiens
US-09-654-328-2

```

Query Match	47.8%	Score	1602	DB	4	Length	796
Best Local Similarity	50.4%	Pred. No.	6.6e-134				
Matches	323	Conservative	98	Mismatches	134	Indels	86
						Gaps	10

```

0Y 17 CMEPLA-----APAR-----AMASPRE--HGPAL,ALTRRSWMWNOFFVIEEYACBEPV 63
Dd 13 CLEMLCHSHAFAPBERGHLPSEFHGHHEKKGKCGQLQSKXGKGMWNOGFVIEEYTGDDPV 72
0Y 64 LIGKHSYDVRGEGRRKTYLLTGEAGYVIVDAETGNHVTXKSIDREPKQOYVTLMAOAVD 123
Dd 73 LVGRHSDDIDSGGNKTYLLSGEAGGTVFVLDGSKGNHAKTYLLDRERAOYVTLMAOAVD 122
0Y 124 RASNRLPEPSEPTIIGQDINDNPRPIFLPGYHAHVAPMSNVGTSVIQTVAHADDBSYG 183
Dd 133 RQINRLPEPSEPTIYKQDINDNPEEFHETHAHVAPRSNVGTSVIQTVAHADDBPYG 192
0Y 184 NSAKLYTVYDGLPFPSVDPQTCGVRTALPNMDETOEELFVIVIOADMGGHMGSLSGST 243
Dd 193 NSAKLYVSIIEGGPYSEVAGTGLIRTALPNMDSRANEKHVIVIOADMGGHMGSLSGST 253
0Y 244 TVTVTLSDVNDNPKPFOGLYQFSVETGAPGTLVGRLAODPDLGDNALMAYSILDEEG 303
Dd 253 KVTITTLVDVNDNPKPFOQLYOMYSSEAVPEEVEGRVKADPDIENGALTVYNIIVGDCG 312
0Y 304 SEAFSISTDQGGDGLTVRKPLDPEOSOSYFRVEANTLIDAYLRPGCFKQVAVRV 363
Dd 313 MBSREITTDYETGEGYIKLKKRVEDTERAHSKTEALNANHIDKFTINSNGFOTYVYKI 372
0Y 364 AVODAPEPPAFTQAAVHTLVPENKAPGTVLQGISADIDSPASPIRISILPHSDPERCFS 422
Dd 373 SVBDADEPPFHLFSPYSIHEVCERMAAGVYGVNAKDDANSPIRYSIDRHTLDDFFT 432
0Y 424 IOPEEGITHPAALDSEARAMENLTVLATELMSGMPGRGVPLLVMEWSAPAAPORSP 483
Dd 433 INEDDGIKTKTKLDEEETAMNITVFPAEI----- 463
0Y 484 VGSVAVGIPQDSSAQSRVQVATQTLDENDNAPQLAEPTDTCDS----AAPGLQIVIR 533
Dd 464 -----HNHQEQVAVAIRVLDVANDNAKKEFAPEGEFTCSBDQTKPLSNQPIVTIS 514
0Y 540 ALDRDEVGNSSHVSFGQP--LGPDPANFTVQDNRDLPA-----WFHPLM 581
Dd 515 ADDKDOTANGPRFITFLPELTIHNPFVTRVDRODTAGVYARAGGFSRKHODLYLPIVI 574
0Y 582 ASASSMHMPAPARGNQPASQGSLSLP--CG--RLGALPSC 620
Dd 575 -----SDGQ,LPWMSNTVITLITIKVCGGDVAGALLSC 604

```

RESULT 7
 US-09-654-328-2
 ; Sequence 2, Application US/09654328
 ; Patent No. 6787136
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Brenner, Michael B.
 ;
 ; APPLICANT: Valencia, Xavier
 ;
 ; TITLE OF INVENTION: Methods and Compositions for Treatment
 ; of Inflammatory Disease Using Cachectin-11 Modulating Agents

RESULT 8
US-08-738-349-2
Sequence 2, Application US/08738344
Patent No. 5859638
GENERAL INFORMATION:
APPLICANT: Takeshi, Sunao
APPLICANT: Okada, Makoto
APPLICANT: Kawai, Shunji
APPLICANT: Tsujimura, Akenoshi

APPLICANT: Amano, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-2

Query Match 47.6%; Score 1596; DB 2; Length 796;
Best Local Similarity 50.7%; Pred. No. 2,3e-133;
Matches 317; Conservative 97; Mismatches 127; Indels 84; Gaps 8;

31 SREHP-----GPAIIKTRRSWVNOFFVIEHYAGPEVLLGKLSVDVREGRT 79
29 SHLPSTFHGHEKKEQVLOKRSRGVWVNOFFVIEHYGPDVVLGRHSDIDSGDNI 88
80 KYLTGEGAGTVEIDATGNIHYTKSLDREKAQYVLLAQAVDRASNRPLEPSPFFIK 139
89 KYLSGEGAGTIFVIDKSGNIHATKTLDBERAAQYTLMAQAVDRDTRNRLPEPSPFFIK 148
140 GQDINDNPPIFLPGPHATVPENSNVGTSTVQYTAHDADDPSTGNSAKLYTVVLGDPFF 199
149 VQDINDNPPEFLHETIYANVPERSNVGTSTVQYASDADDPYTGNSAKLYTSLTEQPYF 208
200 SVDPQGVVRLTALPNMDRETQEEFLVYIAKMGKMGSGSTTVTLTSPDNDNPKF 259
209 SVKQGTIITLALPNMREKEREHYVIAKMGKMGSGSTTKTITLTDVNDNPPKF 268
260 POSTLYPSSVETAGPTGLVRLAODPDLDGNAALMAYSLDGESEAFSITDLOGRDL 319
269 POSTYQMSVSEAVPGEVGRVAKAPDIDENGLVYINLYDGGIGELFEITDYEYODGV 328
320 LTVKAPLDFESQSSYSRVEATNTLLIDPAYLRGPFDDVASVAVVAVODAPPPAFQAY 379
329 VKLKKPVDEFTKRAYSLIKIAPAVNHIDPKTISNGPRDITVYKISVEDADEPMPFLAPSY 388
380 HLTVPENKAGTLVGQISADLDSPASPIRYSILPSPDPCPSIQPEGTHTTAFLDR 439
389 IHEVQENAAAGTAVGVRAHDPDANSPIRYSIDRHTDLDRPFTINPEDGFIKTKPFLDR 448

440 EAWAHNLTVALTELQMSWGPERGVPLVAEWSAPAPQORSPVSAVGIPODSSAQAS 499
445 EETALNTLSVPAEL-----HNRQET 470
500 RVOVALIQTLDENDNAPOLAEPYDTFVCSAAP---GGLIVRLDREYGNSSHSFQ 555
471 KVPVIRVLDVVDNAPKPAAYEGFICSDHPKALSNQPIYVADDDDTANGPRTFS 530
556 GP--LGPANFTVQDNRDLPA-----WFHPLMASASWLMHPAERGN 597
531 LPPEIMHNFTVRNDRNTAGVYARRGGFBRKODPYLDIVL-----SDGI 579
598 QPASQKSSSLP-CG-RLPGALPSC 620
580 PMSSTNLTITIKVCCDVNALLSC 604

RESULT 9
US-08-188-228-42
Sequence 42, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Grete E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-42

Query Match 45.6%; Score 1530.5; DB 1; Length 799;
Best Local Similarity 47.9%; Pred. No. 1.6e-127;
Matches 300; Conservative 110; Mismatches 135; Indels 81; Gaps 9;

39 LILTRRSWVNOFFVIEHYAGPEVLLGKLSVDVREGRTKYLITGEGAGTVEIDAT 98
56 LNRSGRGVWVNOFFVLEFSGPPIVGRHTDLPSSKIKYLSGAGTIFINDIT 115
99 GNHYTKSLDREKAQYVLLAQAVDRASNRPLEPSPFFIKQDINDNPPIFLPGPHAT 158

```

Db 116 GDIHAIRLDRREKAEYTLTQAQVDMETNKELEPPSEFIITKQVODINDNAPEFLNGPHAT 175
QY 159 VPENSNVGTSVIQTADADADPSYNSAKLYVTYLDGLPFESVDPQGTGVRTAI PNMDRE 218
Db 176 VPENSIIGTSTVNTATADADDPVYNSAKLYVSILEGQYFISIEPETAIIKTALPNMDRE 235
QY 219 TQEEFLVYIAQKMGHNGHSGSTTYVTYLSDVNDNPKPEOSLYXOFSTVETAGRTV 278
Db 236 AKEEYLVVIAQKMGHSGSGSLGTTTLVTLTVNDNPKPKAOSLYHFSVPEDVLTGTAI 295
QY 279 GRLAODPDLGDNALMAVYSLDGESEAFSISTDLQGRDGLTVRKPLDFESQSYSPRV 338
Db 296 GRVANDODIGENNAOSSYDIIIDGGTALFELTSDAQAOQGVIRLKRPLDEFETKSYTLKV 355
QY 339 EATNTLIDPAYLRGPFKDVASVAVQADAPPEPAFTQAAHYLTVPENKAPGLTVQISA 398
Db 356 EAANHIDPFRSGRGPFDXTATVKIYVEDADEPEVFSPTYLEHENAALNSVIGQVTA 415
QY 399 ADLSPASPIRYSILPHSDPERCFISOEEGTHTTAAPLDREARAHNLTVALTELGMSW 458
Db 416 RDPDITSSPIRFSIDRHTDLERQFNINADDKITLATPLDRLSWHNSIATET----- 471
QY 459 GPERGWVPLVAVMSAPAPQSPVGSVAVGIPODSSAQASRVQVATQTLDENNDAPOLA 518
Db 472 -----LPAWFPLMLASASSWLHMPAERGNOPASQKSSSL-PCG-RLPGA 616
QY 519 EPYDTFVCDASAPGQLIOVIRALDRDEVGNSSHVSGPLGPD-----ANFTVQDNRD--- 571
Db 498 SEYEAFLECNKGPQGVITQVSAMDKDPKNGHP--FLYSLLPEVNNPNFTIKKEDNSL 555
QY 572 -----LPAWFPLMLASASSWLHMPAERGNOPASQKSSSL-PCG-RLPGA 616
Db 556 SIKXNGFNROKQOEYVLLPIVI-----SDSGNPPLSTSTLTITIRVCCGSDGV 604
QY 617 LPSCQ-----LPLGT---PALGIYLC 634
Db 605 VQSCNVEAYVLPGLSMGALIALIAC 630

```

RESULT 10

US-08-332-638-42

Sequence 42, Application US/08332638

Patent No. 5646250

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/332,638

FILING DATE: 01-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/872,643

FILING DATE: 17 APR 1992

APPLICATION NUMBER: US/08/049,460

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: No. 5646250and, Greta E.

REGISTRATION NUMBER: 35,302

```

REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-332-638-42
Query Match
Best Local Similarity 45.6%; Score 1530.5; DB 1; Length 799;
Matches 300; Conservative 110; Mismatches 135; Indels 81; Gaps 9;

```

39 LIRTRSWYVWQFVYIEYAGEPEVYIGKLSVDVDRGGRKYLITGBAGTVFVIDEAT 98

56 LRSKKGWYVWQFVYIEYAGEPEVYIGKLSVDVDRGGRKYLITGBAGTVFVIDEAT 115

99 GNHVTKSLDREKXQVYLLAQAVDASNRPLEPSEFIITKQVODINDNAPEFLNGPHAT 158

116 GDIHAIRLDRREKAEYTLTQAQVDMETNKELEPPSEFIITKQVODINDNAPEFLNGPHAT 175

159 VPENSNVGTSVIQTADADADPSYNSAKLYVTYLDGLPFESVDPQGTGVRTAI PNMDRE 218

176 VPENSIIGTSTVNTATADADDPVYNSAKLYVSILEGQYFISIEPETAIIKTALPNMDRE 235

219 TQEEFLVYIAQKMGHNGHSGSTTYVTYLSDVNDNPKPEOSLYXOFSTVETAGRTV 278

236 AKEEYLVVIAQKMGHSGSGSLGTTTLVTLTVNDNPKPKAOSLYHFSVPEDVLTGTAI 295

279 GRLAODPDLGDNALMAVYSLDGESEAFSISTDLQGRDGLTVRKPLDFESQSYSPRV 338

296 GRVANDODIGENNAOSSYDIIIDGGTALFELTSDAQAOQGVIRLKRPLDEFETKSYTLKV 355

339 EATNTLIDPAYLRGPFKDVASVAVQADAPPEPAFTQAAHYLTVPENKAPGLTVQISA 398

356 EAANHIDPFRSGRGPFDXTATVKIYVEDADEPEVFSPTYLEHENAALNSVIGQVTA 415

399 ADLSPASPIRYSILPHSDPERCFISOEEGTHTTAAPLDREARAHNLTVALTELGMSW 458

416 RDPDITSSPIRFSIDRHTDLERQFNINADDKITLATPLDRLSWHNSIATET----- 471

459 GPERGWVPLVAVMSAPAPQSPVGSVAVGIPODSSAQASRVQVATQTLDENNDAPOLA 518

472 -----LPAWFPLMLASASSWLHMPAERGNOPASQKSSSL-PCG-RLPGA 616

519 EPYDTFVCDASAPGQLIOVIRALDRDEVGNSSHVSGPLGPD-----ANFTVQDNRD--- 571

498 SEYEAFLECNKGPQGVITQVSAMDKDPKNGHP--FLYSLLPEVNNPNFTIKKEDNSL 555

572 -----LPAWFPLMLASASSWLHMPAERGNOPASQKSSSL-PCG-RLPGA 616

556 SIKXNGFNROKQOEYVLLPIVI-----SDSGNPPLSTSTLTITIRVCCGSDGV 604

617 LPSCQ-----LPLGT---PALGIYLC 634

605 VQSCNVEAYVLPGLSMGALIALIAC 630

RESULT 11

US-08-188-228-54

Sequence 54, Application US/08188228

Patent No. 5597725

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun

```
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-54

Query Match      45.6%; Score 1529.5; DB 1; Length 793;
Best Local Similarity 47.8%; Pred. No. 1.9e-127;
Matches 299; Conservative 111; Mismatches 135; Indels 81; Gaps 9;

QY 39 L L R T R S W N Q P F V I E E Y A G P E P V L I G K L H S P D V R G E G T K Y L T G E G A G T V I D E A T 98
DB 49 L N R S K R G W N Q M V L E F S G P E I L V G R L H T D L D P S K I K I X I L S D G A G T I F Q I N D V T 108
QY 99 G N I H V T S L D R E E K A Q V L L A Q A V D R A S N R P L E P S E F I I K G O D I N D N P I F P L G P Y H A T 158
DB 109 G D I H A I R L D R E E K A E Y T L T A Q A V D M E T S K P L E P S E F I I K V O D I N D N A P E F L N G P Y H A T 168
QY 159 V P E M S N V G T S V I Q V T A H D A D D P S Y G N S A K L V Y T V L D G L P F S V D P O T G V R T A I P M N D R E 218
DB 169 V P E M S I I G T S V T N T A T A D D P Y G N S A K L V S I L S G Q P F S I E P E T A I I K T A L P M N D R E 228
QY 219 T O E F L V I V I O A K M G M G M G L S G S T V T V T L S V N D N P K P F O S I Y Q F S V E T A G E G T I V 278
DB 229 A K E E Y L V I V I O A K M G H S G L S G T T L T V T L T V D N D N P P F A O S L Y H F S V E D V L G T A I 288
QY 279 G R L R A O P D L G D N A L M A Y S I L D G E S E A F S I T D L G R D D L V R K P L D F E S O R S A F R V 338
DB 289 G R V A N D O D I G E N A Q S S Y D I I D G D T A L F E I T S D A Q O D I I L R K P L D E T K S Y T L R D 348
QY 339 E A I N T L I D P A Y L A R G P K D V A S Y R A V A Q D A P E P P A F T O A Y H L T V E N K A P G T L V G O I S A 398
DB 349 E A A N V H I D P R F S G R G P K D A T A K I V E D A D E P P V S S P F Y L E V H E N A L N S V I G Q V T A 408
QY 399 A D D S P A S P I R S Y S T L P S D P E R C E S T O P E C G T I H T A P L D R E A R A H N T L V A T E L G M R W 458
DB 409 R D P D I T S S P I R S T I D R T D L E R G N I N A D G K I T L T P L D R E L S V H N T I T A T E L --- 464
QY 459 G P E R G W P L L V A E W S A P A P O R S P V G S A V G I P O D S A Q A S R V A I Q T L I D E N D A P O L A 518
DB 465 --- 490
QY 519 E P Y D T F V C S A A P G O L I Q V I R A L D R D E V G N S S I V S Q G P L G P D --- A N F T V Q D N R D --- 571
```

```
DB 491 S E Y A F L C E N G K P G V I Q T V S A M D K D P K N G H Y - F L Y S L P E M N M N N F T I K N E D N S L 548
QY 572 -----L P A M H P L I M A S S W L H W P A E R G N Q A S G K S S L - P C G - R L P G A 616
DB 549 S I L A K R G N R K O K E V L Y L P I I I -----S D S G N P L S S T S T I T I R V C C S N D G V 597
QY 617 L P S C Q -----L P L G I ---P A L G I V L C 634
DB 598 V O S C N V E A V L P I G L S M G A L I A I L A C 623

RESULT 12
US-08-332-643-48
Sequence 48, Application US/08332643
Patent No. 5639634
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray &
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-643-48

Query Match      45.6%; Score 1529.5; DB 1; Length 793;
Best Local Similarity 47.8%; Pred. No. 1.9e-127;
Matches 299; Conservative 111; Mismatches 135; Indels 81; Gaps 9;

QY 39 L L R T R S W N Q P F V I E E Y A G P E P V L I G K L H S P D V R G E G T K Y L T G E G A G T V I D E A T 98
DB 49 L N R S K R G W N Q M V L E F S G P E I L V G R L H T D L D P S K I K I X I L S D G A G T I F Q I N D V T 108
QY 99 G N I H V T S L D R E E K A Q V L L A Q A V D R A S N R P L E P S E F I I K G O D I N D N P I F P L G P Y H A T 158
DB 109 G D I H A I R L D R E E K A E Y T L T A Q A V D M E T S K P L E P S E F I I K V O D I N D N A P E F L N G P Y H A T 168
QY 159 V P E M S N V G T S V I Q V T A H D A D D P S Y G N S A K L V Y T V L D G L P F S V D P O T G V R T A I P M N D R E 218
DB 169 V P E M S I I G T S V T N T A T A D D P Y G N S A K L V S I L S G Q P F S I E P E T A I I K T A L P M N D R E 228
```



```

STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-738-349-12

Query Match          44.5%; Score 1493; DB 2; Length 615;
Best Local Similarity 50.9%; Pred. No. 2,3e-124;
Matches 308; Conservative 92; Mismatches 123; Indels 82; Gaps 15;

QY 36 GALLTRRSVWVNOQFVIEBYAGPEPVLLGKLSHDVDRGEGRTKYLITGEGAGTVFVID 95
DB 39 GQVORSKRGVWVNOQFVIEBYETGPDPVLRHLSHSDSDGNIKYLSSEGAGTTFVID 98
QY 96 EATGNIHVTKSLDEEKAQVYLLAQAVRASNRPLEPSPFFIIKGGDINDNPPIFPLGPY 155
DB 99 DKSNGIHATKTLDEEKAQVYLLAQAVDRDTPNPLEPSPFFIYXVDINDNPPF-LHEXY 157
QY 156 HATVPKNSVGTSTVQVTAHDADDPYSYNSAKLYVTLDLPFESVDPQGVVRAIAPMK 215
DB 158 HANVPKNSVGTSTVQVTAHDADDPYNSAKLYVTLDLPFESVDPQGVVRAIAPMK 217
QY 216 DRETQSEFLVVIQAKDGMGNGLSGSTVTVTLSDVNDNPKPFPOSLYQFSVETAGCG 275
DB 218 DREAKEEYHVYIQAQKDMGNGLSGSTTQVTLITLDVNDNPKPFPOSVQ-SVSEAAVQ 276
QY 276 TLVGRLLAODPDLDGMALMAVSLIDGSEAFSISTDLQGRDGLVVRKPLDRESQRTS 335
DB 277 BEVGRVAKDPDLDGSEAFSISTDLQGRDGLVVRKPLDRESQRTS 332
QY 336 FREVATNTLLDPALIRGPFKDVASVAVQADAPPAFTQAAYHLTVENKAPGTLVQ 395
DB 333 LK-EAANVHIDPKRISGPFKDYTVYKL-VEDADEPMTAPAYIHVEQENAAAGTVGR 390
QY 396 ISAADLDSAPSPRISLPLHSDEPSCSIOPEEGTHTTAAPLDREAPAMNLTVLATEIG 455
DB 391 VHKADPDPAANSPIRYSIDRHTDLPFTINPDEGFIKTKPLDREETAMINI-VFAAEI- 448
QY 456 WSMQPERGAVPLVAEWSADPAAPQSPVSAVGIQDSSAQASRYOVAICTLDENDNP 515
DB 449 -----HNRQEKVPAIRVLDVANDNP 470
QY 516 QLAEPYDTFCDSAPAGQLIQVIRALDRDEVGNSSHAVSQGPIDP---ANFTVQDNRL 572
DB 471 KFAAPYEGFICSDKLSNQ-PIVTSADDDDDTANGPFIISLP--PEIHNPENFTVRNDRN 527
QY 573 PA-----WFRPLMASASSWLHWPRAPERNQSPASQCKSSLP-CG-RLPG 615

```

```

DB 528 TAGVYARRGFRKQDYLPRLVIT-----SDGIRPMSTNTLITKCGCDVNG 576
QY 616 ALPSC 620
DB 577 ALLSC 581

RESULT 15
US-08-188-228-44
Sequence 44, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Boston
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-44

Query Match          43.8%; Score 1468; DB 1; Length 532;
Best Local Similarity 54.6%; Pred. No. 3,1e-122;
Matches 271; Conservative 89; Mismatches 98; Indels 38; Gaps 1;

QY 39 LLRTRRSVWVNOQFVIEBYAGPEPVLLGKLSHDVDRGEGRTKYLITGEGAGTVFVIDEAT 98
DB 56 LNRSKRGVWVNOQFVIEBFSGPEPILVGRHTDLPDSKKIKYLSGDSGAGTTFQINDIT 115
QY 99 GNHVTKSLDEEKAQVYLLAQAVRASNRPLEPSPFFIIKGGDINDNPPIFPLGPYHAT 158
DB 116 GDHAIKRLDDEEKAQVYLLAQAVDRDTPNPLEPSPFFIYXVDINDNPPF-LHEXY 175
QY 159 VPKNSVGTSTVQVTAHDADDPYSYNSAKLYVTLDLPFESVDPQGVVRAIAPMK 218
DB 176 VPKNSVGTSTVQVTAHDADDPYVNSAKLYVTLDLPFESVDPQGVVRAIAPMK 235
QY 219 TQSEFLVVIQAKDGMGNGLSGSTVTVTLSDVNDNPKPFPOSLYQFSVETAGCGTV 278

```



```
Db 236 ANEYLVVIQAKMGHSGGLSGTTTLTVTLTVNDNPPKPAQSLYHFSVPEDEVLTGTAI 295
Qy 279 GRLAODPPLGDNALMAYSLIDEGSEAFSISTDLQGRDGLTVKRPPLDPESORSYSPRV 338
Db 296 GRVXANDODIGENAOSSYDIIDGGTALFEITSDAQADGVIRLKPDLFETKSYTLKV 355
Qy 339 EATNTLIDPAYLRGPFKDVASVRVAVODAPBPFAFQAAYHLTVPENKAPGTLVGQISA 398
Db 356 EAAANTHIDPFRFSGRGPFDATATVKIVEDADEPVPFSSPTYLLEVENAALNSVIGQVTA 415
Qy 399 ADLDSAPSPIRYSILPHSDPERCFSGIOPEEGTHTAAPLDREARAHNLTVLATELGSMW 458
Db 416 RDPDITSSPIRFSIDRHIDLERQFNINADGKITLATPLDRELQVWENHISITATEI--- 471
Qy 459 GPERGMVPLLVAMWSAPAPAPQORSFVGSAGVIGIPDSSAQASRVQYAIQTLDENNDAPOLA 518
Db 472 -----RNHSQISRVPAIKVLVDVNDAPPEFA 497
Qy 519 BPYDTFVCDASAPQOL 534
Db 498 SEYEAFLECGKPGQV 513
```

Search completed: December 8, 2004, 10:01:08
Job time : 78.8394 secs

This Page Blank (usp10)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 1.29398 Seconds

(without alignments)
1189.717 Million cell updates/sec

Title: US-09-788-051-6

Perfect score: 95

Sequence: 1 MGVRLLLAMLGWG 16

Scoring table: BIOSUM62

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: PIR_79:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	56.8	408	2	B83333
2	53	55.8	172	1	DMECHD
3	53	55.8	172	2	AF0626
4	53	55.8	172	2	F90758
5	53	55.8	172	2	D85622
6	53	55.8	172	2	AH0174
7	52.5	55.3	222	2	C75250
8	51	53.7	172	2	D82194
9	51	53.7	172	2	G64116
10	50	52.6	490	2	D86879
11	49	51.6	621	2	T46851
12	48	50.5	303	2	B83470
13	47.5	50.0	383	2	AD0183
14	47	49.5	170	2	F87710
15	46	48.4	126	2	C97946
16	46	48.4	126	2	F95078
17	46	48.4	126	2	T12378
18	46	48.4	554	2	T13585
19	46	48.4	927	2	A48085
20	45	47.4	55	2	T10356
21	45	47.4	212	2	S53229
22	45	47.4	305	2	B65048
23	45	47.4	394	2	B85916
24	45	47.4	394	2	AD0842
25	45	47.4	394	2	G81071
26	45	47.4	445	2	D82184
27	45	47.4	786	2	F83292
28	45	47.4	1133	2	A54164
29	44.5	46.8	347	2	A46567

30	44	46.3	255	2	AE0515	Deda family integr
31	44	46.3	307	2	F95949	probable oligopept
32	44	46.3	322	2	AE2160	glycosyltransferas
33	44	46.3	323	2	F95398	probable ABC trans
34	44	46.3	431	1	SAVLC2	large surface anti
35	44	46.3	472	2	AC3534	glu/asp-ENa amido
36	43.5	45.8	270	2	F70878	hypothetical prote
37	43.5	45.8	415	2	AG2044	hypothetical prote
38	43	45.3	124	2	AB2178	hypothetical prote
39	43	45.3	211	1	AS3532	metalloproteinas
40	43	45.3	211	2	JC4630	metalloproteinas
41	43	45.3	216	2	B75469	hypothetical prote
42	43	45.3	263	2	T09841	hypothetical prote
43	43	45.3	281	1	XMBCGP	glycerol facilitat
44	43	45.3	281	2	D91235	glycerol facilitat
45	43	45.3	281	2	D86082	facilitated diffus

ALIGNMENTS

RESULT 1

B83333 Probable MFS transporter PA2500 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C:Accession: B83333

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lam

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path

A:Reference number: AB2950; MUID:20437337; PMID:1094043

A:Accession: B83333

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-408 <STO>

A:Cross-references: UNIPROT:Q910Y2; GB:AE004677; GB:AE004091; NID:99348548; PIDN:AA0581

A:Experimental source: strain PA01

C:Genetics:

A:gene: PA2500

C:superfamily: cynx protein

Query Match	56.8%	Score 54;	DB 2;	Length 408;
Best Local Similarity	76.9%	Pred. No. 3;		
Matches	10;	Conservative	0;	Mismatches 3; Indels 0; Gaps 0;

QY 3 GVVRLLLAMLGW 15

DB 72 GLVALLPLWGRW 84

RESULT 2

DMECHD 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60) - Escherichia coli (

W:Alternate names: beta-hydroxydecanoyl thiolester dehydratase

C:Species: Escherichia coli

C>Date: 30-Jun-1990 #sequence_revision 21-Nov-1997 #text_change 09-Jul-2004

C:Accession: A64836; A28140

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Ci

science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: A64836

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-172 <BIAT>

A:Cross-references: UNIPROT:P18391; GB:AE000197; GB:U00096; NID:q1787180; PIDN:AACT4040

A:Experimental source: strain K-12, substrain MG1655

R:Cronan Jr., U.E.; Li, W.B.; Coleman, R.; Narasimhan, M.; de Mendoza, D.; Schwab, J.W.

J. Biol. Chem. 263, 4641-4646, 1988

A:Title: Derived amino acid sequence and identification of active site residues of Esch

A:Reference number: A28140; MUID:88169574; PMID:2832401
A:Accession: A28140
A:Molecule type: DNA
A:Residues: 1-169, 'LF' <CRO>
C:Genetics:
A:Gene: fabA
A:Map position: 22 min
C:Function:
A:Description: catalyzes two reversible reactions, the dehydration of (R)-3-hydroxydecanal
C:Superfamily: 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase
C:Keywords: carbon-oxygen lyase; fatty acid biosynthesis; homodimer; hydro-lyase
F:70/Active site: Cys #status predicted
F:71/Active site: His #status experimental

Query Match 55.8%; Score 53; DB 1; Length 172;
Best Local Similarity 62.5%; Pred. No. 1.9;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MMGLVRLLLAWLGWG 16
DB 87 MMQLVGFYLGWLGGEG 102

RESULT 3
AF0626
D-3-hydroxydecanoyl-[acyl-carrier-protein] (imported) - Salmonella enterica subsp. enter
C:Species: Salmonella enterica subsp. enterica serovar Typh
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AF0626
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Mout, S.; O'Garra, P.
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Nature 413, 848-852, 2001
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AF0626
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-172 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD08193.1; PID:gl502242; GSPDB:GN00176
C:Genetics:
A:Gene: STY1088
C:Superfamily: 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase

Query Match 55.8%; Score 53; DB 2; Length 172;
Best Local Similarity 62.5%; Pred. No. 1.9;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MMGLVRLLLAWLGWG 16
DB 87 MMQLVGFYLGWLGGEG 102

RESULT 4
P90758
3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60) [similarity] - Escher
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: P90758
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gaswara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A:Reference number: A9629; MUID:21156231; PMID:11258796
A:Accession: F90758
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-172 <HAV>
A:Cross-references: UNIPROT:P18391; GB:BA000007; PIDN:BA034461.1; PID:gl3360498; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952

C:Genetics:
A:Gene: EC01038
C:Superfamily: 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 55.8%; Score 53; DB 2; Length 172;
Best Local Similarity 62.5%; Pred. No. 1.9;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MMGLVRLLLAWLGWG 16
DB 87 MMQLVGFYLGWLGGEG 102

RESULT 5
D85622
3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60) [similarity] - Escher
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: D85622
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: D85622
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-172 <STO>
A:Cross-references: UNIPROT:P18391; GB:AE005174; NID:G12514136; PIDN:AAG55440.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: fabA
C:Superfamily: 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 55.8%; Score 53; DB 2; Length 172;
Best Local Similarity 62.5%; Pred. No. 1.9;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MMGLVRLLLAWLGWG 16
DB 87 MMQLVGFYLGWLGGEG 102

RESULT 6
AH0174
3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60) [imported] - Yersinia
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AH0174
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586930
A:Accession: AH0174
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-172 <KUR>
A:Cross-references: UNIPROT:Q8ZG80; GB:AL590842; PIDN:CAC90259.1; PID:gl5979478; GSPDB:G
C:Genetics:
A:Gene: fabA
C:Superfamily: 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 55.8%; Score 53; DB 2; Length 172;
Best Local Similarity 62.5%; Pred. No. 1.9;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MMGLVRLLLAWLGWG 16

Db 87 MMQLVGFYLGWLGSG 102

RESULT 7

C75250 hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: C75250

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; S.; Shen, M.; Vamathevan, J.U.; Lam, P.; McDonald, L.; Ullrich, T.; Zaleski, C.; M. Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: C75250

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-222 <WHI>

A:Cross-references: UNIPROT:Q9RR69; GB:AE002092; GB:AE000513; NID:G6460455; PIDN:AAF1217

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR2628

A:Map position: 1

C:Superfamily: Deinococcus radiodurans hypothetical protein DR2628

Query Match 55.3%; Score 52.5; DB 2; Length 222;
Best Local Similarity 66.7%; Pred. No. 2.8;
Matches 10; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 3 GLVRLILAWLGWG 16

Db 154 GLARVLAWLGWG 168

RESULT 8

C75250 3-hydroxydecanoyl-(acyl-carrier-protein) dehydratase VC1463 [imported] - Vibrio cholerae

C:Species: Vibrio cholerae

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C:Accession: D82194

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gilm, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Basu, S.; Qin, H.; Dragoi, I.; Sellers, F. l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.W. Nature 406, 477-483, 2000

A:Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: D82194

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-172 <HEI>

A:Cross-references: UNIPROT:Q9RS00; GB:AE004226; GB:AE003852; NID:G9655979; PIDN:AAF9463

A:Experimental source: serogroup O1, strain N16561, biotype El Tor

C:Genetics:

A:Gene: VC1463

A:Map position: 1

C:Superfamily: 3-hydroxydecanoyl-(acyl-carrier-protein) dehydratase

Query Match 53.7%; Score 51; DB 2; Length 172;
Best Local Similarity 56.2%; Pred. No. 3.7;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MMGLVRLILAWLGWG 16

Db 87 MMQLVGFYLGWLGSG 102

RESULT 9

G64116 3-hydroxydecanoyl-(acyl-carrier-protein) dehydratase (EC 4.2.1.60) - Haemophilus influenzae

C:Species: Haemophilus influenzae

C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004

R:Feischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, J. ; Gocayne, J.D.; Scott, J.; Shiley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J. , D.M.; Brandon, R.C.; Pine, L.D.; Fritchman, J.L.; Fritchman, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: G64116

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-177 <RTGS>

A:Cross-references: UNIPROT:P45159; GB:U32812; GB:L42023; NID:G1574784; PIDN:AA022972.1

C:Genetics:

A:Gene: fabA

C:Function:

A:Description: catalyzes two reversible reactions, the dehydration of (R)-3-hydroxydecanoyl-(acyl-carrier-protein) to (R)-3-oxodecanoyl-(acyl-carrier-protein) and the hydration of (R)-3-oxodecanoyl-(acyl-carrier-protein) to (R)-3-hydroxydecanoyl-(acyl-carrier-protein)

A:Pathway: unsaturated fatty acid biosynthesis

C:Superfamily: 3-hydroxydecanoyl-(acyl-carrier-protein) dehydratase

C:Keywords: carbon-oxygen lyase; fatty acid biosynthesis; hydro-lyase

F/15/16/Active site: Cys, His #status predicted

Query Match 53.7%; Score 51; DB 2; Length 177;
Best Local Similarity 56.2%; Pred. No. 3.8;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MMGLVRLILAWLGWG 16

Db 92 MMQLVGFYLGWLGSG 107

RESULT 10

C86879 arginine/ornithine antiporter [imported] - Lactococcus lactis subsp. lactis (strain IL14)

C:Species: Lactococcus lactis subsp. lactis

C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

C:Accession: C86879

R:Polstein, A.; Wincker, P.; Manger, S.; Tallon, O.; Malarme, K.; Weissbach, J.; Ehrlich, S. Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s

A:Reference number: A86525; MUID:21235186; PMID:11337471

A:Accession: C86879

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-490 <STO>

A:Cross-references: UNIPROT:Q9CE15; GB:AE005176; PID:G12725084; PIDN:AA006133.1; GSPDB:K

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: arcD1

C:Superfamily: L-lysine transport protein

Query Match 52.6%; Score 50; DB 2; Length 490;
Best Local Similarity 64.3%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GLVRLILAWLGWG 16

Db 288 GLVRLILAWLGWG 301

RESULT 11

T46851 conserved hypothetical protein yba [imported] - Rhodospirillum rubrum

C:Species: Rhodospirillum rubrum

C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004

C:Accession: T46851

R:Mackenzie, C.; Simmons, A.E.; Kaplan, S. Genetics 153, 525-538, 1999

A:Title: Multiple chromosomes in bacteria. The yin and yang of trp gene localization in

A:Reference number: Z24108; MUID:99442363; PMID:10511537

A:Accession: T46851

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-621 <MAC>

A/Cross-references: UNIPROT:Q9ZFB1; EMBL:AF108766; NID:94185542; PIDN:AA09115.1; PID:94
A/Experimental source: strain 2.4.1
C/Genetics:
A/Gene: ybat

Query Match 51.6%; Score 49; DB 2; Length 621;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 MGLVRLIAMLGNG 16
DB 22 MGLVGLMAYVGLGSG 36

RESULT 12
B83470
hypothetical protein PA1411 [imported] - Pseudomonas aeruginosa (strain PA01)

C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: B83470

R/Source: C.K.; Pham, X.Q.; Ervin, A.L.; Micozucht, S.D.; Martener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.W.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardis, K.; Lim,
J.; Lory, S.; Olson, M.V.
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
gen.
A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Accession: B83470
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-303 <STO>
A/Cross-references: UNIPROT:Q913T3; GB:AE004570; GB:AE004091; NID:99947350; PIDN:AA00480

A/Experimental source: strain PA01
C/Genetics:
A/Gene: PA1411
C/Superfamily: hypothetical protein ydeD

Query Match 50.5%; Score 48; DB 2; Length 303;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 LVRLIAMLGNG 15
DB 50 LVGLMLKMGNG 61

RESULT 13
AD0183
probable exported protein YPO1504 [imported] - Yersinia pestis (strain CO92)

C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C/Accession: AD0183

R/Source: J. Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413: 523-527, 2001

A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360

A/Accession: AD0183
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-383 <XLR>
A/Cross-references: UNIPROT:Q8ZG16; GB:AL590842; PIDN:CA090327.1; PID:915979546; GSPDB:G

C/Genetics:
A/Gene: YPO1504

Query Match 50.0%; Score 47.5; DB 2; Length 383;
Best Local Similarity 53.3%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 2 W-GVRLIAMLGNG 15
DB 93 WGLVRLIAMLGNG 107

RESULT 14
F87710
hypothetical protein CC3720 [imported] - Caulobacter crescentus

C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C/Accession: F87710

R/Source: M.C.; Feldlym, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.R.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98: 4136-4141, 2001

A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: A87249; MUID:21173698; PMID:11259647

A/Accession: F87710
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-170 <STO>
A/Cross-references: UNIPROT:Q9A246; GB:AE005673; NID:913425488; PIDN:AAK25682.1; GSPDB:G

C/Genetics:
A/Gene: CC3720
C/Superfamily: 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase

Query Match 49.5%; Score 47; DB 2; Length 170;
Best Local Similarity 56.2%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 MMGLVRLIAMLGNG 16
DB 85 MMGLVRLIAMLGNG 100

RESULT 15
C97946
conserved hypothetical protein spr0595 [imported] - Streptococcus pneumoniae (strain R6)

C/Species: Streptococcus pneumoniae
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C/Accession: C97946

R/Source: J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.D.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183: 5709-5717, 2001

A/Author: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A/Reference number: A97872; MUID:21429245; PMID:11544234

A/Accession: C97946
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-126 <XLR>
A/Cross-references: UNIPROT:Q97RV8; UNIPROT:Q8DGM7; GB:AE007317; PIDN:AAK9399.1; PID:91

C/Genetics:
A/Gene: spr0595
C/Superfamily: glpB protein

Query Match 48.4%; Score 46; DB 2; Length 126;
Best Local Similarity 46.2%; Pred. No. 14;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MMGLVRLIAMLG 13
DB 6 MMGLVRLIAMLG 18

Search completed: December 8, 2004, 10:27:03
Job time: 5.25398 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 6.41322 Seconds

(Without alignments)
1435.471 Million cell updates/sec

Title: US-09-788-051-6
Perfect score: 95
Sequence: 1 MMGLVRLILAWLGSGW 16

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	241	2	Q86TS8
2	95	100.0	493	2	Q66LQ7
3	95	100.0	781	2	Q6PFX6
4	95	100.0	781	2	AAH57373
5	95	100.0	819	1	CADU_HUMAN
6	54	56.8	172	1	FABA_PHOUL
7	54	56.8	408	2	Q910Y2
8	53	55.8	171	1	FABA_ECOLI
9	53	55.8	171	1	FABA_ECOLI
10	53	55.8	171	1	FABA_SALTY
11	53	55.8	172	1	FABA_YERPE
12	53	55.8	172	1	Q6D6D7
13	53	55.8	177	1	FABA_WIGAR
14	52.5	55.3	222	2	Q9RRE9
15	52	54.7	176	1	FABA_HAEDU
16	52	54.7	194	2	Q7NCAS
17	52	54.7	328	2	Q6ZET7
18	52	54.7	328	2	BAD01813
19	51	53.7	172	1	FABA_CANBF
20	51	53.7	172	1	FABA_VIBGH
21	51	53.7	172	1	FABA_VIBPA
22	51	53.7	172	1	FABA_VIBBU
23	51	53.7	172	1	FABA_VIBRY
24	51	53.7	177	1	FABA_HAEIN
25	51	53.7	177	1	FABA_PASWU
26	51	53.7	348	2	Q9TDS7
27	51	53.7	361	2	Q21680
28	51	53.7	542	2	Q7U446
29	50	52.6	391	2	Q9KXK4
30	50	52.6	391	2	Q86D91
31	50	52.6	447	2	Q7NV89

32	50	52.6	490	2	Q9CE15	Q9CE15 lactococcus
33	50	52.6	526	2	Q9K574	Q9K574 lactococcus
34	49	51.6	170	2	Q68F81	Q68F81 uncultured
35	49	51.6	170	2	AAK38141	AAK38141 unculture
36	49	51.6	175	1	FABA_RHOPA	P61450 rhodospseudo
37	49	51.6	621	2	Q9ZFB1	Q9ZFB1 rhodobacter
38	49	51.6	2042	2	Q8TZ07	Q8TZ07 methanopyru
39	48.5	51.1	253	2	Q7NHM4	Q7NHM4 glaeobacter
40	48	50.5	171	2	Q6TR96	Q6TR96 photobacter
41	48	50.5	171	2	CAG20180	CAG20180 photobact
42	48	50.5	292	2	Q7NXX2	Q7NXX2 chromobacte
43	48	50.5	292	2	Q7ZHX9	Q7ZHX9 thermus the
44	48	50.5	296	2	AA881695	AA881695 thermus t
45	48	50.5	303	2	Q913T3	Q913T3 pseudomonas

ALIGNMENTS

RESULT 1						
ID	Q86TS8	PRELIMINARY;	PRT;	241	AA.	
AC	Q86TS8;					
DT	01-JUN-2003 (TREMBLrel. 24, Created)					
DT	01-OCT-2003 (TREMBLrel. 24, Last sequence update)					
DE	Full-length cDNA 5-PRIME end of clone CS0DE010YPI9 of Placenta of Homo sapiens (human) (Fragment).					
OS	Homo sapiens (Human)					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Placenta;					
RA	Submitted (FEB-2003) to the EMBL/Genbank/DBJ databases.					
CC	-1 SIMILARITY: Contains 2 cadherin domains.					
DR	EMBL; BX248750; CAD6557.1; ..					
DR	HSSP; F12830; 1065.					
DR	GO; GO:0016020; C:membrane; IEA.					
DR	GO; GO:000509; F:calcium ion binding; IEA.					
DR	GO; GO:007156; P:homophilic cell adhesion; IEA.					
DR	InterPro; IPR002126; Cadherin.					
DR	Pfam; PF00028; Cadherin_2.					
DR	PRINTS; PR00205; CADHERIN.					
DR	SMART; SM00112; CA; 2.					
DR	PROSITE; PS00232; CADHERIN_1; 1.					
DR	PROSITE; PS00268; CADHERIN_2; 2.					
KW	Calcium; Calcium-binding.					
FT	NON TER 241					
SQ	SEQUENCE 241 AA; 26348 MW; 4649831B5424604 CRC64;					
Query Match						
Best Local Similarity 100.0%; Score 95; DB 2; Length 241;						
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1	MMGLVRLILAWLGSGW 16				
DB	1	MMGLVRLILAWLGSGW 16				
RESULT 2						
ID	Q96LQ7	PRELIMINARY;	PRT;	493	AA.	
AC	Q96LQ7;					
DT	01-DEC-2001 (TREMBLrel. 19, Created)					
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)					


```

CC      RP SEQUENCE FROM N.A.
CC      RC STRAIN=C57BL/6; TISSUE=Brain;
CC      RA Strausberg R.;
CC      RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC      DR EMBL; BC057373; AAH57373.1;
CC      SQ SEQUENCE 781 AA; 84104 MW; 15996D6EC9835AA CRC64.
CC
CC      Query Match          100.0%; Score 95; DB 2; Length 781;
CC      Best Local Similarity 100.0%; Pred. No. 2.9e-05;
CC      Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
CC
CC      Db      1 MWGLVRLILAMLGWG 16
CC              |||||
CC      RESULT 5
CC      CADO_HUMAN STANDARD; PRT; 819 AA.
CC      AC Q86UP0; Q86UP1; Q9N784;
CC      DT 29-MAR-2004 (Rel. 43, Created)
CC      DT 29-MAR-2004 (Rel. 43, Last sequence update)
CC      DT 05-JUL-2004 (Rel. 44, Last annotation update)
CC      DE Cadherin-24 precursor (UNQ2834/PRO34009).
CC      GN Name=CDH24; Synonyms=CDH11L;
CC      OS Homo sapiens (Human).
CC      OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC      OX NCBI_TaxID=9606;
CC      [1]
CC      RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND INTERACTIONS WITH
CC      RP CATEININS.
CC      RA MEDLINE=22753805; PubMed=12734196; DOI=10.1074/jbc.M304119200;
CC      RA Kafrafiar B.J., Nieman M.T., Wheelock M.J., Johnson K.R.;
CC      RT "Characterization of cadherin-24, a novel alternatively spliced type
CC      II cadherin.", 278:27513-27519(2003).
CC      RL J. Biol. Chem.
CC      [2]
CC      RN SEQUENCE FROM N.A. (ISOFORM 2).
CC      RP MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
CC      RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
CC      RA Chen J., Chow B., Chui C., Crowley C., Curral B., Devel B., Dowd P.,
CC      RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
CC      RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
CC      RA Lewis L., Liao D., Marx M., Robble E., Sanchez C., Schoenfeld J.,
CC      RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
CC      RA Vandelan R., Watanabe C., Weand D., Woods K., Xie M.-H., Yansura D.,
CC      RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
CC      RA Godowski P., Gray A.;
CC      RT "The secreted protein discovery initiative (SPDI), a large-scale
CC      effort to identify novel human secreted and transmembrane proteins: a
CC      bioinformatics assessment.",
CC      RL Genome Res. 13:2265-2270(2003).
CC      [3]
CC      RN SEQUENCE FROM N.A. (ISOFORM 3).
CC      RP TISSUE=Testis;
CC      RA Blum H., Bauserachs S., Mewes H.-W., Gassenhuber J., Niemann S.;
CC      RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC      CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC      They preferentially interact with themselves in a homophilic
CC      manner in connecting cells; cadherins may thus contribute to the
CC      sorting of heterogeneous cell types. Cadherin-24 mediate strong
CC      cell-cell adhesion.
CC      CC -1- SUBUNIT: Associates with alpha-, beta- and delta-catenins.
CC      CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC      CC -1- SUBCELLULAR PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=3;
CC      Name=1; Synonyms=Long form;
CC      IsoId=Q86UP0-1; Sequence=Displayed;
CC      Name=2; Synonyms=Short form;
CC      IsoId=Q86UP0-2; Sequence=VSP_008717;
CC      Name=3;
CC      IsoId=Q86UP0-3; Sequence=VSP_008718 VSP_008719.

```

```
CC Note=No experimental confirmation available;
CC -I- SIMILARITY: Contains 5 cadherin domains.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; AY260900; AAP20590.1; -
DR EMBL; AY260901; AAP20591.1; -
DR EMBL; AY358199; AAO8856.1; -
DR EMBL; AL137477; CAB70758.1; -
DR PIR; T46418; T46418.
DR HSSP; P09803; 11TW.
DR Genew; HGNC:14265; CDH24.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR002123; Cadherin_C_term.
DR Pfam; PF00028; Cadherin_5.
DR Pfam; PF01049; Cadherin_C_1.
DR PRINTS; PR00205; CADHERIN.
DR PROSITE; PS00232; CADHERIN_1; 2.
DR PROSITE; PS0268; CADHERIN_2; 5.
KW Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
KW Multigene family; Repeat; Signal; Transmembrane.
FT SIGNAL 1 Potential.
FT PROPEP 21 44 Potential.
FT CHAIN 45 819 Extracellular (Potential).
FT DOMAIN 45 662 Extracellular.
FT TRANSMEM 642 662 Cytoplasmic (Potential).
FT DOMAIN 663 819 Cadherin 1.
FT DOMAIN 46 150 Cadherin 2.
FT DOMAIN 151 259 Cadherin 3.
FT DOMAIN 260 374 Cadherin 4.
FT DOMAIN 375 517 Cadherin 5.
FT CARBOHYD 446 446 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 548 548 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 563 563 N-linked (GlcNAc...) (Potential).
FT VASPLIC 455 492 Missing (in isoform 2).
FT FT FTTid=VSP_008719.
FT VASPLIC 1 427 Missing (in isoform 3).
FT FT FTTid=VSP_008718.
FT VASPLIC 428 492 EGHTITAPLDREKRAWNTLVLTATELGWSPGRGVPLL
FAEWSAPAPAPQPSRSGSAVGIPQ -> MNIVCTWYCSIH
ALTFSTCIHAAYFMCFLCMLYASCGIHAPHMRLRVNVCV
VMRYCFGLVP (in isoform 3).
FT FT FTTid=VSP_008719.
SQ SEQUENCE 819 AA; 87751 MW; 9083034FF18B7E4A CCCC64;
Query Match 100.0%; Score 95; DB 1; Length 819;
Best Local Similarity 100.0%; Pid. No. 3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
Oy 1 MMGLVRIILLAWLGWG 16
Db 1 MMGLVRIILLAWLGWG 16
RESULT 6
FABA_PHOL
ID_FABA_PHOL STANDARD; PRT; 172 AA.
AC C7MB46;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE 3-hydroxydecanoyl-lacyl-carrier-protein dehydratase (EC 4.2.1.60)
DE (Beta-hydroxydecanoyl thioester dehydrase).
DE Name=faba; OrderedLocNames=plu11772;
OC Photorhabdus luminescens (subsp. launonii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
```

CC Enterobacteriaceae; Photorhabdus.
 RX NCBI_TaxID=141679;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TT01;
 RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
 RA Duchaud E., Kustnok C., Frangeul L., Buchrieser C., Giraudon A.,
 RA Taouat S., Bocs S., Boursaux-Ende C., Chandler M., Charles J.-F.,
 RA Dassa B., Dezoze R., Derzelle S., Freysinet G., Gaudinault S.,
 RA Médigue C., Lancia A., Powell K., Sigulier P., Vincent R., Wingate V.,
 RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
 RA "The genome sequence of the entomopathogenic bacterium Photorhabdus
 luniseiensis.";
 RT Nature 406:958-964(2000).
 RL EMBL, AB004677; AACG5888.1; -
 DR PIR, B83333; B83333.
 KW Complete proteome.
 SQ SEQUENCE 408 AA; 43089 MW; A34FDB70FC656972 CRC64;
 Query Match 56.8%; Score 54; DB 2; Length 408;
 Best Local Similarity 76.9%; Pred. No. 13;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 GVLVRLLLAWLGGW 15
 DB 72 GVLVRLLLPWLGRW 84
 ID FABA_ECOL6 STANDARD; PRT; 171 AA.
 AC Q8FY83;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60)
 GN Name=faba; OrderedLocusNames=1090;
 OS Escherichia coli O6.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Escherichia.
 CC NCBI_TaxID=217993;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O6:H1 / CFT073 / ATCC 700928 / UPEC;
 RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 RA Rasko D., Buckles E.L., Ison S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 of uropathogenic Escherichia coli.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:117020-117024(2002).
 CC -1- FUNCTION: Necessary for the introduction of cis unsaturation into
 fatty acids. Catalyzed the dehydration of (3R)-3-hydroxydecanoyl-
 ACP to E-(2)-decanoyl-ACP and then its isomerization to Z-(3)-
 decenoyl-ACP (By similarity).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxydecanoyl-[acyl-carrier protein]
 = 2,3-decenoyl-[acyl-carrier protein] or 3,4-decenoyl-[acyl-
 carrier protein] + H(2)O.
 CC -1- PATHWAY: Key step in the anaerobic pathway of unsaturated fatty
 acid synthesis in bacteria.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the thioester dehydratase family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC EMBL, BX571865; CAE14065.1; -
 CC PhotoList; P1u172; -
 DR HAMAP, MF_00405; -; 1.
 DR InterPro: IPR010083; Faba.
 DR TIGRFAMs: TIGR01749; Faba; 1.
 KW Complete proteome; Fatty acid biosynthesis; Lyase.
 FT ACT_SITE 71 71 By similarity.
 SQ SEQUENCE 172 AA; 18999 MW; 72D63DF044DAE4E CRC64;
 Query Match 56.8%; Score 54; DB 1; Length 172;
 Best Local Similarity 62.5%; Pred. No. 6.1;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 MNGIVRLLLAWLGGWG 16
 DB 87 MNGIVRFLGWLGGEG 102
 ID Q910Y2 PRELIMINARY; PRT; 408 AA.
 AC Q910Y2;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Probable MFS transporter.
 GN OrderedLocusNames=PA2500;
 OS Pseudomonas aeruginosa.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 CC Pseudomonadaceae; Pseudomonas.
 CC NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PAO1;
 RX MEDLINE=20437337; PubMed=10964043;
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warriner P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,

RA Brody L.L., Coulter S.N., Folger K.R., Kae A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reiter J., Sater M.H., Hancock R.E.W., Lory S., Olsen M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
 opportunistic pathogen.";
 RT Nature 406:958-964(2000).
 RL EMBL, AB004677; AACG5888.1; -
 DR PIR, B83333; B83333.
 KW Complete proteome.
 SQ SEQUENCE 408 AA; 43089 MW; A34FDB70FC656972 CRC64;
 Query Match 56.8%; Score 54; DB 2; Length 408;
 Best Local Similarity 76.9%; Pred. No. 13;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 GVLVRLLLAWLGGW 15
 DB 72 GVLVRLLLPWLGRW 84
 ID FABA_ECOL6 STANDARD; PRT; 171 AA.
 AC Q8FY83;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60)
 GN Name=faba; OrderedLocusNames=1090;
 OS Escherichia coli O6.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Escherichia.
 CC NCBI_TaxID=217993;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O6:H1 / CFT073 / ATCC 700928 / UPEC;
 RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 RA Rasko D., Buckles E.L., Ison S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 of uropathogenic Escherichia coli.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:117020-117024(2002).
 CC -1- FUNCTION: Necessary for the introduction of cis unsaturation into
 fatty acids. Catalyzed the dehydration of (3R)-3-hydroxydecanoyl-
 ACP to E-(2)-decanoyl-ACP and then its isomerization to Z-(3)-
 decenoyl-ACP (By similarity).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxydecanoyl-[acyl-carrier protein]
 = 2,3-decenoyl-[acyl-carrier protein] or 3,4-decenoyl-[acyl-
 carrier protein] + H(2)O.
 CC -1- PATHWAY: Key step in the anaerobic pathway of unsaturated fatty
 acid synthesis in bacteria.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the thioester dehydratase family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC EMBL, AE016758; AAN79558.1; ALT_INIT.
 DR HSSP, P18931; IMKA.
 DR HAMAP, MF_00405; -; 1.
 DR InterPro: IPR010083; Faba.
 DR TIGRFAMs: TIGR01749; Faba; 1.
 KW Complete proteome; Fatty acid biosynthesis; Lyase.
 FT INIT_MET 0 0 By similarity.

FT ACT SINE 70 70 By similarity.
SQ SEQUENCE 171 AA; 18665 MW; 3D8C55A01DD72220 CRC64;

Query Match 55.8%; Score 53; DB 1; Length 171;
Best Local Similarity 62.5%; Pred. No. 8.5;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 MMGLVRLTLAWLGGWG 16
Db 86 MMGLVGYFLGMDGGEG 101

RESULT 9

FABA_ECOLI STANDARD; PRT; 171 AA.

AC P18351; 059383;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60)
OS (Beta-hydroxydecanoyl thioester dehydratase)
GN Name=faba; OrderedLocustNames=00954, 21304, ECol038, SF0954, S1020;
OS Escherichia coli O157:H7, and
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
CX NCBI_TaxID=562, 83334, 623;

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC SPECIES=E.coli; STRAIN=K12;
RX MEDLINE=86169574; PubMed=2832401;
RA Cronan J.E., Jr., Li W.-B., Coleman R., Narasimhan M., de Mendoza D.,
RA Schwab J.M.,
RT "Derived amino acid sequence and identification of active site
RT residues of Escherichia coli beta-hydroxydecanoyl thioester
RL dehydratase";
RL J. Biol. Chem. 263:4641-4646(1988).

REVISION TO 169-171.

RC SPECIES=E.coli;
RX MEDLINE=92370687; PubMed=1505031;

RA Henry M.F., Cronan J.E., Jr.,
RT "A new mechanism of transcriptional regulation: release of an
RT activator triggered by small molecule binding.";
RL Cell 70:671-679(1992).

SEQUENCE FROM N.A.

RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatter F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Valdes J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.,
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).

SEQUENCE FROM N.A.

RC SPECIES=E.coli; STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemura S., Inada T., Itoh T., Kajihara M., Kanei K., Kashibuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Samped G., Seki Y., Takami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano W., Horikuchi T.,
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).

SEQUENCE FROM N.A.

RC SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;

RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobleck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blatter F.R.,
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).

SEQUENCE FROM N.A.

RC SPECIES=E.coli; STRAIN=O157:H7 / RIMD 0509352 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
RA Kihara S., Shida T., Hattori M., Shitagawa H.,
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).

SEQUENCE FROM N.A.

RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.,
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).

SEQUENCE FROM N.A.

RC SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=2259024; PubMed=12704152;
RA Wei J., Goldberg W.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G., III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blatter F.R.,
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).

WOTANTS FABA6 AND FABA2.

RC SPECIES=E.coli; STRAIN=K12;
RX MEDLINE=96404784; PubMed=8808925;
RA Rock C.O., Tsay J.-T., Heath R., Jackowski S.,
RT "Increased unsaturated fatty acid production associated with a
RT suppressor of the fabA6(fts) mutation in Escherichia coli.";
RL J. Bacteriol. 178:5382-5387(1996).

X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RC SPECIES=E.coli;
RX MEDLINE=96398612; PubMed=8805534;
RA Leesong M., Henderson B.S., Gillig J.R., Schwab J.M., Smith J.L.,
RT "Structure of a dehydratase-isomerase from the bacterial pathway for
RT biosynthesis of unsaturated fatty acids: two catalytic activities in
RT one active site.";
RL Structure 4:253-264(1996).

-1- FUNCTION: Necessary for the introduction of cis unsaturation into
fatty acids. Catalyzed the dehydration of (3R)-3-hydroxydecanoyl-
ACP to E-(2)-decanoyl-ACP and then its isomerization to Z-(3)-
decanoyl-ACP.

-1- CATALYTIC ACTIVITY: (3R)-3-hydroxydecanoyl-[acyl-carrier protein]
= 2,3-decanoyl-[acyl-carrier protein] or 3,4-decanoyl-[acyl-
carrier protein] + H(2)O.

-1- PATHWAY: Key step in the anaerobic pathway of unsaturated fatty
acid synthesis in bacteria.

-1- SUBUNIT: Homodimer.

-1- SIMILARITY: Belongs to the thioester dehydratase family.
This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

EMBL; J01186; AA96496.1; ALT INIT.
 EMBL; AE000197; AAC74040.1; -
 EMBL; D90733; BA35712.1; -
 EMBL; AE005285; AAG55440.1; -
 EMBL; AP002554; BAB34461.1; -
 EMBL; U37057; AAC4389.1; -
 EMBL; U56977; AAC4399.1; -
 EMBL; AE015125; AAM2583.1; -
 EMBL; AE016981; AAP6468.1; -
 PIR; A64836; DMECHD.
 PIR; D85622; D85622.
 PIR; F90758; F90758.
 PDB; IMKA; X-ray; A/B=1-171.
 PDB; IMKB; X-ray; A/B=1-171.
 ECODBASE; H017.2; 6TH EDITION.
 ECHOBASE; EB0269; -
 EcGene; EG10273; faba.
 HAMAP; MF_00405; -; 1.
 InterPro; IPR010083; Faba.
 TIGRfams; TIGR01749; faba; 1.
 3D-structure; Complete proteome; Direct protein sequencing;
 KM Fatty acid biosynthesis; Lyase.
 FT INIT MET 0
 FT ACT SITE 70 70 P -> L (in allele FBA6; TS).
 FT VARIANT 75 75 G -> D (in allele FBA2; TS).
 FT VARIANT 101 101 R -> H (in Ref. 8).
 FT CONFLICT 17 17 M -> I (in Ref. 8).
 FT CONFLICT 36 36 M -> I (in Ref. 8).
 FT CONFLICT 151 151 G -> C (in Ref. 8).
 FT STRAND 7 7
 FT HELIX 9 16
 FT TURN 17 18
 FT TURN 31 33
 FT STRAND 38 43
 FT TURN 47 50
 FT STRAND 53 59
 FT TURN 62 63
 FT HELIX 65 68
 FT TURN 69 73
 FT HELIX 79 96
 FT TURN 97 98
 FT STRAND 102 108
 FT STRAND 111 113
 FT TURN 119 120
 FT STRAND 123 135
 FT STRAND 139 149
 FT TURN 150 151
 FT STRAND 152 165
 FT TURN 169 171
 SQ SEQUENCE 171 AA; 18838 MW; 3D8C55A01DCD0B20 CRC64;

Query Match 55.8%; Score 53; DB 1; Length 171;
 Best Local Similarity 62.5%; Pred. No. 8.5;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 MMGLVRLIAMIIGMG 16
 Db 86 MMGLVRYLGLWGGSG 101

RESULT 10
 FABA_SALT
 ID FABA_SALT STANDARD; PRT; 171 AA.
 AC O8XEV3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

01-OCT-2004 (Rel. 45, Last annotation update)
 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60)
 DE (beta-hydroxydecanoyl) thioester dehydratase
 GN Name=faba; OrderedLocNames=TM1067, STY1068, t1853;
 OS Salmonella typhimurium, and
 CC Salmonella typhi.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Salmonella.
 CC NCB TaxID=602, 601;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP SPECIES=S. typhi; STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RC MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
 RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
 RA McClelland M., Sanders K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of salmonella enterica serovar Typhimurium
 LT2.";
 RL Nature 413:852-856(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S. typhi; STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
 RA Parhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
 RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatina M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Felwell T., Hamlin N., Hague A., Hien T.T., Holroyd S., Jagsels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Goira P., Parry C.,
 RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrall B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S. typhi; STRAIN=Ty2 / ATCC 700931;
 RX MEDLINE=22531367; PubMed=12644504;
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.C.,
 RA Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;
 RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
 and CT18.";
 RL J. Bacteriol. 185:2330-2337(2003).
 CC -1- FUNCTION: Necessary for the introduction of cis unsaturation into
 fatty acids. Catalyzed the dehydration of (3R)-3-hydroxydecanoyl-
 ACP to E-(2)-decanoyl-ACP and then its isomerization to Z-(3)-
 decenoyl-ACP (By similarity).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxydecanoyl-[acyl-carrier protein]
 = 2,3-decenoyl-[acyl-carrier protein] or 3,4-decenoyl-[acyl-
 carrier protein] + H(2)O.
 CC -1- PATHWAY: Key step in the anaerobic pathway of unsaturated fatty
 acid synthesis in bacteria.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the thioester dehydratase family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

EMBL; AE008746; AAL20000.1; -
 EMBL; AL627269; CAD08193.1; -
 EMBL; AE016840; AAC09471.1; -
 HSSP; P18391; IMKA.
 DR StyGene; SG27277; faba.
 DR HAMAP; MF_00405; -; 1.
 DR InterPro; IPR010083; Faba.

DR TIGR01749, fabA, 1.
 Complete proteome; Fatty acid biosynthesis; Lyase.
 KM Complete proteome; Fatty acid biosynthesis; Lyase.
 FT INIT MET 0 By similarity.
 ACT SITE 70 By similarity.
 SQ SEQUENCE 171 AA; 18916 MW; 3D9FC816D520BC20 CRC64;

Query Match 55.8%; Score 53; DB 1; Length 171;
 Best Local Similarity 62.5%; Pred. No. 8.6;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MMGLVRLLLAWLGWNG 16
 Db 86 MMGLVGFYLGWLGEG 101

RESULT 11

FABA_YERPE STANDARD; PRT; 172 AA.
 AC Q8ZG80;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 45, Last annotation update)
 DT 01-OCT-2004 (Rel. 42, Last sequence update)
 DE 3-Hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60)
 GN Name=faba; OrderedLocustNames=YF01430, Y2740, YP0875;
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Yersinia.
 NX NCBI_taxid=632;
 RN (1)

RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / Biovar Orientalis;
 RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
 RA Parthill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 RA Pretlie M.B., Sebailha M., James K.D., Chuchter C.M., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Taranga A.-M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Feltwell T., Hamlin N., Holtroyd S., Jagels K., Karlyshev A.V.,
 RA Leather S., Moul S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.;
 RT "Genome sequence of Yersinia pestis, the causative agent of plague."
 RL Nature 413:523-527(2001).
 RN (2)

RP SEQUENCE FROM N.A.
 RC STRAIN=KIM5 / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Nilles M.W., Watson J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of Yersinia pestis KIM."
 RL J. Bacteriol. 184:4601-4611(2002).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=91001 / Biovar Mediaevalis;
 RA Song Y., Tong Z., Wang L., Han Y., Zhang T., Pei D., Wang J., Zhou D.,
 RA Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
 RA Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
 RA Yang R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -I- FUNCTION: Necessary for the introduction of cis unsaturation into
 fatty acids. Catalyzed the dehydration of (3R)-3-hydroxydecanoyl-
 ACP to E-(2)-decanoyl-ACP and then its isomerization to Z-(3)-
 decenoyl-ACP (By similarity).
 CC -I- CATALYTIC ACTIVITY: (3R)-3-hydroxydecanoyl-[acyl-carrier protein]
 = 2,3-decenoyl-[acyl-carrier protein] or 3,4-decenoyl-[acyl-
 carrier protein] + H(2)O.
 CC -I- PATHWAY: Key step in the anaerobic pathway of unsaturated fatty
 acid synthesis in bacteria.
 CC -I- SUBUNIT: Homodimer (By similarity).
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -I- SIMILARITY: Belongs to the thioester dehydratase family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL; A014148; CAC90259.1; -
 DR EMBL; A013876; AAM86292.1; ALT_INIT.
 DR EMBL; A017130; AAS61132.1; ALT_INIT.
 DR PIR; A0174; A0174.
 DR HSSP; P18391; 1MKA.
 DR HAMAP; MF_00405; -; 1.
 DR InterPro; IPR01083; Faba.
 DR TIGR01749, fabA, 1.
 KM Complete proteome; Fatty acid biosynthesis; Lyase.
 FT ACT SITE 71 By similarity.
 SQ SEQUENCE 172 AA; 18810 MW; 19037054D0A721EC CRC64;

Query Match 55.8%; Score 53; DB 1; Length 172;
 Best Local Similarity 62.5%; Pred. No. 8.6;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MMGLVRLLLAWLGWNG 16
 Db 87 MMGLVGFYLGWLGEG 102

RESULT 12

Q6D6D7 PRELIMINARY; PRT; 172 AA.
 AC Q6D6D7;
 DT 01-OCT-2004 (TEMBLrel. 28, Created)
 DT 01-OCT-2004 (TEMBLrel. 28, Last sequence update)
 DT 01-OCT-2004 (TEMBLrel. 28, Last annotation update)
 DE 3-Hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC
 4.2.1.60).
 GN Name=faba; ORFNames=BCA1748;
 OS Yersinia carotovora subsp. atroseptica SCRI1043.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Pectobacterium.
 NX NCBI_taxid=218491;
 RN (1)

RP SEQUENCE FROM N.A.
 RC STRAIN=SCRI1043;
 RA Bell K.S., Sebailha M., Pritchard L., Holden M., Hyman L.J.,
 RA Holeva M.C., Thomson N.R., Bentley S.D., Chuchter C., Mungall K.,
 RA Aklin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
 RA Fraser A., Hance Z., Hauser H., Jagels K., Moul S., Norbertczak H.,
 RA Omond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
 RA Salmond G.P.C., Birch P.R.J., Barrett B.G., Parthill J., Toth I.K.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX950851; CAG74653.1; -

KM Lyase. 172 AA; 18963 MW; 6B4C06941629D4 CRC64;

Query Match 55.8%; Score 53; DB 2; Length 172;
 Best Local Similarity 62.5%; Pred. No. 8.6;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MMGLVRLLLAWLGWNG 16
 Db 87 MMGLVGFYLGWLGEG 102

RESULT 13
 FABA_WIGER STANDARD; PRT; 177 AA.
 ID FABA_WIGER
 AC Q8D204;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60)
 GN Name=faba; OrderedLocNames=MGSR3000;
 OS Migglesworthia gossypii
 CC Enterobacteriaceae; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Migglesworthia.
 NCBI_TaxID=36870;
 RX MEDLINE=2229718; PubMed=12219091; DOI=10.1038/ng986;
 RA Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,
 RA Akeoy S.;
 RT "Genome sequence of the endocellular obligate symbiont of tsetse
 RT files, Migglesworthia gossypii.",
 RL Nat. Genet. 32:402-407(2002).
 CC -1- FUNCTION: Necessary for the introduction of cis unsaturation into
 CC fatty acids. Catalyzed the dehydration of (3R)-3-hydroxydecanoyl-
 CC ACP to E-(2)-decanoyl-ACP and then its isomerization to Z-(3)-
 CC decenoyl-ACP (By similarity).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxydecanoyl-[acyl-carrier protein]
 CC = 2,3-decenoyl-[acyl-carrier protein] or 3,4-decenoyl-[acyl-
 CC carrier protein] + H(2)O.
 CC -1- PATHWAY: Key step in the anaerobic pathway of unsaturated fatty
 CC acid synthesis in bacteria.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the thioester dehydratase family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AB063522; BAC24446.1; -
 DR HSSP; P18391; IMKA.
 DR HAMAP; MF_00405; -; 1.
 DR InterPro; IPR010083; FABA.
 DR TIGRFAMs; TIGR01749; faba; 1.
 KM Complete proteome; Fatty acid biosynthesis; Lyase.
 FT ACT_SITE 71 71
 SQ SEQUENCE 177 AA; 20109 MW; 53237E5162914988 CRC64;
 QY Query Match 55.8%; Score 53; DB 1; Length 177;
 Best Local Similarity 62.5%; Pred. No. 8.8;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 MGGLVRLIAMLGWG 16
 Db 87 MGQLVGFYLGMLGKG 102
 RESULT 14
 ID Q9RR69 PRELIMINARY; PRT; 222 AA.
 AC Q9RR69;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein DR2628.
 GN OrderedLocNames=DR2628;
 OS Deinococcus radiodurans.
 CC Bacteria; Deinococcus-thermus; Deinococci; Deinococcales;
 CC Deinococcaceae; Deinococcus.
 NCBI_TaxID=1299;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,

RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L.A., Uitterlinden T.R., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 RT radiodurans R1.",
 RL Science 286:1571-1577(1999).
 DR EMBL; AE002092; AAP12174.1; -
 DR TIGR; C75250; C75250.
 KM Complete proteome; Hypothetical protein.
 SQ SEQUENCE 222 AA; 24482 MW; A1B9F407DF89A9A CRC64;
 QY Query Match 55.3%; Score 52.5; DB 2; Length 222;
 Best Local Similarity 66.7%; Pred. No. 13;
 Matches 10; Conservative 2; Mismatches 2; Indels 1; Gaps 1;
 QY 3 GLAVLLIAM-LGSGWG 16
 Db 154 GLAVLVAMGLSGWG 168
 RESULT 15
 ID FABA_HAEU STANDARD; PRT; 176 AA.
 AC Q7UJ43;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60)
 DE (Beta-hydroxydecanoyl thioester dehydratase).
 GN Name=faba; OrderedLocNames=HD0181;
 OS Haemophilus ducreyi.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 CC Pasteurellaceae; Haemophilus.
 NCBI_TaxID=730;
 RX MEDLINE=12219091; PubMed=12219091; DOI=10.1038/ng986;
 RA Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,
 RA Akeoy S.;
 RT "Genome sequence of the endocellular obligate symbiont of tsetse
 RT files, Migglesworthia gossypii.",
 RL Nat. Genet. 32:402-407(2002).
 CC -1- FUNCTION: Necessary for the introduction of cis unsaturation into
 CC fatty acids. Catalyzed the dehydration of (3R)-3-hydroxydecanoyl-
 CC ACP to E-(2)-decanoyl-ACP and then its isomerization to Z-(3)-
 CC decenoyl-ACP (By similarity).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxydecanoyl-[acyl-carrier protein]
 CC = 2,3-decenoyl-[acyl-carrier protein] or 3,4-decenoyl-[acyl-
 CC carrier protein] + H(2)O.
 CC -1- PATHWAY: Key step in the anaerobic pathway of unsaturated fatty
 CC acid synthesis in bacteria.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the thioester dehydratase family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AE017151; AAP5174.1; -
 DR HAMAP; MF_00405; -; 1.
 DR InterPro; IPR010083; FABA.
 DR TIGRFAMs; TIGR01749; faba; 1.
 KM Complete proteome; Fatty acid biosynthesis; Lyase.
 FT ACT_SITE 75 75
 SQ SEQUENCE 176 AA; 19280 MW; 21DE115843D569DC CRC64;

Wed Dec 8 11:46:32 2004

us-09-788-051-6.rup

Page 9

Query Match 54.7%; Score 52; DB 1; Length 176;
Best Local Similarity 56.2%; Pred. No. 12;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Oy 1 MMGLVRLLLAWLGGWG 16
Db 91 MMGLVGFPLGWI GGK 106
Search completed: December 8, 2004, 10:24:35
Job time : 8.41322 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OK protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 6.62102 Seconds

(without alignments)
866.886 Million cell updates/sec

Title: US-09-788-051-6

Perfect score: 95

Sequence: 1 MWGLVRLMLMLGSGWG 16

Scoring table: BIOSUM62

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	16	7	ADD29447 Human cad
2	95	100.0	493	5	AD116946 Human NOV
3	95	100.0	607	5	AB553295 Human pol
4	95	100.0	636	7	ADD29445 Human pol
5	95	100.0	781	5	AB553296 Human pol
6	95	100.0	781	5	AA448736 Human cad
7	95	100.0	781	5	AB534078 Human PRO
8	95	100.0	781	5	AD116604 Human NOV
9	95	100.0	781	5	AD116606 Human NOV
10	95	100.0	781	6	ABR40114 Human cel
11	95	100.0	781	6	ADA01366 Human PRO
12	95	100.0	781	6	ADA43795 Human sec
13	95	100.0	781	6	ADA43563 Human sec
14	95	100.0	781	6	ADA01238 Human PRO
15	95	100.0	781	7	ADA01122 Human sec
16	95	100.0	781	7	ADA43679 Human sec
17	95	100.0	781	7	ADA06941 Human PRO
18	95	100.0	781	7	ADA06429 Human PRO
19	95	100.0	781	7	ADB99722 Human PRO
20	95	100.0	781	7	ADB87005 Human PRO
21	95	100.0	781	7	ADB66160 Human sec
22	95	100.0	781	7	ADB99638 Human PRO
23	95	100.0	781	7	ADB99493 Human hum
24	95	100.0	781	7	ADB66044 Human sec
25	95	100.0	781	7	ADC23442 Human tra

26	95	100.0	781	7	ADC26135 Human PRO
27	95	100.0	781	7	AD604962 Human PRO
28	95	100.0	781	7	AD611268 Human PRO
29	95	100.0	781	7	AD688199 Human PRO
30	95	100.0	781	7	AD695494 Human sec
31	95	100.0	781	7	AD606424 Human PRO
32	95	100.0	781	7	AD638199 Human PRO
33	95	100.0	781	7	AD688315 Human PRO
34	95	100.0	781	7	AD690896 Human sec
35	95	100.0	781	7	AD699451 Human sec
36	95	100.0	781	7	AD606544 Human PRO
37	95	100.0	781	7	AD605495 Human PRO
38	95	100.0	781	7	AD682496 Human PRO
39	95	100.0	781	8	AD651749 Human sec
40	95	100.0	781	8	AD651865 Human sec
41	95	100.0	781	8	AD637723 Human sec
42	95	100.0	781	8	AD637607 Human sec
43	95	100.0	781	8	AD695378 Human sec
44	95	100.0	781	8	AD638078 Human PRO
45	95	100.0	781	8	AD676167 Human PRO

ALIGNMENTS

RESULT 1	
ID	ADD29447
AC	ADD29447 standard; protein; 16 AA.
DT	15-JUN-2004 (first entry)
DE	Human cadherin-like protein signal peptide.
KW	cadherin-like protein; transmembrane protein; cadherin domain; homotypic cell-cell adhesion; cytotactin; osteopathic; cancer; osteopetrosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis metastatic tumour; human.
OS	Homo sapiens.
PN	US200314491-A1.
PD	31-JUL-2003.
PF	16-FEB-2001; 2001US-00788051.
PR	03-FEB-2000; 2000US-00496914. 27-APR-2000; 2000US-00560875.
PA	(GDB/) GDBOLE S D. (KLOC/) KLO C. (ARTE/) ARTERBURN M C. (YEUN/) YEUNG G. (PALE/) PALENCIA S. (TANG/) TANG Y T. (LITC/) LIU C. (DRMA/) DRMANAC R T.
PI	Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT; Liu C, Dimaac RT;
DR	WPI; 2003-829799/77.
PT	Novel isolated human secreted cadherin-like polypeptide useful for treating diseases such as cancers, osteopetrosis, Paget's disease, osteomalacia, hyperostosis, osteopetrosis.
PS	Claim 11; SEQ ID NO 6; 63pp; English.
CC	This invention relates to a novel isolated human secreted cadherin-like protein and the DNA sequence which encodes it. Cadherins are a family of

CC transmembrane proteins which share a common cadherin domain in their
CC extracellular region. The extracellular portion mediates homotypic cell-
CC cell adhesion that is calcium dependent. Modulators of the protein of the
CC invention may have cytostatic or osteoparalytic activity. The invention may
CC allow development of therapeutic useful for the treatment of diseases
CC such as cancers, osteoporosis, Paget's disease, osteomalacia,
CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
CC invention may also be useful as markers for prognosis of metastatic
CC tumours. The present sequence is that of the signal peptide of the human
CC secreted cadherin-like protein which was used during the exemplification
CC of the invention.

XX
XX Sequence 16 AA;
SQ

Query Match 100.0%; Score 95; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MGVLRLLAMLGWG 16
Db 1 MGVLRLLAMLGWG 16

RESULT 2
AD16946
ID AD16946 standard; protein: 493 AA.
XX
XX AD16946;
AC
XX
XX 15-APR-2004 (first entry)
DT
XX
DE Human NOVX protein homologue SeqID 482.
XX
XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
XX inflammation; autoimmune disorder; allergy; blood disorder;
XX acquired immunodeficiency syndrome; AIDS; obesity; asthma;
XX immunoglobulin (Ig) A nephropathy; cirrhosis; arthritis;
XX Alzheimer's disease; infection; str.

XX Homo sapiens.
OS
XX WO200268649-A2.
PN
XX
XX 06-SEP-2002.
PD
XX
XX 31-JAN-2002; 2002MO-US002785.
PF
XX
XX 31-JAN-2001; 2001US-0265395P.
PR
XX 31-JAN-2001; 2001US-0265412P.
PR
XX 31-JAN-2001; 2001US-0265514P.
PR
XX 02-FEB-2001; 2001US-0265517P.
PR
XX 05-FEB-2001; 2001US-0266406P.
PR
XX 07-FEB-2001; 2001US-0266757P.
PR
XX 07-FEB-2001; 2001US-0266975P.
PR
XX 08-FEB-2001; 2001US-0267057P.
PR
XX 09-FEB-2001; 2001US-0267459P.
PR
XX 15-FEB-2001; 2001US-0267823P.
PR
XX 26-FEB-2001; 2001US-0268974P.
PR
XX 27-FEB-2001; 2001US-0271664P.
PR
XX 27-FEB-2001; 2001US-0271839P.
PR
XX 02-MAR-2001; 2001US-0271855P.
PR
XX 02-MAR-2001; 2001US-0272788P.
PR
XX 14-MAR-2001; 2001US-0275925P.
PR
XX 14-MAR-2001; 2001US-0275947P.
PR
XX 14-MAR-2001; 2001US-0275950P.
PR
XX 14-MAR-2001; 2001US-0275989P.
PR
XX 15-MAR-2001; 2001US-0276448P.
PR
XX 15-MAR-2001; 2001US-0276450P.
PR
XX 16-MAR-2001; 2001US-0276397P.
PR
XX 20-MAR-2001; 2001US-0278652P.
PR
XX 26-MAR-2001; 2001US-0278775P.

PR 26-MAR-2001; 2001US-0278789P.
PR 29-MAR-2001; 2001US-0279882P.
PR 29-MAR-2001; 2001US-0279884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282992P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285133P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 29-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312889P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313390P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.

XX
XX (CURA-) CURAGEN CORP.
XX
XX Tchernov VT, Spytek KA, Zernusen BD, Parturajan M, Shinkets RA;
PI Li L, Gangolli EA, Padigaru M, Anderson DM, Rastelli L, Miller CE;
PI Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CE;
PI Furtak K, Grosse WM, Alsobrook JP, Iepley DM, Rieger DK, Burgess CE;
XX
XX WPI; 2002-706998/76.
DR
XX
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
PT
XX
XX Disclosure; SEQ ID NO 482; 1498pp; English.
PS
XX
XX This invention relates to a novel nucleic acids, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOVX polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig) A nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC cytostatic, cardiac, antiinflammatory, immunosuppressive, antiallergic,
CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
CC antiautismic, nephroprotective, antiarthritic, hepatoprotective,
CC neuroprotective, nootropic, antibacterial, vitacide, antiparasitic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
CC of the invention.
XX
XX Sequence 493 AA;
SQ

Query Match 100.0%; Score 95; DB 5; Length 493;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MMGLVRLILAWLGSGWG 16
|||
Db 1 MMGLVRLILAWLGSGWG 16

RESULT 3
ABBS3295
ID ABBS3295 standard; protein; 607 AA.

XX AC ABBS3295;
XX DT 12-FEB-2002 (first entry)
XX DE Human polypeptide #35.

XX KW Human; nootropic; neuroprotective; anticonvulsant; antidepressant;
KW neuroleptic; tranquilizer; antiarrhythmic; cardiact; antidiabetic;
KW antiinflammatory; antihypertensive; hepatotropic; virucide; antidiabetic;
KW nephrotropic; anorectic; cytostatic; vaccine; neurological disease;
KW cardiovascular disease; respiratory disease; liver disease;
KW renal disease; skeletal muscle disease; gastrointestinal disease;
KW placental disease; testicular cancer; male fertility; pancreatic disease.

XX OS Homo sapiens.
XX FN WC00181363-A1.
XX PD 01-NOV-2001.

XX PF 26-APR-2001; 2001WO-US013360.
XX PR 27-APR-2000; 2000US-0199963P.
XX PR 11-MAY-2000; 2000US-0203336P.
XX PR 25-MAY-2000; 2000US-0207087P.
XX PR 26-MAY-2000; 2000US-0207546P.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.
XX PA (SMIK) SMITHKLINE BEECHAM PLC.

XX PI Agarwal P, Murdock FR, Rizvi SK, Smith RF, Xiang Z, Kabinick KS;
XX PI Lai Y, Xie Q;
XX DR WPI: 2002-041392/05.
XX DR N-PSDB; ABA90360.

XX PT Novel polypeptides and polynucleotides useful as a vaccine for preventing
XX PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesias.
XX PS Claim 1; Page 106-108; 116pp; English.

XX CC The invention relates to an isolated polypeptide comprising a 277, 480,
CC 583, 581, 628, 424, 639, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
CC 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,
CC 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
CC given in the specification. The polypeptides, modulators of the
CC polypeptides and antibodies against the polypeptides are useful for
CC treating diseases such as neurological and psychiatric diseases including
CC Alzheimer's, paraneoplastic, Huntington's disease, myotonic
CC dystrophy, anorexia and depression; cardiovascular diseases including
CC congestive heart failure, Hodgkin's disease and myocardial infarction;
CC respiratory diseases including asthma, chronic obstructive pulmonary
CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
CC diseases including hypercholesterolemia, cirrhosis, viral and nonviral
CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
CC renal disease including renal failure, acute tubular necrosis and
CC glomerulonephritis; skeletal muscle diseases including Eulenburg's
CC disease, hypoglycaemia and obesity; gastrointestinal diseases including

CC myotonia congenita and intestinal obstruction; lymph diseases including
CC lymphagiectasia; diseases of placenta including choriocarcinoma; diseases
CC of testes including testicular cancer, male reproductive diseases
CC including low testosterone and male infertility; and disease of pancreas
CC including diabetic ketosidosis, Type 1 and 2 diabetes and obesity. The
CC present sequence is a polypeptide of the invention
XX SQ Sequence 607 AA;

Query Match 100.0%; Score 95; DB 5; Length 607;
Best Local Similarity 100.0%; Pred. No. 5.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MMGLVRLILAWLGSGWG 16
|||
Db 1 MMGLVRLILAWLGSGWG 16

RESULT 4
ADD29445
ID ADD29445 standard; protein; 636 AA.

XX AC ADD29445;
XX DT 15-JAN-2004 (first entry)
XX DE Human cadherin-like protein amino acid sequence.

XX KW cadherin-like protein; transmembrane protein; cadherin domain;
KW homotypic cell-cell adhesion; cytotactic; osteopetrosis; cancer;
KW osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
KW metastatic tumour; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT Reptide 1..16
XX FT Protein /label=Signal_peptide
XX FT 17..636
XX FT /label=Mature_human_cadherin-like_protein

XX PN US200314491-A1.

XX PD 31-JUL-2003.

XX PF 16-FEB-2001; 2001US-00788051.

XX PR 03-FEB-2000; 2000US-00496914.
XX PR 27-APR-2000; 2000US-00560875.

XX PA (GODE/) GODEBOLE S D.

XX PA (KUOC/) KUO C.

XX PA (ARTE/) ARTERBURN M C.

XX PA (YEUN/) YEUNG G.

XX PA (PALE/) PALENCIA S.

XX PA (TANG/) TANG Y T.

XX PA (LITU/) LITU C.

XX PA (DRMA/) DRMANAC R T.

XX PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;
XX PI Liu C, Drmanac RT;

XX DR WPI: 2003-829799/77.
XX DR N-PSDB; ADD29461, ADD29446.

XX PT Novel isolated human secreted cadherin-like polypeptide useful for
XX PT treating diseases such as cancers, osteoporosis, Paget's disease,
XX PT osteomalacia, hyperostosis, osteopetrosis.
XX PS Claim 11; SEQ ID NO 4; 63pp; English.
XX CC This invention relates to a novel isolated human secreted cadherin-like
XX CC protein and the DNA sequence which encodes it. Cadherins are a family of

XX Claim 9; Page 105; 11pp; English.
PS
CC The invention relates to human cadherin family polypeptide designated
CC 57805 with osteopathic, hepatotropic, antipneumococcal, antidiabetic,
CC neoprotective, antirheumatic, antipneumococcal, antidiabetic,
CC immunosuppressive, antineoplastic, antipneumococcal, antidiabetic,
CC antiallergic, antipneumococcal, antipneumococcal, antidiabetic,
CC immunomodulatory, vasotropic, virucide, cytostatic, thrombolytic,
CC analgesic and anabolic activity. The 57805 molecules are useful for
CC diagnosing and treating disorders which include disorders associated with
CC bone metabolism, immune disorders, cardiovascular disorders, liver
CC disorders, viral diseases, pain or metabolic disorders. Especially bone
CC metabolism including osteoporosis, rickets, osteosclerosis, cirrhosis;
CC immune disorders including autoimmune disease including diabetes mellitus
CC arthritis, including rheumatoid arthritis and osteoarthritis, multiple
CC sclerosis, systemic lupus, dermatitis, psoriasis, Crohn's disease,
CC asthma, thrombocytopenia, Graves' disease, graft-versus-host disease,
CC allergy; cardiovascular disorders, thrombus, hypertension,
CC atherosclerosis, arrhythmias and cardiomyopathy; liver disorders,
CC glycogen storage disease, vascular disorders, chronic heart failure,
CC portal vein thrombosis; viral diseases; metabolic or pain disorders
CC include obesity, anorexia nervosa and diabetes, inflammation, infection
CC and ischaemia, irritable bowel syndrome. The polynucleotides are also
CC useful in gene therapy
XX
SQ Sequence 781 AA;
Query Match 100.0%; Score 95; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 MMGLVRLLLAWLGWG 16
Db 1 MMGLVRLLLAWLGWG 16
RESULT 7
ABG34078 ID ABG34078 standard; protein; 781 AA.
XX
AC ABG34078;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human Pro peptide #49.
XX
KM Human; PRO; secreted protein; transmembrane protein; genetic disorder;
KM tumour; cancer.
XX
OS Homo sapiens.
XX
PN WO200224888-A2.
XX
PD 28-MAR-2002.
XX
PF 29-AUG-2001; 2001WO-US027099.
XX
PR 01-SEP-2000; 2000US-0228996P.
PR 05-SEP-2000; 2000US-0230621P.
PR 22-SEP-2000; 2000US-0235147P.
PR 10-NOV-2000; 2000WO-US030873.
PR 12-JAN-2001; 2001US-0261878P.
PR 16-JAN-2001; 2001US-0261910P.
PR 16-JAN-2001; 2001US-0261939P.
PR 16-JAN-2001; 2001US-0262150P.
PR 25-JAN-2001; 2001US-0264385P.
PR 02-FEB-2001; 2001US-0266421P.
PR 09-FEB-2001; 2001US-0267623P.
PR 28-FEB-2001; 2001WO-US006520.
PR 09-MAR-2001; 2001US-0274399P.
PR 03-APR-2001; 2001US-0280982P.

PR 04-APR-2001; 2001US-0282129P.
PR 04-APR-2001; 2001US-0282199P.
PR 09-MAY-2001; 2001US-0290589P.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
XX (GENTH) GENENTECH INC.
XX
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
DR WFI; 2002-362426/39.
DR N-PSDB; ABK70009.
XX
PT New PRO polypeptides and polynucleotides encoding the polypeptides,
PT useful in gene therapy, chromosome identification, tissue typing, or for
XX genetic analysis of individuals with genetic disorders.
XX
Claim 11; Fig 98; 21pp; English.
CC This invention relates to the cDNA and protein sequences of novel
CC secreted and transmembrane polypeptides PRO polypeptides. The invention
CC also comprises a method for producing the proteins of the invention by
CC recombinant means and antibodies specific for the protein of the
CC invention. The antibody may be used for detecting the PRO proteins of the
CC invention and may be used to modify their activity. Polynucleotides may
CC be used as hybridisation probes for a cDNA library to isolate the full-
CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation
CC probes for mapping the gene which encodes that PRO and for genetic
CC analysis of individuals with genetic disorders, in assays to identify
CC other proteins or molecules involved in binding reaction, to generate
CC transgenic animals or knock-out animals which in turn are useful in the
CC development and screening of therapeutically useful reagents, for
CC chromosome identification, and tissue typing. The PRO polypeptides are
CC useful in gene therapy, and as molecular weight markers for protein
CC electrophoresis purposes. The sequences may also be used to detect
CC overexpression on PRO polypeptides in cancerous tumours and for screening
CC for differentially expressed genes using microarray technology. The
CC present sequence represents a human PRO protein of the invention
XX
SQ Sequence 781 AA;
Query Match 100.0%; Score 95; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 MMGLVRLLLAWLGWG 16
Db 1 MMGLVRLLLAWLGWG 16
RESULT 8
AD116604 ID AD116604 standard; protein; 781 AA.
XX
AC AD116604;
XX
DT 15-APR-2004 (first entry)
XX
DE Human NOVX protein to treat human pathological conditions SegID140.
XX
XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
XX inflammation; autoimmune disorder; allergy; blood disorder;
XX acquired immunodeficiency syndrome; AIDS; obesity; asthma;
XX immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
XX Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
XX cytostatic; cardiant; antiinflammatory; immunosuppressive; antiallergic;
XX haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;
XX antisthmatic; nephrotropic; antiarthritic; hepatotropic;

XX	MO2002068649-A2.
FN	
XX	
PD	06-SEP-2002.
XX	
PF	31-JAN-2002; 2002MO-US002785.
XX	
PR	31-JAN-2001; 2001US-0265395P.
XX	
PR	31-JAN-2001; 2001US-0265412P.
XX	
PR	31-JAN-2001; 2001US-0265514P.
XX	
PR	31-JAN-2001; 2001US-0265517P.
XX	
PR	02-FEB-2001; 2001US-0266406P.
XX	
PR	03-FEB-2001; 2001US-0266767P.
XX	
PR	07-FEB-2001; 2001US-0266795P.
XX	
PR	07-FEB-2001; 2001US-0267057P.
XX	
PR	08-FEB-2001; 2001US-0267459P.
XX	
PR	09-FEB-2001; 2001US-0267823P.
XX	
PR	15-FEB-2001; 2001US-0268974P.
XX	
PR	26-FEB-2001; 2001US-0271664P.
XX	
PR	27-FEB-2001; 2001US-0271839P.
XX	
PR	27-FEB-2001; 2001US-0271855P.
XX	
PR	02-MAR-2001; 2001US-0272788P.
XX	
PR	02-MAR-2001; 2001US-0273046P.
XX	
PR	14-MAR-2001; 2001US-0275925P.
XX	
PR	14-MAR-2001; 2001US-0275947P.
XX	
PR	14-MAR-2001; 2001US-0275950P.
XX	
PR	14-MAR-2001; 2001US-0275989P.
XX	
PR	15-MAR-2001; 2001US-0276448P.
XX	
PR	15-MAR-2001; 2001US-0276450P.
XX	
PR	16-MAR-2001; 2001US-0276397P.
XX	
PR	16-MAR-2001; 2001US-0276768P.
XX	
PR	20-MAR-2001; 2001US-0278652P.
XX	
PR	26-MAR-2001; 2001US-0278775P.
XX	
PR	26-MAR-2001; 2001US-0278778P.
XX	
PR	29-MAR-2001; 2001US-0279682P.
XX	
PR	29-MAR-2001; 2001US-0279684P.
XX	
PR	30-MAR-2001; 2001US-0280147P.
XX	
PR	11-APR-2001; 2001US-0282992P.
XX	
PR	11-APR-2001; 2001US-0283083P.
XX	
PR	20-APR-2001; 2001US-0285133P.
XX	
PR	23-APR-2001; 2001US-0285749P.
XX	
PR	03-MAY-2001; 2001US-0286327P.
XX	
PR	03-MAY-2001; 2001US-0288504P.
XX	
PR	29-MAY-2001; 2001US-0294074P.
XX	
PR	30-MAY-2001; 2001US-0294473P.
XX	
PR	08-JUN-2001; 2001US-0296947P.
XX	
PR	18-JUN-2001; 2001US-0298959P.
XX	
PR	19-JUN-2001; 2001US-0299324P.
XX	
PR	13-AUG-2001; 2001US-0312020P.
XX	
PR	16-AUG-2001; 2001US-0312889P.
XX	
PR	16-AUG-2001; 2001US-0312908P.
XX	
PR	21-AUG-2001; 2001US-0313390P.
XX	
PR	28-AUG-2001; 2001US-0315470P.
XX	
PR	31-AUG-2001; 2001US-0316447P.
XX	
PR	07-SEP-2001; 2001US-0318115P.
XX	
PR	07-SEP-2001; 2001US-0318118P.
XX	
PR	12-SEP-2001; 2001US-0318740P.
XX	
PR	19-SEP-2001; 2001US-0323379P.
XX	
PR	18-OCT-2001; 2001US-0330245P.
XX	
PR	18-OCT-2001; 2001US-0330308P.
XX	
PR	14-NOV-2001; 2001US-0332701P.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
XX	
PI	Tchernev VT, Spytek KA, Zethusen BD, Faturajan M, Shinkets RA;
XX	
PI	Li L, Gangolfi EA, Padigara M, Anderson DW, Rattelli L, Miller CE;
XX	
PI	Gielach VL, Tappier RJ, Guev VY, Colman SD, Wolenc AR, Pena CEA;
XX	
PI	Furtak K, Grosse WM, Alsobrook JP, Lepley DW, Rieger DK, Burgess CE
XX	
XX	WPI; 2002-706998/76.
XX	
XX	N-PSDB; ADI16605.
XX	

PT	treating NOXV-associated disorders', e.g. cancer, cardiomyopathy,
PT	atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT	pharmacogenomics.
PS	Claim 1; SEQ ID NO 142; 1498BP; English.
XX	
CC	This invention relates to a novel nucleic acids, and encoded polypeptides
CC	thereof, which have properties related to the stimulation of biochemical
CC	or physiological responses in a cell, tissue, organ or organism.
CC	Specifically, it refers to the use of biologically active fragments for
CC	diagnostic and prognostic assays and furthermore in the treatment of
CC	diverse pathological conditions. The present invention describes novel
CC	human and murine NOXV proteins, as well as methods to modulate their
CC	expression using antisense oligos, ribozymes and peptide nucleic acids.
CC	The NOXV polypeptides, polymucleotides and antibodies are useful in
CC	treating or preventing NOXV-associated disorders, e.g. cardiomyopathy,
CC	atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC	treating or preventing diseases such as inflammation, autoimmune
CC	disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC	(AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
CC	arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC	and epilepsy. Accordingly, these molecules have many activities including
CC	cystostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
CC	haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
CC	antianasthmatic, nephroprotective, antihypertensive, hepatotropic,
CC	neuroprotective, neurotropic, antibacterial, antiviral, antiparasitic,
CC	relaxant and anticonvulsant. In addition, they are useful in screening
CC	assays to identify small molecules that modulate or inhibit, for example,
CC	neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC	used as in chromosome mapping, tissue typing, preventive medicine and
CC	pharmacogenomics. This polypeptide is a human NOXV protein of the
CC	invention.
SO	
XX	
SQ	Sequence 781 AA;
	Query Match 100.0%; Score 95; DB 5; Length 781;
	Best local similarity 100.0%; Pred. No. 6.9e-05;
	Matches 16; Conservative 0; Mismatches 0; Indels 0;
Oy	1 MMGLVRLLLMLLGGWG 16
Ds	1 MMGLVRLLLMLLGGWG 16
RESULT 10	
ABR40114	ID ABR40114 standard; protein; 781 AA.
AC	XX ABR40114;
DT	XX 04-JUL-2003 ((first entry))
DE	XX Human cell adhesion and extracellular matrix protein, CADECW-11.
XX	
KM	Human; anti-HIV; antifibrotic; cerebroprotective; antiparkinsonian;
KM	anticonvulsant; nootropic; neuroprotective; immunosuppressive;
KM	dermatological; anti-inflammatory; cytostatic; antiarteriosclerotic;
KM	gene therapy; cell adhesion; extracellular matrix; CADECW;
KM	immune system disorder; AIDS; allergy; neurological disorder; stroke;
KM	Parkinson's disease; epilepsy; developmental disorder; Down's syndrome;
KM	cerebral palsy; connective tissue disorder; systemic lupus erythematosus;
KM	genetic disorder; Alport's syndrome; cell proliferative disorder; cancer;
OS	XO Homo sapiens.
XX	
FN	WO2003027230-A2.
XX	
PD	03-APR-2003.
XX	
PF	02-AUG-2002; 2002WC-US024649.
XX	

PR 03-AUG-2001; 2001US-0310119P.
 PR 17-AUG-2001; 2001US-0313081P.
 PR 31-AUG-2001; 2001US-0316771P.
 PR 07-SEP-2001; 2001US-0317896P.
 PR 21-SEP-2001; 2001US-0324781P.
 PR 05-OCT-2001; 2001US-0327606P.
 PR 12-OCT-2001; 2001US-0328960P.
 PR 09-NOV-2001; 2001US-0344471P.
 PR 17-MAY-2002; 2002US-0381291P.
 XX
 XX (INCYTE GENOMICS INC.)
 XX
 XX Burford N, Warren BA, Duggan BW, Mason PM, Richardson TW, Yue H;
 PI Forsythe JY, Elliott VS, Griffith JA, Gorvad AE, Azimzai Y;
 PI Kallik D, Xu Y, Honchell CD, Baughn MR, Gietzen KJ, Lee S;
 PI Wajia NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Ramkumar J;
 DR WPI; 2003-354645/33.
 DR N-PSDB; ACC00402.
 XX
 XX New human cell adhesion and extracellular matrix proteins (CADECM),
 PT useful for diagnosing, treating or preventing disorders associated with
 PT aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies
 PT or stroke.
 XX
 XX Claim 1; Page 192-194; 234pp; English.
 XX
 XX The present invention relates to novel human cell adhesion and
 CC extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding
 CC sequences (ACC00392-ACC00413, and ABR40104-ABR40125). The coding sequences
 CC and proteins are useful in diagnosing, treating and preventing disorders
 CC associated with aberrant expression of CADECM, such as immune system
 CC disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,
 CC Parkinson's disease or epilepsy), developmental disorders (e.g. Down's
 CC syndrome or cerebral palsy), connective tissue disorders (e.g. systemic
 CC lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell
 CC proliferative disorders (e.g. cancer or atherosclerosis)
 CC
 XX Sequence 781 AA;
 SQ
 Query Match 100.0%; Score 95; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 6.9e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMGLVRLILAWLGWG 16
 DB 1 MMGLVRLILAWLGWG 16
 RESULT 11
 ADA01366
 ID ADA01366 standard; protein; 781 AA.
 XX
 XX ADA01366;
 AC
 XX 06-NOV-2003 (first entry)
 DT
 XX Human PRO polypeptide #49.
 DE
 XX Human, PRO; secreted polypeptide; transmembrane polypeptide;
 KM tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
 KM adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
 KM microvascular endothelial cell; endothelial cell tube formation;
 KM sports-related joint problem; articular cartilage defect; osteoarthritis;
 KM rheumatoid arthritis; osteopathic; anti-rheumatic; anti-arthritis.
 XX
 XX Homo sapiens.
 OS
 XX US2003068779-A1.
 FN
 XX 10-APR-2003.
 PD
 XX 16-SEP-2002; 2002US-00245107.
 PF

XX 09-MAY-2001; 2001US-0290589P.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX
 XX (GENTEC GENENTECH INC.)
 XX
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WL, Zhang Z;
 PI Fong S;
 DR WPI; 2003-625484/59.
 DR N-PSDB; ADA01365.
 XX
 XX Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
 PT stimulating proliferation of human microvascular endothelial cells, and
 PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
 PT cells.
 XX
 XX Claim 1; Fig 98; 307pp; English.
 XX
 XX The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
 CC colon, breast, prostate, rectal, cervical and liver tumours). The
 CC polynucleotides are useful in molecular biology, including uses as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
 CC be used in preparing PRO polypeptides by recombinant techniques and in
 CC generating either transgenic animals or knock-out animals which are
 CC useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides or antibodies are used in preparing a
 CC medicament for treating a condition responsive to the polypeptides or
 CC antibodies, such as tumours, for stimulating and inhibiting proliferation
 CC of human microvascular endothelial cells, for inducing endothelial cell
 CC tube formation and for treating sports-related joint problems, articular
 CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
 CC represents a human PRO polypeptide of the invention.
 CC
 XX Sequence 781 AA;
 SQ
 Query Match 100.0%; Score 95; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 6.9e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMGLVRLILAWLGWG 16
 DB 1 MMGLVRLILAWLGWG 16
 RESULT 12
 ADA43795
 ID ADA43795 standard; protein; 781 AA.
 XX
 XX ADA43795;
 AC
 XX 20-NOV-2003 (first entry)
 DT
 XX Human secreted/transmembrane polypeptide PRO34009.
 DE
 XX Human, PRO; secreted protein; transmembrane protein;
 KM endothelial cell tube formation; chondrocyte cell differentiation;
 KM microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KM breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KM liver tumour; cytostatic; vaccine.
 XX
 XX Homo sapiens.
 OS
 XX US2003064474-A1.
 FN

XX 03-APR-2003.
PD 16-SEP-2002; 2002US-00245859.
XX 29-AUG-2001; 2001WO-US027099.
XX 18-JUL-2002; 2002US-00197942.
XX (GENTH) GENENTECH INC.
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX WPI; 2003-605867/57.
DR N-PSDB; ADA43794.
XX
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PT PRO2183, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
PS Claim 11; Fig 98; 308pp; English.
XX
CC The invention relates to an isolated secreted/transmembrane (PRO)
CC polypeptide, having at least 80% sequence identity to a sequence selected
CC from any one of the 57 amino acid sequences given in specification, or to
CC a sequence encoded by a nucleic acid molecule selected from any one of
CC the nucleic acids deposited under any of the ATCC accession numbers given
CC in specification, or a sequence having at least 80% identity to PRO
CC lacking its associated signal peptide, an extracellular domain of PRO
CC with or without its associated signal peptide. Also included are vectors,
CC transformed host cells, anti-PRO antibodies, the nucleic acid encoding
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC an oligonucleotide probe derived from any one of the above nucleotide
CC sequences. PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO313, PRO20080
CC and PRO2183 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumour in a mammal, including tumours of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence represents a PRO protein.
XX
SQ Sequence 781 AA;
Query Match 100.0%; Score 95; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. NO. 6.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 20-NOV-2003 (first entry)
XX Human secreted/transmembrane polypeptide PRO34009.
DE Human; PRO: secreted protein; transmembrane protein;
XX endothelial cell tube formation; chondrocyte cell differentiation;
XX microvascular endothelial cell; tumour, lung tumour, colon tumour;
XX breast tumour, prostate tumour; rectal tumour; kidney tumour;
XX liver tumour; cytosol; vaccine.
XX
OS Homo sapiens.
XX
XX US2003073196-A1.
XX
XX 17-APR-2003.
XX
XX 18-SEP-2002; 2002US-00246210.
XX
XX 04-APR-2001; 2001US-0282199P.
XX 29-AUG-2001; 2001WO-US027099.
XX 18-JUL-2002; 2002US-00197942.
XX
XX (GENTH) GENENTECH INC.
XX
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
XX Fong S;
XX WPI; 2003-743814/70.
XX N-PSDB; ADA43562.
XX
XX
XX New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
XX PRO2183 useful for stimulating the proliferation or differentiation of
XX chondrocyte cells and detecting the presence of a tumor in a mammal.
XX
XX Claim 11; Fig 98; 307pp; English.
XX
XX The invention relates to an isolated secreted/transmembrane (PRO)
XX polypeptide, having at least 80% sequence identity to a sequence selected
XX from any one of the 57 amino acid sequences given in specification, or to
XX a sequence encoded by a nucleic acid molecule selected from any one of
XX the nucleic acids deposited under any of the ATCC accession numbers given
XX in specification, or a sequence having at least 80% identity to PRO
XX lacking its associated signal peptide, an extracellular domain of PRO
XX with or without its associated signal peptide. Also included are vectors,
XX transformed host cells, anti-PRO antibodies, the nucleic acid encoding
XX PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
XX administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
XX PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
XX an oligonucleotide probe derived from any one of the above nucleotide
XX sequences. PRO6018 polypeptide is useful for stimulating the
XX proliferation or differentiation of chondrocyte cells. PRO313, PRO20080
XX and PRO2183 polypeptides are useful for stimulating the proliferation of
XX human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
XX polypeptides are useful for inhibiting the proliferation of human
XX microvascular endothelial cells. PRO polypeptides are useful for
XX detecting the presence of tumour in a mammal, including tumours of lung,
XX colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
XX PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
XX PRO34274 polypeptides are useful for inducing endothelial cell tube
XX formation. PRO or the antibody are useful in the preparation of a
XX medicament for treating a condition responsive to PRO polypeptide. The
XX oligonucleotide probes are useful for isolating genomic and cDNA
XX nucleotide sequences, for measuring or detecting the expression of an
XX associated gene, and as antisense probes. PRO nucleic acid is useful as a
XX hybridisation probe, in chromosome and gene mapping, in the generation of
XX antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
XX PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
XX present sequence represents a PRO protein.
XX
SQ Sequence 781 AA;
Query Match 100.0%; Score 95; DB 6; Length 781;

Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMGLVRLLLAMLGWG 16
1 MMGLVRLLLAMLGWG 16

RESULT 14
ADA01238
ID ADA01238 standard; protein: 761 AA.

AC ADA01238;
DT 06-NOV-2003 (first entry)

DE Human PRO polypeptide #49.

XX Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
KW cancer; lung; colon; breast; prostate; rectum; kidney; liver;
KW microvascular endothelial cell; endothelial cell tube formation.

OS Homo sapiens.

PN US2003068782-A1.

PD 10-APR-2003.

PF 16-SEP-2002; 2002US-00245851.

PR 27-APR-1999; 99US-0131271P.
PR 29-OCT-1999; 99US-0162506P.
PR 02-DEC-1999; 99WO-US028551.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.

PA (GENTH) GENENTECH INC.

PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
PI Fong S;

DR WPI; 2003-625487/59.
DR N-PSDB; ADA01237.

PT Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
PT preparation of a medicament for treating a condition responsive to PRO
PT polypeptide, and as therapeutic agents e.g. vaccines.

PS Claim 11; Fig 98; 308pp; English.

XX The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
CC prostate, rectal, kidney and liver tumours). The polynucleotides are
CC useful in molecular biology, including uses as hybridisation probes, in
CC chromosome and gene mapping, in generating antisense RNA and DNA and in
CC gene therapy. The polynucleotides may also be used in preparing PRO
CC polypeptides by recombinant techniques and in generating either
CC transgenic animals or knock-out animals which are useful in the
CC development and screening of therapeutically useful reagents. The PRO
CC polypeptides or antibodies are used in preparing a medicament for
CC treating a condition responsive to the polypeptides or antibodies, such
CC as tumours, for stimulating and inhibiting proliferation of human
CC microvascular endothelial cells and for inducing endothelial cell tube
CC formation. This sequence represents a human PRO polypeptide of the
XX invention.

SEQ Sequence 761 AA;

Query Match 100.0%; Score 95; DB 6; Length 761;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMGLVRLLLAMLGWG 16
1 MMGLVRLLLAMLGWG 16

RESULT 15
ADA01122
ID ADA01122 standard; protein: 761 AA.

AC ADA01122;

DT 06-NOV-2003 (first entry)

DE Human secreted/transmembrane polypeptide PRO34009.

XX Human; PRO; secreted protein; transmembrane protein;
KW endothelial cell tube formation; chondrocyte cell differentiation;
KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
KW liver tumour; cytostatic; vaccine.

OS Homo sapiens.

PN US2003068780-A1.

PD 10-APR-2003.

PF 16-SEP-2002; 2002US-00245143.

PR 02-AUG-2000; 2000US-0222695P.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.

PA (GENTH) GENENTECH INC.

PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
PI Fong S;

DR WPI; 2003-625485/59.
DR N-PSDB; ADA01121.

PT Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
PT preparation of a medicament for treating a condition responsive to PRO
PT polypeptide, and as therapeutic agents e.g. vaccines.

PS Claim 11; Fig 98; 307pp; English.

XX The invention relates to an isolated secreted/transmembrane (PRO)
CC polypeptide, having at least 80% sequence identity to a sequence selected
CC from any one of the 57 amino acid sequences given in specification, or to
CC a sequence encoded by a nucleic acid molecule selected from any one of
CC the nucleic acids deposited under any of the ATCC accession numbers given
CC in specification, or a sequence having at least 80% identity to PRO
CC lacking its associated signal peptide, an extracellular domain of PRO
CC with or without its associated signal peptide. Also included are vectors,
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
CC PRO10775, PRO21207, PRO20993 or PRO34274 polypeptide or its agonist) and
CC an oligonucleotide probe derived from any one of the above nucleotide
CC sequences. PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC and PRO21383 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human

CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumour in a mammal, including tumours of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO4499, PRO6108, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence represents a PRO protein.
XX
SQ Sequence 781 AA;

Query Match 100.0%; Score 95; DB 7; Length 781;
Best Local Similarity 100.0%; Pred. NO. 6.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMGLVRLILAVLGWG 16
|||
1 MMGLVRLILAVLGWG 16

Search completed: December 8, 2004, 10:13:03
Job time : 7.62102 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 10:13:18 ; Search time 16.3495 Seconds
(without alignments)
349.544 Million cell updates/sec

Title: US-09-788-051-6

Perfect score: 95

Sequence: 1 MWGLVRLMLMGWG 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 158576 segs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	95	100.0	16	10	US-09-788-051-6
2	95	100.0	493	15	US-10-072-012-482
3	95	100.0	607	15	US-10-258-951-74
4	95	100.0	636	10	US-09-788-051-4
5	95	100.0	781	9	US-09-860-868-2
6	95	100.0	781	14	US-10-245-752-98
7	95	100.0	781	14	US-10-245-859-98
8	95	100.0	781	14	US-10-245-103-98
9	95	100.0	781	14	US-10-245-107-98
10	95	100.0	781	14	US-10-245-143-98
11	95	100.0	781	14	US-10-245-171-98
12	95	100.0	781	14	US-10-245-851-98
13	95	100.0	781	14	US-10-245-883-98

14	95	100.0	781	14	US-10-237-535-98	Sequence 98, Appl
15	95	100.0	781	14	US-10-238-183-98	Sequence 98, Appl
16	95	100.0	781	14	US-10-238-283-98	Sequence 98, Appl
17	95	100.0	781	14	US-10-238-370-98	Sequence 98, Appl
18	95	100.0	781	14	US-10-245-055-98	Sequence 98, Appl
19	95	100.0	781	14	US-10-245-147-98	Sequence 98, Appl
20	95	100.0	781	14	US-10-245-730-98	Sequence 98, Appl
21	95	100.0	781	14	US-10-245-739-98	Sequence 98, Appl
22	95	100.0	781	14	US-10-246-210-98	Sequence 98, Appl
23	95	100.0	781	14	US-10-239-196-98	Sequence 98, Appl
24	95	100.0	781	14	US-10-243-024-98	Sequence 98, Appl
25	95	100.0	781	14	US-10-243-409-98	Sequence 98, Appl
26	95	100.0	781	14	US-10-245-621-98	Sequence 98, Appl
27	95	100.0	781	14	US-10-245-880-98	Sequence 98, Appl
28	95	100.0	781	14	US-10-245-023-98	Sequence 98, Appl
29	95	100.0	781	14	US-10-243-035-98	Sequence 98, Appl
30	95	100.0	781	14	US-10-243-185-98	Sequence 98, Appl
31	95	100.0	781	14	US-10-245-427-98	Sequence 98, Appl
32	95	100.0	781	14	US-10-245-473-98	Sequence 98, Appl
33	95	100.0	781	14	US-10-245-770-98	Sequence 98, Appl
34	95	100.0	781	14	US-10-245-877-98	Sequence 98, Appl
35	95	100.0	781	14	US-10-246-976-98	Sequence 98, Appl
36	95	100.0	781	14	US-10-243-320-98	Sequence 98, Appl
37	95	100.0	781	14	US-10-162-435-13	Sequence 13, Appl
38	95	100.0	781	14	US-10-242-743-98	Sequence 98, Appl
39	95	100.0	781	14	US-10-242-845-98	Sequence 98, Appl
40	95	100.0	781	14	US-10-237-636-98	Sequence 98, Appl
41	95	100.0	781	14	US-10-238-325-98	Sequence 98, Appl
42	95	100.0	781	14	US-10-238-346-98	Sequence 98, Appl
43	95	100.0	781	14	US-10-238-411-98	Sequence 98, Appl
44	95	100.0	781	14	US-10-243-124-98	Sequence 98, Appl
45	95	100.0	781	14	US-10-243-425-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-09-788-051-6
; Sequence 6, Application US/09788051
; Publication No. US20030144491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dimaac, Radoje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES A
; FILE REFERENCE: HYS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-6

Query Match 100.0%; Score 95; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWGLVRLMLMGWG 16

Db 1 MMGLVRLLLAWLGGWG 16

RESULT 2

US-10-072-012-482
; Sequence 482, Application US/10072012
; Publication No. US2004003493A1
; GENERAL INFORMATION:
; APPLICANT: Tchermey, Velizar
; APPLICANT: Szytek, Kimberly
; APPLICANT: Zernusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esna
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grose, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieser, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 482
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-482

Query March 100.0%; Score 95; DB 15; Length 493;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMGLVRLLLAWLGGWG 16
DB 1 MMGLVRLLLAWLGGWG 16

RESULT 3

US-10-258-951-74
; Sequence 74, Application US/10258951
; Publication No. US20040033504A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kahnlick, Karen
; APPLICANT: Lai, Ying-Ta
; APPLICANT: Xie, Qing
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50025
; CURRENT APPLICATION NUMBER: US/10/258,951
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/13360
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/199,963
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/203,336
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 60/207,087
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/207,546
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-951-74

Query March 100.0%; Score 95; DB 15; Length 607;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMGLVRLLLAWLGGWG 16
DB 1 MMGLVRLLLAWLGGWG 16

RESULT 4

US-09-788-051-4
; Sequence 4, Application US/09788051
; Publication No. US20030144491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiacyun
; APPLICANT: Arceburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dimanac, Radjoe T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AND
; FILE REFERENCE: HYS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-4

Query Match 100.0%; Score 95; DB 10; Length 636;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MMGLVRLILAMLGWG 16
|||||
DB 1 MMGLVRLILAMLGWG 16

RESULT 5
US-09-860-868-2

; Sequence 2, Application US/09860868
; Patent No. US20020076757A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A.J.
; TITLE OF INVENTION: 57805, A NOVEL HUMAN CACHERIN FAMILY
; FILE REFERENCE: 1048-050001
; CURRENT APPLICATION NUMBER: US/09/860,868
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 60/205,674
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-860-868-2

Query Match 100.0%; Score 95; DB 9; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MMGLVRLILAMLGWG 16
|||||
DB 1 MMGLVRLILAMLGWG 16

RESULT 6
US-10-245-752-98

; Sequence 98, Application US/10245752
; Publication No. US20030064473A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gueney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanebe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C66
; CURRENT APPLICATION NUMBER: US/10/245,752
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; TYPE: PRT

; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-752-98

CY 1 MMGLVRLILAMLGWG 16
|||||
DB 1 MMGLVRLILAMLGWG 16

RESULT 7
US-10-245-859-98

; Sequence 98, Application US/10245859
; Publication No. US20030064474A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gueney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanebe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C78
; CURRENT APPLICATION NUMBER: US/10/245,859
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT

ORGANISM: Homo Sapien
US-10-245-859-98

Query Match 100.0%; Score 95; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMGLVRLILAWLGSGW 16
DB 1 MMGLVRLILAWLGSGW 16

RESULT 8
US-10-245-103-98

Sequence 98, Application US/10245103
Publication No. US2003006879A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C12
CURRENT APPLICATION NUMBER: US/10/245,103

PRIOR FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-103-98

Query Match 100.0%; Score 95; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMGLVRLILAWLGSGW 16
DB 1 MMGLVRLILAWLGSGW 16

RESULT 9
US-10-245-107-98

Sequence 98, Application US/10245107
Publication No. US2003006879A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C71
CURRENT APPLICATION NUMBER: US/10/245,107

PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-107-98

Query Match 100.0%; Score 95; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMGLVRLILAWLGSGW 16
DB 1 MMGLVRLILAWLGSGW 16

RESULT 10
US-10-245-143-98

Sequence 98, Application US/10245143
Publication No. US2003006879A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin

```

1  APPLICANT: Fong, Sherman
2  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
3  TITLE OF INVENTION: ACIDS ENCODING THE SAME
4  FILE REFERENCE: P3630R1C90
5  CURRENT APPLICATION NUMBER: US/10/245,143
6  PRIOR FILING DATE: 2002-09-16
7  PRIOR APPLICATION NUMBER: 10/197942
8  PRIOR FILING DATE: 2002-07-18
9  PRIOR APPLICATION NUMBER: 60/059114
10 PRIOR FILING DATE: 1997-09-17
11 PRIOR APPLICATION NUMBER: 60/065046
12 PRIOR FILING DATE: 1997-10-24
13 PRIOR APPLICATION NUMBER: 60/065027
14 PRIOR FILING DATE: 1997-11-10
15 PRIOR APPLICATION NUMBER: 60/079689
16 PRIOR FILING DATE: 1998-03-27
17 PRIOR APPLICATION NUMBER: 60/086478
18 PRIOR FILING DATE: 1998-05-22
19 PRIOR APPLICATION NUMBER: 60/087607
20 PRIOR FILING DATE: 1998-06-02
21 PRIOR APPLICATION NUMBER: 60/089801
22 PRIOR FILING DATE: 1998-06-18
23 PRIOR APPLICATION NUMBER: 60/090557
24 PRIOR FILING DATE: 1998-06-24
25 PRIOR APPLICATION NUMBER: 60/090689
26 PRIOR FILING DATE: 1998-06-25
27 Remaining Prior Application data removed - See File Wrapper or PALM.
28 NUMBER OF SEQ ID NOS: 116
29 SEQ ID NO 98
30 LENGTH: 781
31 TYPE: PRT
32 ORGANISM: Homo Sapien
33 US-10-245-143-98

```

```

Query Match 100.0%; Score 95; DB 14; Length 761;
Best Local Similarity 100.0%; Pred. NO. 0.00032;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ox 1 MMGLVRLLLAMLGWG 16
|||||
Db 1 MMGLVRLLLAMLGWG 16

RESULT 11
US-10-245-771-98
Sequence 98, Application US/10245771
Publication NO. US20030068781A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvarcoff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Auecia
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Collin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C98
CURRENT APPLICATION NUMBER: US/10/245,771
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10

```

```

P R I O R   A P P L I C A T I O N   N U M B E R : 60/0796659
P R I O R   F I L I N G   D A T E : 1998-03-27
P R I O R   A P P L I C A T I O N   N U M B E R : 60/086478
P R I O R   F I L I N G   D A T E : 1998-05-22
P R I O R   A P P L I C A T I O N   N U M B E R : 60/087607
P R I O R   F I L I N G   D A T E : 1998-06-02
P R I O R   A P P L I C A T I O N   N U M B E R : 60/089801
P R I O R   F I L I N G   D A T E : 1998-06-18
P R I O R   A P P L I C A T I O N   N U M B E R : 60/090557
P R I O R   F I L I N G   D A T E : 1998-06-24
P R I O R   A P P L I C A T I O N   N U M B E R : 60/090669
P R I O R   F I L I N G   D A T E : 1998-06-25
    Remaining Prior Application data removed - See File Wrapper or PALM
?     NUMBER OF SEQ ID NOS: 116
?
?     SEQ ID NO: 98
?     LENGTH: 781
?
?     TYPE: PRMT
?
?     ORGANISM: Homo Sapien
US-10-245-771-98

```

```

Query March 100.0%; Score 95; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MMGLVRLILAWLGGWG 16
|||||
1 MMGLVRLILAWLGGWG 16

RESULT 12
US-10-245-851-98
; Sequence 98, Application US/10245851
; Publication No. US2003068782A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watande, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C93
CURRENT APPLICATION NUMBER: US/10/245.851
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116

```

SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-851-98

Query Match 100.0%; Score 95; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMGLVRLILAMLGSGWG 16
DB 1 MMGLVRLILAMLGSGWG 16

RESULT 13
US-10-245-883-98

Sequence 98, Application US/10245883
Publication No. US20030068783A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C70
CURRENT FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
REMARKS: Remaining Prior Application data removed - See File Wrapper or PAM.

US-10-245-883-98
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien

Query Match 100.0%; Score 95; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMGLVRLILAMLGSGWG 16
DB 1 MMGLVRLILAMLGSGWG 16

RESULT 14
US-10-237-535-98

Sequence 98, Application US/10237535

Publication No. US20030073188A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C3
CURRENT FILING DATE: 2002-09-06
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091358
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/106932
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/115554
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119342
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/123957
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123972
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: 60/127372
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/131271
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/13459
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/135725
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135729
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135750
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/138385
PRIOR FILING DATE: 1999-06-09

PRIOR APPLICATION NUMBER: 60/140653
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144732
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144790
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145228
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146843
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/148188
PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/148513
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/149327
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149395
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/150114
PRIOR FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: 60/151700
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/151734
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/170262
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/177118
PRIOR FILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: 60/179851
PRIOR FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 60/180921
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: 60/187202
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/198587
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 60/199614
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 60/206330
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206368
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/209832
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 60/218371
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/222695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/229896
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/230621
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/232887
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/235147
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/261878
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/261910
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/261939
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/262150

PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/264395
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/266421
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/267623
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/274399
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/280982
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/282129
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/282199
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/290589
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 09/180997
PRIOR FILING DATE: 1998-11-19
PRIOR APPLICATION NUMBER: 09/267213
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 09/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/403297
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 09/423741
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: 09/709238
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 09/802706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 09/872035
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/924419
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/927796
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/929404
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 09/931836
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 09/941992
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 09/946374
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 10/001054
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 10/081056
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: 10/119480
PRIOR FILING DATE: 2002-04-09

Query Match 100.0%; Score 95; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MMGLVRLILAVIGSWG 16

DB 1 MMGLVRLILAVIGSWG 16

RESULT 15
US-10-238-183-98
Sequence 98, Application US/10238183
Publication No. US20030073189A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin

APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C11
CURRENT APPLICATION NUMBER: US/10/238,183
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079669
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091358
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/106932
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/115554
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119342
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/123957
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123972
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: 60/127372
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/131271
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/133459
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/135725
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135729
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135750
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/138385
PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: 60/140653
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144732
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144758

PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144790
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145228
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146843
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/148188
PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/148513
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/149327
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149395
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/150114
PRIOR FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: 60/151700
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/151734
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/170262
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/177118
PRIOR FILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: 60/179851
PRIOR FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 60/180921
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: 60/187202
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/198587
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 60/199614
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 60/206330
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206368
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/209832
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 60/218371
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/222695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/229896
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/230621
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/232887
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/235147
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/261878
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/261910
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/261939
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/262150
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/264395
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/266421
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/267623
PRIOR FILING DATE: 2001-02-09

Wed Dec 8 11:46:31 2004

us-09-788-051-6.rapb

;; PRIOR APPLICATION NUMBER: 60/274399
;; PRIOR FILING DATE: 2001-03-09
;; PRIOR APPLICATION NUMBER: 60/280982
;; PRIOR FILING DATE: 2001-04-03
;; PRIOR APPLICATION NUMBER: 60/282129
;; PRIOR FILING DATE: 2001-04-04
;; PRIOR APPLICATION NUMBER: 60/282199
;; PRIOR FILING DATE: 2001-04-04
;; PRIOR APPLICATION NUMBER: 60/290589
;; PRIOR FILING DATE: 2001-05-09
;; PRIOR APPLICATION NUMBER: 09/180997
;; PRIOR FILING DATE: 1998-11-19
;; PRIOR APPLICATION NUMBER: 09/267213
;; PRIOR FILING DATE: 1999-03-12
;; PRIOR APPLICATION NUMBER: 09/380137
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/380138
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/403297
;; PRIOR FILING DATE: 1999-10-18
;; PRIOR APPLICATION NUMBER: 09/423741
;; PRIOR FILING DATE: 1999-11-10
;; PRIOR APPLICATION NUMBER: 09/709238
;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: 09/802706
;; PRIOR FILING DATE: 2001-03-09
;; PRIOR APPLICATION NUMBER: 09/872035
;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 09/924419
;; PRIOR FILING DATE: 2001-08-06
;; PRIOR APPLICATION NUMBER: 09/927796
;; PRIOR FILING DATE: 2001-08-09
;; PRIOR APPLICATION NUMBER: 09/929404
;; PRIOR FILING DATE: 2001-08-13
;; PRIOR APPLICATION NUMBER: 09/931836
;; PRIOR FILING DATE: 2001-08-16
;; PRIOR APPLICATION NUMBER: 09/941992
;; PRIOR FILING DATE: 2001-08-28
;; PRIOR APPLICATION NUMBER: 09/946374
;; PRIOR FILING DATE: 2001-09-04
;; PRIOR APPLICATION NUMBER: 10/001054
;; PRIOR FILING DATE: 2001-11-30
;; PRIOR APPLICATION NUMBER: 10/052586
;; PRIOR FILING DATE: 2002-01-15
;; PRIOR APPLICATION NUMBER: 10/081056
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: 10/119480
;; PRIOR FILING DATE: 2002-04-09

Query Match: 100.0%; Score 95; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMGLVRLLLAWLGWG 16
1 MMGLVRLLLAWLGWG 16

Search completed: December 8, 2004, 11:34:26
Job time: 16.3495 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model
Run on: December 8, 2004, 09:16:13 / Search time 1.90791 Seconds
(without alignments)
556.152 Million cell updates/sec

Title: US-09-788-051-6
Perfect score: 95
Sequence: 1 MWGLVRLMLMGWG 16

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/aa/5A.COMB.pdp:*
2: /cgn2_6/ptodata/1/aa/5B.COMB.pdp:*
3: /cgn2_6/ptodata/1/aa/6A.COMB.pdp:*
4: /cgn2_6/ptodata/1/aa/6B.COMB.pdp:*
5: /cgn2_6/ptodata/1/aa/PTCUS.COMB.pdp:*
6: /cgn2_6/ptodata/1/aa/backfiles.pdp:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	56.8	555	4	US-09-252-991A-31521
2	53	55.8	173	4	US-09-543-681A-7869
3	53	55.8	195	4	US-09-489-039A-12028
4	48	50.5	86	4	US-09-513-999C-4272
5	48	50.5	373	4	US-09-252-991A-24381
6	47	49.5	500	4	US-09-540-236-3439
7	46	48.4	126	4	US-09-583-110-2867
8	45	47.4	860	4	US-09-252-991A-26112
9	45	47.4	1147	2	US-08-131-365B-38
10	45	47.4	1147	2	US-08-668-123-38
11	44	46.3	169	4	US-09-328-352-6931
12	44	46.3	273	4	US-09-489-039A-12374
13	44	46.3	346	5	PCT-US96-10602-2
14	44	46.3	582	4	US-09-489-039A-10786
15	43.5	45.8	361	4	US-09-328-352-7040
16	43	45.3	12	2	US-08-764-640-136
17	43	45.3	12	2	US-08-973-225-136
18	43	45.3	12	3	US-09-244-298A-136
19	43	45.3	12	3	US-09-516-704-136
20	43	45.3	12	4	US-09-540-090-136
21	43	45.3	12	4	US-09-832-230A-136
22	43	45.3	439	4	US-09-583-110-3057
23	42.5	44.7	112	4	US-09-205-258-1097
24	42	44.2	157	4	US-09-270-767-32124
25	42	44.2	157	4	US-09-270-767-47341
26	42	44.2	210	3	US-08-849-764C-4
27	42	44.2	210	3	US-09-262-087-4

28	42	44.2	210	4	US-08-463-261B-10	Sequence 10, Appl
29	42	44.2	211	1	US-08-588-163-4	Sequence 4, Appl
30	42	44.2	211	2	US-09-111-070-4	Sequence 4, Appl
31	42	44.2	211	4	US-09-540-530-3	Sequence 3, Appl
32	42	44.2	211	4	US-08-134-231C-13	Sequence 13, Appl
33	42	44.2	211	4	US-08-728-160-13	Sequence 13, Appl
34	42	44.2	309	4	US-09-489-039A-10582	Sequence 10582, A
35	42	44.2	317	2	US-08-864-799-4	Sequence 4, Appl
36	42	44.2	317	2	US-08-864-799-5	Sequence 5, Appl
37	42	44.2	348	4	US-09-489-039A-8632	Sequence 8632, Ap
38	42	44.2	538	3	US-09-040-005-2	Sequence 2, Appl
39	42	44.2	538	3	US-09-523-217-115	Sequence 115, App
40	42	44.2	538	4	US-09-404-641-2	Sequence 2, Appl
41	42	44.2	538	4	US-09-923-246-115	Sequence 115, App
42	42	44.2	538	4	US-10-295-723-115	Sequence 115, App
43	42	44.2	538	4	US-10-414-186-2	Sequence 2, Appl
44	42	44.2	538	4	US-09-825-561A-2	Sequence 2, Appl
45	42	44.2	539	4	US-09-248-766A-16542	Sequence 16542, A

ALIGNMENTS

```
RESULT 1
US-09-252-991A-31521
; Sequence 31521, Application US/09252991A
; Patent No. 6651795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31521
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31521

Query Match      56.8%; Score 54; DB 4; Length 555;
Best Local Similarity 76.9%; Pred. No. 6.7;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3  GLVRLMLMGW 15
Db      219  GLVRLMLMGW 231

RESULT 2
US-09-543-681A-7869
; Sequence 7869, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRENN
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7869
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7869
```

Query Match 55.8%; Score 53; DB 4; Length 173;
Best Local Similarity 62.5%; Pred. No. 2.8;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MGVLRLLIWLGMG 16
Db 88 MVLVGYLWLGSEG 103

RESULT 3

US-09-489-039A-12028
; Sequence 12028, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO: 12028
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12028

Query Match 55.8%; Score 53; DB 4; Length 195;
Best Local Similarity 62.5%; Pred. No. 3.2;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MGVLRLLIWLGMG 16
Db 110 MVLVGYLWLGSEG 125

RESULT 4

US-09-513-999C-4272
; Sequence 4272, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO: 4272
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SIGNAL
; LOCATION: -22..-1
; OTHER INFORMATION: score 10
; OTHER INFORMATION: seq FILATLTIASTWA/LT
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 13
; OTHER INFORMATION: Xaa=Glu or Gly
US-09-513-999C-4272

Query Match 50.5%; Score 48; DB 4; Length 86;
Best Local Similarity 72.7%; Pred. No. 6.9;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 5 VRLILSLWWSGW 15
Db 70 VRLILSLWWSGW 80

RESULT 5

US-09-252-991A-24381
; Sequence 24381, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 24381
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24381

Query Match 50.5%; Score 48; DB 4; Length 373;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 LVRLILSLWWSGW 15
Db 120 LVRLILSLWWSGW 131

RESULT 6

US-09-540-236-3439
; Sequence 3439, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO: 3439
; LENGTH: 500
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-3439

Query Match 49.5%; Score 47; DB 4; Length 500;
Best Local Similarity 87.5%; Pred. No. 57;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LLAWLWGM 15
Db 164 LVAWLWGM 171

RESULT 7

US-09-583-110-2867
; Sequence 2867, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

FILE REFERENCE: PATH00-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 2867
LENGTH: 126
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-583-110-2867

Query Match 48.4%; Score 46; DB 4; Length 126;
Best Local Similarity 46.2%; Pred. No. 19;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 MMGLVRLILAMWG 13
DB 6 LMALILAMWG 18

RESULT 8
US-09-252-991A-26112
Sequence 26112, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26112
LENGTH: 860
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26112

Query Match 47.4%; Score 45; DB 4; Length 860;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 3 GLVRLILAMWG 16
DB 624 GLAQLQLTLPKRG 637

RESULT 9
US-08-131-365B-38
Sequence 38, Application US/08131365B
Patent No. 5527690
GENERAL INFORMATION:
APPLICANT: Brown, Michael S.
APPLICANT: Briggs, Michael R.
APPLICANT: Wang, Xiaodong
APPLICANT: Goldstein, Joseph L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESSES:
ADDRESSES: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston

STATE: Texas
COUNTRY: U.S.A.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/131,365B
FILING DATE: 01-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:372/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1147 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-131-365B-38

Query Match 47.4%; Score 45; DB 1; Length 1147;
Best Local Similarity 47.1%; Pred. No. 2.5e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

OY 1 MMGLVRLILAMWG 15
DB 628 LMLIRHLQLRWGRW 644

RESULT 10
US-08-668-123-38
Sequence 38, Application US/08668123
Patent No. 5891631
GENERAL INFORMATION:
APPLICANT: Brown, Michael S.
APPLICANT: Briggs, Michael R.
APPLICANT: Wang, Xiaodong
APPLICANT: Goldstein, Joseph L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESSES:
ADDRESSES: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/668,123
FILING DATE: 14-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/131,365
FILING DATE: 01-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:372/PAR
TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1147 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-668-123-38

Query Match 47.4%; Score 45; DB 2; Length 1147;
Best Local Similarity 47.1%; Pred. No. 2.5e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 1 MGGLVRL--AWLGM 15
Db 628 LMLIRHLQRLWGRW 644
RESULT 11
US-09-328-352-6931
Sequence 6931, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-035A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6931
LENGTH: 169
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-6931

Query Match 46.3%; Score 44; DB 4; Length 169;
Best Local Similarity 66.7%; Pred. No. 50;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 VRLIWLWLGWG 16
Db 113 IGLIWLWLGWG 124
RESULT 12
US-09-489-039A-12374
Sequence 12374, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12374
LENGTH: 273
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12374

Query Match 46.3%; Score 44; DB 4; Length 273;
Best Local Similarity 87.5%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 13
PCT-US96-10602-2

Sequence 2, Application PC/TUS96.10602
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: INHIBITION OF HEPATITIS B REPLICATION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10602
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017,814
FILING DATE: 20-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/282001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10602-2

Query Match 46.3%; Score 44; DB 5; Length 346;
Best Local Similarity 47.6%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 3; Indels 8; Gaps 1;

Qy 2 MGGLVRL-----LWLG 14
Db 285 WALRLSWLNLVPLWLG 305
RESULT 14
US-09-489-039A-10786
Sequence 10786, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 10786
LENGTH: 582
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10786

```

Query Match          46.3%;   Score 44;   DB 4;   Length 582;
Best Local Similarity 53.3%;   Pred. No. 1.8e+02;
Matches      8;   Conservative    2;   Mismatches    5;   Indels    0;   Gaps    0;

```

```
Qy      1 MWGLVRLLLAWIGW 15
          :| | | | | :| |
Db      20 LWLLVALLVIGAW 34
```

```

RESULT 15
US-09-328-352-7040
: Sequence 7040, Application US/09328352
: Patent No. 6562358
: GENERAL INFORMATION:
: APPLICANT: Gary L. Breton et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
: TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: GTC99-03PA
: CURRENT APPLICATION NUMBER: US/09/328,352
: CURRENT FILING DATE: 1999-06-04
: NUMBER OF SEQ ID NOS: 8252
: SEQ ID NO 7040
: LENGTH: 361
: TYPE: PR1
: ORGANISM: Acinetobacter baumannii
US-09-328-352-7040

```

Query Match	45.8%	Score 43.5;	DB 4;	Length 361;
Best Local Similarity	42.1%;	Pred. No. 1.3e+02;		
Matches	8;	Conservative	4;	Mismatches 4;
			Indels	3;
			Gaps	1;

```
QY      1 MWGLVRL--LLAWLTGWS 16
      :||: : |||||
Db     101 VWGIPVITIGILAWLTWWS 119
```

Search completed: December 8, 2004, 10:01:09
Job time : 2.90791 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 50.1417 Seconds
(without alignments)
1189.717 Million cell updates/sec

Title: us-09-788-051-7
Perfect score: 3259
Sequence: 1 CMGRLLAAPAPAPAMAGSRHPG.....LPSCQLPLGLPALGIVLCAS 620

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR.79:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1602	49.2	796 2 A38992	cadherin 11 precurs
2	1596	49.0	796 2 A53584	OB-cadherin precurs
3	1593	48.9	796 2 148277	cadherin-11 - mous
4	1593	48.9	796 2 149556	cadherin-11 - mous
5	1529.5	46.9	793 2 D38992	cadherin 8 - human
6	1441	44.2	789 2 152701	K-cadherin - rat
7	1440	44.2	790 2 137016	cadherin-6 - human
8	1431.5	43.9	785 2 150180	cadherin-7 - chick
9	1412.5	43.3	790 2 G02678	cadherin-14 - huma
10	1400	43.0	790 2 150178	cadherin-6b - chic
11	1389.5	42.6	790 2 151638	P-cadherin - Afric
12	1368.5	42.0	794 2 159372	cadherin 12 - huma
13	935.5	28.7	784 2 151206	cadherin 5 precurs
14	601	18.4	906 1 IUMSCN	N-cadherin precurs
15	596	18.3	913 1 ICHCHR	R-cadherin precurs
16	594.5	18.2	906 1 IYXLC2	N-cadherin 2 precu
17	594	18.2	906 1 IYHUCN	N-cadherin 2 precurs
18	592	18.2	877 1 IYHUCN	N-cadherin precurs
19	591	18.1	912 1 IYHUCN	N-cadherin precurs
20	586	18.0	887 1 IYHUCN	R-cadherin precurs
21	585	18.0	913 1 A47543	R-cadherin precurs
22	581	17.8	882 1 IYHUCN	cadherin 1 precurs
23	581	17.8	905 1 IYXLC1	N-cadherin 1 precu
24	574.5	17.6	712 1 IYHUCN	N-cadherin precurs
25	574.5	17.6	717 2 IYHUCN	T-cadherin precurs
26	567	17.4	916 2 C38992	cadherin 4 precurs
27	563.5	17.3	713 2 B38992	cadherin 13 precurs
28	552.5	17.0	814 2 G02678	cadherin-15 precurs
29	543.5	16.4	2809 2 T10213	G-cadherin - sea u

30	531	16.3	732 1 IYHUCB	B-cadherin precurs
31	531	16.3	783 2 I50116	N-cadherin precurs
32	524	16.1	884 1 IUMSCN	E-cadherin precurs
33	523.5	16.1	896 2 I45858	desmocollin - bovi
34	521	16.0	884 2 S34438	uvomorulin - bovi
35	519	15.9	871 2 S47518	cadherin - Afric
36	512	15.7	3034 2 T14119	seven-pass transme
37	510.5	15.7	826 2 B53363	desmocollin, type
38	510.5	15.7	896 2 A55363	desmocollin, type
39	507	15.6	730 1 IUMSCN	M-cadherin - mouse
40	502.5	15.4	822 1 IUMSCP	P-cadherin precurs
41	502.5	15.4	829 1 IYHUCP	cadherin 3 precurs
42	496	15.2	3097 2 T00021	DN-cadherin - furi
43	491	15.1	840 2 I37281	Desla precursor -
44	491	15.1	894 2 I37281	Desla precursor -
45	487	14.9	770 2 B48910	desmocollin 1b pre

ALIGNMENTS

RESULT 1

A38992
cadherin 11 precursor - human
N:Alternate names: OB-cadherin, osteoblast
C:Species: Homo sapiens (man)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: A38992
R/Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A>Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous
A/Reference number: S24305; MUID:91283540; PMID:2059658
A/Accession: A38992
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-796 <SUZ>
A/Cross-references: UNIPROT:P55287; GB:U34056; NID:G506403; PIDN:AAA5622.1; PID:G50640
C/Genetics:
A:Gene: GDB:CDH11; OB
A/Cross-references: GDB:512891; OMIM:600023
A/Map position: 16q22.1-16q22.1
C/Superfamily: cadherin; cadherin repeat homology
C/Keywords: calcium binding; cell adhesion; duplication
F/56-159/Domain: cadherin repeat homology <CR1>
F/162-268/Domain: cadherin repeat homology <CR2>
F/271-383/Domain: cadherin repeat homology <CR3>
F/386-488/Domain: cadherin repeat homology <CR4>

Query Match

Best Local Similarity 49.2%; Score 1602; DB 2; Length 796;
Matches 323; Conservative 98; Mismatches 134; Indels 86; Gaps 10;

QY	1	CMGRLLA-----APAR-----AMAGSR--HGCPALPFRRSWMNQFVIEEYAPREPV	47
DB	13	CLQMLCHSAFAPBERGHLPSPFHGHEKKGQVYQRIKRWGYNQFVIEEYTPDDV	72
QY	48	LICKLMSVDYRGGRKTYLLTGEAGTVFVIDEATGNHVTSLDREERQAQVLLQAQVD	107
DB	73	LVGRLLMSDIDSGDNIKYILSGGAGTIVIDDKSGNIAATKLDREERQAQVLLQAQVD	132
QY	108	RASNRLPEPSEFIIIGQDINNPFFPLGPHATPEMSNGTSVIOYTAADADPSYG	167
DB	133	RDNRPLPEPSEFIVAVQDINDNPEFLHETTHANVPESNNGTSVIOYTAADADPTVG	192
QY	168	NSAKLVYTVLDGLPFFSVDPQGTGVVTAIPNDRETQEEFLVYIQAKDNGHNGGLSGST	227
DB	193	NSAKLVYSILIEGQPYFSVEAQGTGIRTPALPNDRFAKEEYHVYIQAKDNGHNGGLSGST	252
QY	228	TIVTVTLDVVDNPPKPKQSIYQFSVETAGPGLVGRRLAQQPDDGLNMLMYSITLDEGS	287
DB	253	KVITITLVDVNDPPKPKPQRYQMSVSEAAVPGSEVERVAKQPDIGENGLVITNIVDGSG	312
QY	288	SEAFSISTDQGDGLITVRKPLDFESQRSYSFRVATITLIDPAYLRGPFEDVASVAV	347

Db 313 MESFEITTDYTOGVVILKKPVDPEFERAVSLKVEANVHIDPKFISNGPFDOTVTKI 372
Qy 348 AVQDAPPEPAFTQAAHNLTVPENKAPGTLVGOISAAALDSPAIRYSILPHSDPERCSF 407
Db 373 SVEDDEPMPFLASVYHEVOENAAAGVGRVAKDPDAAANSPIRISIDRHLDLDFFT 432
Qy 408 IQPEEGTHTAAPLDRAPAMHNLTVLATELGSWGPGRGVPLLVAMSAAPAAPQSRP 467
Db 433 INPEDGFKTKTLPDLRETAALNITVFAAEI----- 463
Qy 468 VGSVAGVLPDSSAASQVAVIQTLDENDNAPOLAEYDTFVCDSE-----AAGQLIQVIR 533
Db 464 -----NHRQEAQVPAIRVLVDNDNAPKFAAYEGFICESDQTKPLSNQPIVTIS 514
Qy 524 ALDRDEVANSNVSVFQGP--LGPDPANFTVODNRDLPA-----WPHFLM 565
Db 515 ADDXDDPDANGBRPIFSLPPEIHNPNFTVARDNNTGAVYARRGGRKODLYLPIVI 574
Qy 566 ASASSWLMHPPAERGNQAPAGKSSSLP-CG-RUPGALPSC 604
Db 575 -----SDGIIPPMSTNTLITIKVCGCDVNGALISC 604

RESULT 2

OB-cadherin precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: A53584
R:Okazaki, M.; Takeshita, S.; Kawai, S.; Kikuno, R.; Tsujimura, A.; Kido, A.; Amann, E.
J. Biol. Chem. 269, 12092-12098, 1994
A:Title: Molecular cloning and characterization of OB-cadherin, a new member of cadherin
A:Reference number: A53584, MUID:94216322, PMID:8163513
A:Accession: A53584
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-796 <OKA>
A:Cross-references: UNIPROT:P55288; GB:D1253; NID:g994774; PIDN:BA04797.1; PID:g994775
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: transmembrane protein
C:KeyWords: transmembrane protein
F:56-159/Domain: cadherin repeat homology <CR1>
F:162-268/Domain: cadherin repeat homology <CR2>
F:386-488/Domain: cadherin repeat homology <CR4>

Query Match 49.0%; Score 1596; DB 2; Length 796;
Best Local Similarity 50.7%; Pred. No. 2.8e-98;
Matches 317; Conservative 97; Mismatches 127; Indels 84; Gaps 8;
Qy 15 SREHP-----GPAALRTTRSGVWVNOQFVIEEYAGPEPVLIGKLSHDVDRGERT 63
Db 29 SHLHPSFHGHKEKGEQVLRKSKRGVWVNOQFVIEEYAGPEPVLIGKLSHDVDRGERT 88
Qy 64 KYLLTGAGAGTVFVIDEATGNIHVTKSLDREKAOYVLLAOAVDRASNRPLEPSPFTIK 123
Db 89 KYLLSGGAGTIFVIDKSGNIHATKTLDBEERAOYTLMAOAVDRDTRNPLEPSPFTIK 148
Qy 124 GODINDNPPFIFLGPYHATVPENSNVGTSVIQTADHADDPSYGNSAKLYTVTLSDNNDPPK 183
Db 149 VQDINDNPPFELHEIYHANVPERSNVGTSVIQTADHADDPSYGNSAKLYTVTLSDNNDPPK 208
Qy 184 SVDPOGVAVRAIPNMDRETOEFLVYIOAKDNGHNGISGTTVTVTLSDVNDNPPK 243
Db 209 SVAQGTGIRITAPNMDREKAEHVVYIOAKDNGHNGISGTTVTVTLSDVNDNPPK 268
Qy 244 POSLYQSVVETAGPGLVGRLAODPDLDGNALMAYSILDEGSEAFSISTDLQGRDL 303
Db 269 POSYQMSVEAAPGSEVGRVAKDPDIDGENGLVTYNIYDGGIELFETITDYETQDGV 328
Qy 304 LTVAKPLDESSQSVSYFRVATNTLIDPALRRGPKDVAASVVAQDAPEPAFTQAA 363
Db 329 VKLKKVDFETKAYSLKIEANVHIDPKFISNGPFDOTVTKISVEDADEPMPFLASV 388

Qy 364 HLTVPENKAPGTLVGOISAAALDSPAIRYSILPHSDPERCSFIOPEEGTHTAAPLDR 423
Db 389 IHEVOENAAAGTVGRVAKDPDAAANSPIRISIDRHLDLDFFTINPEDGFKTKTLPDR 448
Qy 424 EAPAMHNLTVLATELGSWGPGRGVPLLVAMSAAPAAPQSRVGSAGVLPDSSAASQAS 483
Db 449 EETAMNLSVFAAEI-----HNRQET 470
Qy 484 RVQVAVIQTLDENDNAPOLAEYDTFVCDSEAP-----GQLIQVIRALDRDEVANSNVSVFQ 539
Db 471 KVPVAVIRVLVDNDNAPKFAAYEGFICESDHPKLSNQPITYVTSADDDODDPAAPRPIFS 530
Qy 540 GP--LGPDPANFTVODNRDLPA-----WPHFLMASASSWLMHPPAERGN 581
Db 531 LPPEIHNPNFTVARDNNTGAVYARRGGRKODLYLPIVI-----SDGII 579
Qy 582 QPASGKSSSLP-CG-RUPGALPSC 604
Db 580 PMSSTNTLITIKVCGCDVNGALISC 604

RESULT 3

cadherin-11 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48277
R:Hoffmann, I.; Balling, R.
Dev. Biol. 169, 337-346, 1995
A:Title: Cloning and expression analysis of a novel mesodermally expressed cadherin.
A:Reference number: I48277; MUID:95265886; PMID:7750649
A:Accession: I48277
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-796 <RES>
A:Cross-references: UNIPROT:P55288; EMBL:X77557; NID:g642796; PIDN:CA054674.1; PID:g66606
C:Superfamily: cadherin; cadherin repeat homology
F:56-159/Domain: cadherin repeat homology <CDH>

Query Match 48.9%; Score 1593; DB 2; Length 796;
Best Local Similarity 50.6%; Pred. No. 4.4e-98;
Matches 316; Conservative 96; Mismatches 127; Indels 84; Gaps 8;
Qy 15 SREHP-----GPAALRTTRSGVWVNOQFVIEEYAGPEPVLIGKLSHDVDRGERT 63
Db 29 SHLHPSFHGHKEKGEQVLRKSKRGVWVNOQFVIEEYAGPEPVLIGKLSHDVDRGERT 88
Qy 64 KYLLTGAGAGTVFVIDEATGNIHVTKSLDREKAOYVLLAOAVDRASNRPLEPSPFTIK 123
Db 89 KYLLSGGAGTIFVIDKSGNIHATKTLDBEERAOYTLMAOAVDRDTRNPLEPSPFTIK 148
Qy 124 GODINDNPPFIFLGPYHATVPENSNVGTSVIQTADHADDPSYGNSAKLYTVTLSDNNDPPK 183
Db 149 VQDINDNPPFELHEIYHANVPERSNVGTSVIQTADHADDPSYGNSAKLYTVTLSDNNDPPK 208
Qy 184 SVDPOGVAVRAIPNMDRETOEFLVYIOAKDNGHNGISGTTVTVTLSDVNDNPPK 243
Db 209 SVAQGTGIRITAPNMDREKAEHVVYIOAKDNGHNGISGTTVTVTLSDVNDNPPK 268
Qy 244 POSLYQSVVETAGPGLVGRLAODPDLDGNALMAYSILDEGSEAFSISTDLQGRDL 303
Db 269 POSYQMSVEAAPGSEVGRVAKDPDIDGENGLVTYNIYDGGIELFETITDYETQDGV 328
Qy 304 LTVAKPLDESSQSVSYFRVATNTLIDPALRRGPKDVAASVVAQDAPEPAFTQAA 363
Db 329 VKLKKVDFETKAYSLKIEANVHIDPKFISNGPFDOTVTKISVEDADEPMPFLASV 388
Qy 364 HLTVPENKAPGTLVGOISAAALDSPAIRYSILPHSDPERCSFIOPEEGTHTAAPLDR 423
Db 389 IHEVOENAAAGTVGRVAKDPDAAANSPIRISIDRHLDLDFFTINPEDGFKTKTLPDR 448

QY 424 EAAWHLTVLATELGWGWPERGWVPLVAEWSAPAPQSPVGSANGIPQDSSAQAS 483
| : : : : :
DB 449 EETWMLNISVPAADI-----HNRHQT 470
QY 484 RVQVAITQTLDENNDNAPOLAEPTDFVCDSPAAP-----GQLIQVIRALDRDEVGSSHSVQ 539
| : : : : :
DB 471 KVPVAIRVLVDNDNAPFAAPFEGFICESDHPKALSNQPIVTSADQDDDTANPFRIFS 530
QY 540 GP--LGPDAFTVQDNRLDPA-----WFHPLMASASWMLWMPAERGN 581
| : : : : :
DB 531 LPPEIMNPNFTVRNDNDNTAGVYARRGCFGRQKODPYLLPIVY-----SDGGL 579
QY 582 QPASQKSSSLP-CG-RLPGALPSC 604
| : : : : :
DB 580 PPMSTVTLTIKVCQCDVNGALLSC 604

RESULT 4

149556
cadherin-11 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 149556
R:Kimura, Y.; Matsumi, H.; Inoue, T.; Shimamura, K.; Uchida, N.; Ueno, T.; Miyazaki, T.
Dev. Biol. 169,347-358, 1995
A/Title: Cadherin-11 expressed in association with mesenchymal morphogenesis in the head
A/Reference number: 149556; MUID:95269887; PMID:7750650
A/Accession: 149556
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-796 <R5>
A/Cross-references: UNIPROT:P55288; GB:D11963; NID:g974190; PIDN:BAA06730.1; PID:g974191
C/Superfamily: cadherin; cadherin repeat homology
F:156-159/Domain: cadherin repeat homology <CDH>

Query Match 48.9%; Score 1593; DB 2; Length 796;
Best Local Similarity 50.6%; Pred. No. 4,4e-98;
Matches 317; Conservative 95; Mismatches 128; Indels 86; Gaps 8;

QY 15 GREHP-----GPA.LRTSRWVWNOFVIEEYAGPEPVLIGKLSVDVREGRT 63
| : : : : :
DB 29 SHLPSEFGHEKEGQVLQSRKRWVWNOFVIEETGDPVLVGRHSDIDSGDGN 88
QY 64 KYLLTGBGAGTVFVIDEATGNVHTKSLDREKAQVYLLAQAVRASNPPEPSEPIIK 123
| : : : : :
DB 89 KYLLSGBGAGTVFVIDSGNTHATKTLDREBAQVYLLMAQAVRDNRPLEPSEPIIVK 148
QY 124 QGDINDNPFIPPLGPNATVPEKSNVGTSVIQVTAHDADDSYNSAKLYVTVLGLPFF 183
| : : : : :
DB 149 VQDINDNPEPLHEIYHANVPERSNVGTSVIQVTAHDADDSYNSAKLYVTVLGLPFF 208
QY 184 GVDQGTGVRRAIPMDRETOEELVYVQAQDMGSHSGSTTVTVTLSDVNDNPKF 243
| : : : : :
DB 209 SVEAQGTGIRTAIPMDREAEYEHVYVQAQDMGSHSGSTTVTVTLSDVNDNPKF 268
QY 244 POSLYQFVSVTAGFGLVGRLLRAQDPLGNALMAYSILDEGESEAFSISTDLQGRGL 303
| : : : : :
DB 269 POSLYQMSVSAAYAGEEVRGKADPDIGENGLVTVTVDDGDELFEITDDETQGV 328
QY 304 LTVKPLDPEQSRKSFVENVTNTLIDPAYLRGPFQDVASVRAVQDAPPPAFQAAV 363
| : : : : :
DB 329 VKLKPVDPEFKRAVSLKIEANVHIDPKFISNGFKDTVTKVLSVEDADPPVFLAPSY 388
QY 364 HLTVENAPGTLVQGISAADDSPASIRYSILPHSDPERCFSIQPEEGTITHAAPLDR 423
| : : : : :
DB 389 IHEQENAAAGTVARVAKDPDANSIRYSIDRHTDLDRFFINPDGFIKTKXLDLR 448
QY 424 EAAWHLTVLATELGWGWPERGWVPLVAEWSAPAPQSPVGSANGIPQDSSAQAS 483
| : : : : :
DB 449 EETWMLNISVPAADI-----HNRHQT 470
QY 484 RVQVAITQTLDENNDNAPOLAEPTDFVCDSPAAP-----GQLIQVIRALDRDEVGSSHSVQ 539

DB 471 KVPVAIRVLVDNDNAPFAAPFEGFICESDHPKALSNQPIVTSADQDDDTANPFRIFS 530
QY 540 GP--LGPDAFTVQDNRLDPA-----WFHPLMASASWMLWMPAERGN 581
| : : : : :
DB 531 LPPEIMNPNFTVRNDNDNTAGVYARRGCFGRQKODPYLLPIVYISD-----GG 578
QY 582 QPASQKSSSLP-CG-RLPGALPSC 604
| : : : : :
DB 579 PPMSTVTLTIKVCQCDVNGALLSC 604

RESULT 5

D38992
cadherin 8 - human
C/Species: Homo sapiens (man)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
C/Accession: D38992
R:Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous
A/Reference number: S24305; MUID:91283540; PMID:2059658
A/Accession: D38992
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-793 <SUZ>
A/Cross-references: GB:LJ4060; NID:g506411; PIDN:AAA35628.1; PID:g506412
C/Genetic: GDB:CDH8
A/Gene: GDB:CDH8
A/Cross-references: GDB:5822911
C/Superfamily: cadherin; cadherin repeat homology
C/Keywords: calcium binding; cell adhesion; duplication
F:163-269/Domain: cadherin repeat homology <CDH>

Query Match 46.9%; Score 1529.5; DB 2; Length 793;
Best Local Similarity 47.8%; Pred. No. 7,4e-94;
Matches 299; Conservative 111; Mismatches 135; Indels 81; Gaps 9;

QY 23 L.LRTSRWVWNOFVIEEYAGPEPVLIGKLSVDVREGRTKYLLTGBGAGTVFVIDEAT 82
| : : : : :
DB 49 LNRSKRGWVWNOFVIEESGPEPLVGRHLDLPGRSKKIKYLLSGBGAGTIFQINDVT 108
QY 83 GNTHVTKSLDREKAQVYLLAQAVRASNPPEPSEPIIKQDINDNPFIPPLGPNAT 142
| : : : : :
DB 109 GDHAIKRLDREKEKLEYTLTAQVDMETSKPEPSEPIIKQDINDNAPPELNPENYAT 168
QY 143 VEMSNVGTSVIQVTAHDADDSYNSAKLYVTVLGLPFFSVDQTVGVRRAIPMDRE 202
| : : : : :
DB 169 VPMSTLIGTSVTVNTRTDADDPVYNSAKLYVTVLGLPFFSVDQTVGVRRAIPMDRE 228
QY 203 TOEELVYVQAQDMGSHSGSTTVTVTLSDVNDNPKFPOSLYQFVSVTAGFGLV 262
| : : : : :
DB 229 AKEEVLYVQAQDMGSHSGSTTVTVTLSDVNDNPKFPOSLYQFVSVDVGLGTAL 288
QY 263 GRLRAQDPLGNALMAYSILDEGESEAFSISTDLQGRGLTVKPLDPEQSRKSFV 322
| : : : : :
DB 289 GRKAKDQDQIGENAGSYDIDGDTALPETSDQAQDQITRLRKLDFETKSTYLLKD 348
QY 323 EATNTLIDPAYLRGPFQDVASVRAVQDAPPPAFQAAVHILTVPENKAPGLVQGIS 382
| : : : : :
DB 349 EAAWHLTVLATELGWGWPERGWVPLVAEWSAPAPQSPVGSANGIPQDSSAQAS 408
QY 383 ADIDSPASIRYSILPHSDPERCFSIQPEEGTITHAAPLDRBARAHNLTVLATELGW 442
| : : : : :
DB 409 RPDIDISSPISRIDHTLERQFNINADGKITLATPDRLSVHNHTITLATEI----- 464
QY 443 GPERGWVPLVAEWSAPAPQSPVGSANGIPQDSSAQASRVQVAITQTLDENNDNAPOLA 502
| : : : : :
DB 465 -----RNHSQISVPAIKVLDVNDNAPFA 490
QY 503 EPTDTVCSAAPQQLIQVIRALDRDEVGSSHSVQGLD-----ANFTVQDNRD--- 555
| : : : : :
DB 491 SEYEAFICENKRGQVITQVTSAMDKDPKNGHY--FLVSLPEWVNNPNFTIKKQEDNSL 548

QY 556 -----LPAWFHPLMASASWLMWPPAEKGNOPASQKSSSL-PCG-RLPGA 600
DB 549 SLAKHNGFNKQKQEVILPIL-----SDSGNPPPLSTLTITRVCGCSNDGV 557
QY 601 LPSCQ-----LPLGI---PALGIYLC 618
DB 598 VQSCNVEAYVPIGLSMGALITAILAC 623

RESULT 6

152701
K-cadherin - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: 152701
R:Shimoyama, Y.; Gotch, M.; Terasaki, T.; Kitajima, M.; Hirohashi, S.
Cancer Res. 55, 2206-2211, 1995
A:Title: Isolation and sequence analysis of human cadherin-6 complementary DNA for the f
A:Reference number: 152701; MUID:95262134; PMID:7743525
A:Accession: 152701
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-789 <RES>
A:Cross-references: UNIPROT:P55280; GB:D25290; NID:g435460; PIDN:BAA04975.1; PID:g435461
A:Gene: KCAD
C:Superfamily: cadherin, cadherin repeat homology
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 44.2%; Score 1441; DB 2; Length 789;
Best Local Similarity 45.0%; Pred. No. 5,7e-88;
Matches 289; Conservative 116; Mismatches 155; Indels 82; Gaps 7;

QY 13 AGSEHPGALLRRSRWVNOQFVIEYAGPEPVILGKLSVDVDEGRTKYLTEGAG 72
DB 42 ANSHNE-----LSRSKRSMMNQFLLBEYTSQYQYVGKLSDDGSLKYLISGDA 97
QY 73 GIVFVIDEATGNINHTKSLDREKQAYVLLAQAVDRASNRLPEPSEFIKQDINDNP 132
DB 98 GDLTIENNGDILATRLDREKQAYVLLAQAVDRASNRLPEPSEFIKQDINDNP 157
QY 133 IFFLPYHATVPEMSNVTSVIOYTAHADDDPSYNSAKLYVTLDELPEFSYDPOGVV 192
DB 158 IFTKDYVTAIVPEMAADVGTFVQYATADDDPTYSNKAQVYSILQGPYFVSSESTGII 217
QY 193 RTAENMDETOEFLVLIQAKMGHGLSGSTVTVTLSDVNNPKFPQSLYQESV 252
DB 218 KTAALNDRNRDQYQVIAKMGHGLSGSTVTVTLSDVNNPKFPQSLYQESV 277
QY 253 VETAGPGLVRLAODPDLGDNALMAVSIIDGEGSEAFSISTDLQGRGLTVRKPLDF 312
DB 278 PESPPGTPIGRIKASADAVGENAIEYSITDGEHDMFDVINDQTOGIIITVKLDF 337
QY 313 ESQSYSFREYATNTLIDPAVLRGPKVAVSVAVQDAPEPAPTAQAHVLPENKA 372
DB 338 EKKRVYTLKVEASNPILBPRFLVIGPKSATVRIIVDDVDEPVSKEAYILQIREDAQ 397
QY 373 PGLVQGISAADSPASPIRYSILPHSDPERCFSTIOPEGTHTAALDREARAHNLT 432
DB 398 INTTIGVAADDPAAKNPKYKSYVDRTDMRIFNIDSGNSIFTSKLDRETLMHNT 457
QY 433 VLATELGMSWSPRGWVPLVAEMSAAPAPQKSPVGSANGIIPQSSAQASRQVAIQT 492
DB 458 VITETI-----NNPKQSSRVPLIYIKVL 479
QY 493 DEANDNPQALPEYDTFVCDASAPQOLIQTALDRDEVGNSSHVSGPGLGDA-----NF 548
DB 480 DVANDNPEFAFEYETFCVCAKADQILQTHAVDKDPPYSGHOFSS--LAPBAAGSNF 537
QY 549 TVQDNRD-----LPAWFHPLMASASWLMWPPA-----E 578
DB 538 TIQDNKNTAGITRKNQYRHEMSTYLLPVVISDND-----YVQSGSTGTVTVRVACDH 593

QY 579 RGNOPASQKSSSLPCGRPLPGALPSCQPLGIPLGIYLCAS 620
DB 594 EGNMOSCHAEALIHPTGLSTGALVAILCTIYLLVTVVLFPA 635

RESULT 7

137016
cadherin-6 - human
C:Species: Homo sapiens (man)
C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C:Accession: 137016
R:Shimoyama, Y.; Gotch, M.; Terasaki, T.; Kitajima, M.; Hirohashi, S.
Cancer Res. 55, 2206-2211, 1995
A:Title: Isolation and sequence analysis of human cadherin-6 complementary DNA for the f
A:Reference number: 137016; MUID:95262134; PMID:7743525
A:Accession: 137016
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-790 <RES>
A:Cross-references: UNIPROT:P55285; GB:D31784; NID:g974184; PIDN:BAA06562.1; PID:g974185
A:Gene: GDB:CDH6
A:Cross-references: GDB:5822908
C:Superfamily: cadherin, cadherin repeat homology
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 44.2%; Score 1440; DB 2; Length 790;
Best Local Similarity 45.1%; Pred. No. 6.6e-88;
Matches 285; Conservative 118; Mismatches 151; Indels 78; Gaps 6;

QY 23 LFRFRSVMNQFVIEYAGPEPVILGKLSVDVDEGRTKYLTEGAGTVIDEAT 82
DB 48 LNRKRSMMNQFLLBEYTSQYQYVGKLSDDGSLKYLISGAGDLFINENT 107
QY 83 GNHHTKSLDREKQAYVLLAQAVDRASNRLPEPSEFIKQDINDNP 142
DB 108 GDIQATKLDREKQAYVLLAQAVDRASNRLPEPSEFIKQDINDNP 167
QY 143 VPENSNVTSVIOYTAHADDDPSYNSAKLYVTLDELPEFSYDPOGVV 202
DB 168 VPENSDVGTFFVQYATADDDPTYSNKAQVYSILQGPYFVSSESTGII 227
QY 203 TOEFLVYIQAQKMGHGLSGSTVTVTLSDVNNPKFPQSLYQESV 262
DB 228 NREQYQVYIQAQKMGHGLSGSTVTVTLSDVNNPKFPQSLYQESV 287
QY 263 GRLPADQPDIGDNLMAVSIIDGEGSEAFSISTDLQGRGLTVRKPLDESGQSYFRV 322
DB 288 GRIPASDADYGENAIEYSITDGEHDMFDVINDQTOGIIITVKLDF 347
QY 323 EATNTLIDPAVLRGPKVAVSVAVQDAPEPAPTAQAHVLPENKA 382
DB 348 EASNPEYEPFLYIGPPEDSATVRIIVDDVDEPVSKEAYILQIREDAQ 407
QY 383 ADLSPASPIRYSILPHSDPERCFSTIOPEGTHTAALDREARAHNLT 442
DB 408 QDPAAKNPKYKSYVDRTDMRIFNIDSGNSIFTSKLDRETLMHNT 463
QY 443 GREKMWPLVAEMSAAPAPQKSPVGSANGIIPQSSAQASRQVAIQT 502
DB 464 -----NNPKQSSRVPLIYIKVL 489
QY 503 EYDTFVCDASAPQOLIQTALDRDEVGNSSHVSGPGLGDA-----NF 555
DB 490 EYDTFVCDASAPQOLIQTALDRDEVGNSSHVSGPGLGDA-----NF 547
QY 556 -----LPAWFHPLMASASWLMWPPA-----E 578
DB 548 GILTRKNQYRHEMSTYLLPVVISDND-----YVQSGSTGTVTVRVACDH 603
QY 589 SSSLPGRPLPGALPSCQPLGIPLGIYLCAS 620
DB 604 ALIHPTGLSTGALVAILCTIYLLVTVVLFPA 635

RESULT 8
 150180
 C/Species: Gallus gallus (chicken)
 C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
 C/Accession: 150180
 R/Nakagawa, S.; Takeichi, M.
 Development 121, 1321-1332, 1995
 A/Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spec
 A/Reference number: 150178; MUID:95309115; PMID:7540531
 A/Accession: 150180
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-785 <NAK>
 A/Cross-references: UNIPROT:Q90763; GB:D42150; NID:9868000; PIDN:BA07721.1; PID:9868001
 F:156-262/Domain: cadherin repeat homology <CDH>

Query Match 43.9%; Score 1431.5; DB 2; Length 785;
 Best Local Similarity 45.7%; Pred. No. 2.4e-87;
 Matches 296; Conservative 103; Mismatches 166; Indels 83; Gaps 8;

6 AARARAAAGSEHP--GPALRTSRSMWNOQFVIEEYAGPEPYLIGKLSVDVDRGEGRT 63
 27 AEPSP-----SRKRYFGSGRTKRSWVNOQFVLEHMGSDPLVYKLSVDVDRGEGRT 82
 64 KYLTGEGAGTVFVIDEATGNHVTKSLDREKAQYVLLAQAVDRASNPRLPEPSEFTIK 123
 83 KYLSGEGASSIFIIDENTGDIHATKRLDREKAQYVLLAQAVDRASNPRLPEPSEFTIK 142
 124 GODINDNPPIFPLGAPYATPEMNGVTSYIOVTAHADDPSSYNSAKLYTVLDGPPF 183
 143 IQDINDPEKFLDGPYTAGVPEKSPVGSVQVATADPTVYKNSARVYSLIQGPYF 202
 184 SVDPQGVVATVAINMDRETQEEFLVYIOAKDMGNGHGLSGSTTVTLVDVNDPPEK 243
 203 SVEKGTGIKTALPNMDREARDQYLVIOAKDMVGNGHGLSGSTTVTLVDVNDPPEK 262
 244 PQSLYQGSVETAPGTLVGRAPDPLDGNALMAYSLIDGSSAFSISTDIQGRDL 303
 263 FRRSYQNVPEPSLPLASVVAIKADADVGNAEMEKIYDGDGLGVFKLSVDRDQEG 322
 304 LTVKPKPLDFESQSYSEKVEATNTLIDPAYLRGPFQVAVSVRAVQADAPPAFTQAY 363
 323 ITTKEKLDPEKFTYITIRISANAHVDRPLSLGPFSDMTTKIYEDVDEPVEFTSRX 382
 364 HLYPENKAPGLVGOISADLDSPASPIRYSILPHSDPERCSIQEESTHTAFLDR 423
 383 SMVSEAKYGTIIIGTAAHDPDASNPVYSIDRNLDLERYFIIDANSVITAKSLDR 442
 424 EARMHNLVLTATLGLSMWGPGRGVPLVLAEMSAAPQRPSPVGSAAVGIPODSSAQAS 483
 443 ETNAVHNTVLAEM-----SQNPQIG 464
 484 RVQVAIOTLDENDNAPQALAPYDTFVDSAPAGQLIOVIRALDRDEV--GNSSHVSQGP 541
 465 RGVVAITLIDINDNAPPEAMEYETTVCEMAGPQIIOKISALDRDPNGHQFYSILAE 524
 542 LGPANTFTVQDNRLPA-----WFHPLMASASSWLHMPAERGN---581
 525 AANHNFTLQDNKNTATVLTFRNGFRROEQSVYLLPIFIVDSGS---PSLSSTNTLTI 580
 582 -----OPASQSSSLPCRLPGAL---PSCOLPIGIPALGIV 616
 591 RVCCDDADGIAQTQNAEAYILIPAGLSGALIALIACVTLTLVLLIV 628

RESULT 9
 G02678
 C/Species: Homo sapiens (man)

C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
 C/Accession: G02678
 R/Shibata, T.; Shimoyama, Y.; Gotch, M.; Hirohashi, S.
 Submitted to the EMBL Data Library, May 1996
 A/Reference number: H01584
 A/Accession: G02678
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-790 <SHI>
 A/Cross-references: UNIPROT:Q13634; EMBL:U59325; NID:g1389852; PIDN:AA02933.1; PID:5136
 F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 43.3%; Score 1412.5; DB 2; Length 790;
 Best Local Similarity 45.9%; Pred. No. 4.5e-86;
 Matches 288; Conservative 100; Mismatches 152; Indels 87; Gaps 9;

25 FRRASWVNOQFVIEEYAGPEPYLIGKLSVDVDRGEGRTKYLTGEGAGTVFVIDEATGN 84
 50 RPKRGWVNOQFVLEHMGSDPLVYKLSVDVDRGEGRTKYLTGEGAGTVFVIDEATGN 109
 85 HVTKSLDREKAQYVLLAQAVDRASNPRLPEPSEFTIKGODINDNPPIFPLGYPHATVP 144
 110 IHSTKSLDREKAQYVLLAQAVDRASNPRLPEPSEFTIKGODINDNPPIFPLGYPHATVP 169
 145 EMSNVGTSYIOVTAHADDPSSYNSAKLYTVLDGPPFSDVDPQGVVATVAINMDRETQ 204
 170 EMSDWGTSYVQVATADPTVYKNSARVYSLIQGPYFSDPKGVATVIRALHMDREAR 229
 205 EEFLLVIOAKDMGNGHGLSGSTTVTLVDVNDPPEKPOLYQSVETAPGTLVGR 264
 230 EHYSVIIOAKDMAQGVNGHGLSGSTTVTLVDVNDPPEKPOLYQSVETAPGTLVGR 289
 265 LAAQPELDGNALMAYSLIDGSSAFSISTDIQGRDLITRKRLDREKSGSYFRVBA 324
 290 IYANDADTGSNADMVYSIINGDGWGISISTDKETREBGLSLKPLNEKKKSYTLNLEG 349
 325 TMTLIDPAYLRGPFQVAVSVRAVQADAPPAFTQAYHLYPENKAPGLVGOISAD 384
 350 ANTHIDPFRSHLGPCKDAMTKLIIGVDDEPLFEMPBYLMEVYNAGIGVTVLAQD 409
 385 LDPASPIRYSILPHSDPERCSIQEESTHTAFLDRAPAMHNLVLTATLGLSMWGP 444
 410 PDSTNSLVRYFINVAVEDREFINIDANTGITRTVLRREETPNWNIIVTASEI----- 463
 445 ERGWPLVLAEMSAAPQRPSPVGSAAVGIPODSSAQASRVQVAIOTLDENDNAPQALAP 504
 464 -----DNDLLSHTVGIRVLDVANDNPPELARE 491
 505 YTFVCDASAPQQLIOVIRALDRDEVGSSSHVSF---QGPLGPANTFTVQDNRLPA- 558
 492 YDIIVCENSKPQVHTIISATDKDPFANGPPNFPLDRLLPVPN--NFTLKDNEMNTASI 549
 559 -----WFHPLMASASSWLHMPAERGNQPAQSGKSSS---PCGRPLG 599
 550 LTRRRFRFTVQDVYLLPIMISD-----GGLP-SLSSSTLITRVACACER-DG 595
 600 ALPSCOLPIGIPALG-----IYLC 618
 596 RVRTCHAAEAFLSAGLSTGALIALIILC 622

RESULT 10
 150178
 C/Species: Gallus gallus (chicken)
 C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
 C/Accession: 150178
 R/Nakagawa, S.; Takeichi, M.
 Development 121, 1321-1332, 1995
 A/Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-eg
 A/Reference number: 150178; MUID:95309115; PMID:7540531
 A/Accession: 150178

Best Local Similarity 44.4%; Pred. No. 3.6e-83;
Matches 282; Conservative 114; Mismatches 154; Indels 85; Gaps 11;

```
QY 14 GSREHPGALLTRRSWVWNOFVIEEYAGEPVLICKLHSDVDVREGRTKYLITGEGAG 73
Db 44 GORSH---FORVVRGWVWNOFVLEEMGESEPOYVSKLHSDLDKGGTAVYTLSDGAG 99
QY 74 TVFIDATGNIHTKSLDREKQOYVLLAQVNRANRPLRPESEFIIIGODINNP 133
Db 100 TVFIDETGDIHAIKSLDREKQOYVLLAQVNRANRPLRPESEFIIIGODINNP 139
QY 134 FPLGPHATVEMSNVGTSVIQTAVHADDPVSGNSAKLYTVLIDGLPFPSVDPTGVVR 193
Db 160 FLDPGYATVEMSPVGAIVYLQVATADDDPTGNSARVYSLIQGPVPSIDPKTVIR 219
QY 194 TAIEMRETOEEELVYLQAKDMGNGHGLSGSTTVYTLSDVNDNPKPKPSIYOSVY 253
Db 220 TALPMREVEKEQVQLIQAKDMGNGHGLSGSTTVYTLSDVNDNPKPKPSIYOSVY 279
QY 254 ETAPGRTVGRADPDLGNALMAYSIIDGEGSEAFSISTDLQGRDGLTVAKPLDFE 313
Db 280 ESSPTGSAIGIRAVDPFGONAEIVYVPGDGNLFDTVTDDEDTQEGVILKLPDFE 339
QY 314 SQRSYSPFEVATNTLIDPVAIRRGPFQDVASVAVQAPPPAFTQAAVHLTVENKAP 373
Db 340 TKKAVTFKVDASNLHLDRHFSAGPFKDTATVKLSVLDVDEPPVFSKPLTYMEVEDTPV 399
QY 374 GTIVGQISAALDPSASPIRYSILPHSDPERCFISIOPEEGTITHAALDSEARAHNLTV 433
Db 400 GTIIGAVYADLDGSSAVRFTIDKSDGDSYFTIDNEGTLINELIDRSIKQVFSI 459
QY 434 LATEIGMSWGPGRVPLLVAEWMSAPAPQPSRPSVGSVGIPODSSAQASRVYAIOTLD 493
Db 460 IASKYS-----NFL-----TSKVNILINVL 481
QY 494 ENDAPQOLAEYDTFVCDASAPRGOLIQTALDRDEVNSHVSFOGFLGDA---NFT 549
Db 482 VNEPPEPVSVEYVAVCNAPRGQIQIVSADBDLSPAGQOFSFR--LPEEAIKENFT 539
QY 550 VQDRDLP-----WEPHLMASAGSLWHPAERGNQPSAQSGSSLP 593
Db 540 VRDRNNYAGIETRRNGSRQQLYFIPVYIEDSSV-----PVQ-----SSTNTTIR 588
QY 594 CGRL--PGALPSCQ---LPLGIPA---LGIYIC 618
Db 589 VCRCDSDGTILSCVNEAIFLPVGLSTGALIALILC 623
```

RESULT 13

10HUC5
Cadenherin 5 precursor - human
N/Alternate names: 784 antigen; cadherin, endothelial-specific; VE-cadherin
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1993 #sequence revision 13-Sep-1996 #text_change 09-Jul-2004
R/Accession: S49893; S24305; A43418
R/Breviario: F.; Cavada, L.; Corada, M.; Martin-Padura, I.; Goley, D.; Introna, M.; Lamp
submitted to the EMBL Data Library, June 1994
A/Description: Molecular and functional properties of VE-cadherin (784/cadherin-5) a nov
A/Reference number: S49893
A/Accession: S49893
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-784

A/Cross-references: UNIPROT:P33151; EMBL:X79981; NID:G599833; P1DN:CAA6306.1; P1D:G5998
R/Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous s
A/Reference number: S24305; MUID:91283540; PMID:2059658
A/Accession: S24305
A/Molecule type: mRNA
A/Residues: 5-516, 'I', 518-784 <SUZ>
A/Cross-references: EMBL:X59796; NID:G639976; P1DN:CAA42468.1; P1D:G29593
R/Lampugnani, M.G.; Resnati, M.; Rattieri, M.; Pigotti, R.; Pisacane, A.; Houen, G.; Rucco,

J. Cell Biol. 118, 1511-1522, 1992

A/Title: A novel endothelial-specific membrane protein is a marker of cell-cell contact;
A/Reference number: A43418; MUID:92394977; PMID:1522121

A/Accession: A43418

A/Molecule type: protein

A/Residues: 48-60, 'X', 62, 'X', 64, 108-116, 'X', 118-123, 237-238, 'X', 240, 'X', 242-252, 'X', 254.

A/Experimental source: cultured endothelial cells

A/Note: sequence extracted from NCBI backbone (NCBI:P113040, NCBI:P113045, NCBI:P113047,
C/Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought to
C/Genetics:

A/Gene: GDB:CDH5

A/Cross-references: GDB:134230; CMIN:601120

A/Map position: 16q22.1-16q22.1

C/Superfamily: cadherin; cadherin repeat homology

C/Keyword: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane pr

F1-25/Domain: signal sequence #status predicted <SIG>

F1-26-47/Domain: propeptide #status predicted <PRO>

F1-48-784/Product: cadherin 5 #status predicted <NAT>

F1-48-593/Domain: extracellular #status predicted <EXT>

F1-50-151/Domain: cadherin repeat homology <CR1>

F1-154-258/Domain: cadherin repeat homology <CR2>

F1-261-372/Domain: cadherin repeat homology <CR3>

F1-375-479/Domain: cadherin repeat homology <CR4>

F1-481-587/Domain: cadherin repeat homology <CR5>

F1-594-620/Domain: transmembrane #status predicted <TM>

F1-621-784/Domain: intracellular #status predicted <INT>

F1-736-753/Region: serine-rich

F1-61,112,157,362,442,523,535/Binding site: carbohydrate (Asn) (covalent) #status predic

Query Match 28.7%; Score 935.5; DB 1; Length 784;
Best Local Similarity 39.9%; Pred. No. 2.4e-54;

Matches 225; Conservative 83; Mismatches 201; Indels 55; Gaps 12;

```
QY 1 CMGRLAAPARAWAGSRHPG-----PALTRRSWVWNOFVIEEYAGEPVLIGKL 52
Db 14 CIGLAAVAANAAGA--NAQRDTHSLPETHRQRDMWQNMHIDEKNTSLYHNKGI 71
QY 53 HSDVDRGSRRTYLLTGBCAGTVFVIDEATGNIHTKSLDREKQOYVLLAQVNRANR 112
Db 72 KSVSR--KNAAYLLKGEVGVGVVDAETGVPFAIERDRNISBYHLTAIVDKDSE 129
QY 113 PLRPESEFIIIGODINNPPIPLGPHATVEMSNVGTSVIQTAVHADDPVSGNSAKL 172
Db 130 NLETPSSFTIKVNDVNDMPVTHRLFNASVSSAGVSVSYAVADDDPTVDHASY 189
QY 173 VYTVLDGLPFPSVDPTGVVTAIPNMDRETOEEELVYLQAKDMGNGHGLSGSTTVYT 232
Db 190 MVOILKGEYFAID-NSGRIITITKSLDREKQARFIVEADAG-LRGDSGTATVLT 247
QY 233 LSVNDNPKPKPSQIYQFESVETAGRTVGRADPDLGNALMAYSIIDGEGSEAFS 292
Db 248 LQDINDNPFPTQKTFFVEDTRVGSVGLFVDEDPDRNMTKISILSGDYODAT 307
QY 293 ISTDLQGRDGLTVRKPDLFESQRSYSPFEVATNTLIDPVAIRRGPFQDVASVAVQDA 352
Db 308 IENPANNNGIILKPKMLDYEXIQYSFVEATCTPIDRYN-SPAGRAQVINITV 366
QY 353 PEPPATQAAVHLTVPEN-KAGTLYVQGISAADLDSAPPIYSLPHSDPERCSIOE 411
Db 367 DEPPITQOQFHYHOLENKKP--LIGVLADPPAARHSIGYSIRTSKQOFPVV-CK 423
QY 412 EGTHTAALDREARAHNLTVLATELGMSWGPGRGVPLLVAEWSAPAPQPSRPSVGS 471
Db 424 KGIIVNKKLDREYVWYLVYAKEL-----DS 452
QY 472 VGIPDSSAQASRVQVAYITLDENDNAPOLAEYDTFVCDASAPRGOLIVPALDREVG 531
Db 453 TGRP--TGKESIVQVHLEVDENNAPAFAPQKVCENAHQVLQISAIKDI-- 507
QY 532 NSGHVSFOGFLGPDANFTVQDNRD 555
Db 508 TPANVAFKTLTNTENNFTLTDND 531
```

RESULT 14

JM5CN
N-cadherin precursor, neuronal - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: A32759; A46163
R:Myatani, S.; Shimamura, K.; Hatta, M.; Nagafuchi, A.; Nose, A.; Matsunaga, M.; Hatta, Science 245, 631-635, 1999
A:Title: Neutral cadherin: role in selective cell-cell adhesion.
A:Reference number: A32759; MUID:89346748; PMID:2762814
A:Accession: A32759
A:Molecule type: mRNA
A:Residues: 1-906 <MTY>
A:Cross-references: UNIPROT:P15116; GB:M1131; NID:g192327; PIDN:AAA37353.1; PID:g309125
R:Myatani, S.; Copeland, N.G.; Gilbert, D.O.; Jenkins, N.A.; Takeichi, M.
Proc. Natl. Acad. Sci. U.S.A. 89, 8443-8447, 1992
A:Title: Genomic structure and chromosomal mapping of the mouse N-cadherin gene.
A:Reference number: A46163; MUID:92409532; PMID:11528849
A:Accession: A46163
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 835-906 <MT2>
A:Cross-references: GB:S45011; NID:g256010; PIDN:AA23356.1; PID:g256011
A:Note: sequence extracted from NCBI backbone (NCBIN:113759, NCBI:P113760)
C:Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought to
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane pro
F:1-27/Domain: signal sequence #status predicted <SIG>
F:128-153/Domain: propeptide #status predicted <PRO>
F:160-906/Product: N-cadherin #status predicted <EXT>
F:160-906/Product: extracellular #status predicted <EXT>
F:162-267/Domain: cadherin repeat homology <CR1>
F:237-242/Region: cadherin binding #status predicted
F:237-382/Domain: cadherin repeat homology <CR2>
F:385-487/Domain: cadherin repeat homology <CR3>
F:500-605/Domain: cadherin repeat homology <CR4>
F:606-714/Domain: cadherin repeat homology <CR5>
F:715-766/Domain: transmembrane #status predicted <TM>
F:747-906/Domain: intracellular #status predicted <INT>
F:865-878/Region: serine-rich
F:190,273,325,402,572,651,692/Binding site: carbohydrate (Asn) (covalent) #status predic

Query Match 18.4%; Score 601; DB 1; Length 906;
Best Local Similarity 33.9%; Pred. No. 5,4e-32;
Matches 190; Conservative 76; Mismatches 214; Indels 80; Gaps 21;
17 EHPGALLRTRRSWVWVQFVIEYAGPEPVILGKLSHSDVDRGGRKTYLTGEGAGT-- 74
149 KHSG-ALCRKRDVIRPILNPKSRGPFQBLVIRSDDKLS-LRISVIGSGADQPP 206
75 --VFVIDEATGNIVHTKSLDREKAQVYLLAQAVDRASNPFLPSEFIIKGGDINDNP 132
207 TGFIINPISGQLSVTKPLDRELARFHLRAHVDINGNQ-VENPIDIVINVIDMNDNP 265
133 IEPGPHATPEMSNVGTSVIQTAHADDDPSYGNASAKLYTVVLGDL-----FFSVD 186
266 EFLHGVNKGSPBSKRGTYVMTVTAIDADDPAALN-GMLRYILSCAPSTSPENKFTTN 324
187 PQTVGVTATAPNDRETOEELVYVIOAKDMGSH-MGSLSGSTTVTTLSDVNDNPKFPQ 245
325 NETGDIITVAAGDREKVOQYTLIIQATDEGNPTGLSTATAVATVTDVNDNPEPFA 384
246 SLVPSVETRAGETVLGRLAODPDLG-----NALMAYSLIDGESSEAFSISTDLQGD 301
385 MTFPGEVPENR-VDVIAANTLTVDKQPHTPAWNA-AVRISSGDEPTGRFALITDPSND 441
302 GLTLVRKPLDFESQSSYFVEATNTLIDPAYLRG--PFKDVASVRAVQDAPPEPPAF 358
442 GIVTVVAFIDFETRMVLTVALENCY-----PLAKGIQHPGSTAIVSVTVIDVNNPFF 497
359 TQAAHILTVENKAPGLTVGQISPADLDS-PASPIRYSILPHSDPERCSIOPEBGTHT 417

DB 498 APNPKIIQEGELHAGTMTLTITADDPDRVQONIRYTKL--SDPAMWLKIDPVNGQITT 555
QY 418 AAPLDREA-----RAWHNLTVLATELGWSGPERGWPLVAWESAPAPQSPFVSAVG 473
DB 556 IAVLDRESPVYQNNIYNATFLASDNG-----IPFW-----SGTG 589
QY 474 IPQSSAASASVQVALQTLDENDNAPOLAEPRDFVGDASAPQGLQIVGALDSEVNS 533
DB 590 TLQ-----IYLLDINDNAPVL-POEATCETPEPNSI--NIALDIDIDPNA 634
QY 534 SHVSQGLPG---DANFTV 550
DB 635 GPFAFDLPLSPVTKRMWTI 654

RESULT 15

ICHCN
N-cadherin precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: JH0424
R:Imazuka, H.; Miyatani, S.; Takeichi, M.
Neuron 7, 69-79, 1991
A:Title: R-cadherin: a novel Ca2+-dependent cell-cell adhesion molecule expressed in the
A:Reference number: JH0424; MUID:91299341; PMID:1712604
A:Accession: JH0424
A:Molecule type: mRNA
A:Residues: 1-913 <INT>
A:Cross-references: UNIPROT:P24503; GB:D14459; GB:D00849; NID:g222854; PIDN:BA03356.1;
A:Experimental source: retina
C:Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought to
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication; glycoprotein; retina; transmembr
F:1-26/Domain: signal sequence #status predicted <SIG>
F:127-166/Domain: propeptide #status predicted <PRO>
F:167-913/Product: R-cadherin #status predicted <MT>
F:167-721/Domain: extracellular #status predicted <EXT>
F:169-274/Domain: cadherin repeat homology <CR1>
F:244-249/Region: cadherin binding #status predicted
F:277-389/Domain: cadherin repeat homology <CR2>
F:392-504/Domain: cadherin repeat homology <CR3>
F:507-612/Domain: cadherin repeat homology <CR4>
F:613-721/Domain: cadherin repeat homology <CR5>
F:722-753/Domain: transmembrane #status predicted <TM>
F:754-913/Domain: intracellular #status predicted <INT>
F:870-885/Region: serine-rich
F:180,409,554,629,658,699/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.3%; Score 596; DB 1; Length 913;
Best Local Similarity 33.3%; Pred. No. 1.2e-31;
Matches 185; Conservative 77; Mismatches 226; Indels 68; Gaps 19;
16 REH-FGPALTRTRRSWVWVQFVIEYAGPEPVILGKLSHSDVDRGGRKTYLTGEGAG- 73
153 RQHSAGKLRRQKEDWVIRPINVPENSRGPPQQLVIRSDKDK-EIHIRYSITGVADQ 211
74 ---TVFVIDEATGNIVHTKSLDREKAQVYLLAQAVDRASNPFLPSEFIIKGGDINDN 150
212 PMEVEFSDIPVSGMYVTRPDRERASVYHLRAAVVMNGK-VENPIDIYIYVIDMNDN 270
131 PPIPLGPHATPEMSNVGTSVIQTAHADDDPSYGNASAKLYTVVLGDL-----FFS 184
271 RPEFINGVYNSGVDEGKPGTYVMTVTAINDADSTAN-GWVRIRIYTOQPSQSMFT 329
185 VDPQTVGVTATAPNDRETOEELVYVIOAKDMGSHG-GLSGSTTVTTLSDVNDNPKF 243
330 INSETGDIITVAAGDREKVOQYVIVQATDMENLVYGSNTATAITVTDVNDNPEP 389
244 PQSLYQPSVETAGPGLTVGRLAODPDL--GDNALMAYSLIDGESSEAFSISTDLQGD 301
DB 390 TTSYSGEVEPNR-VVVVAVNLTMDDDQHSRPMNAIYIILISGDPGHTIRIDPTNE 448
302 GLTLVRKPLDFESQSSYFVEATNTLIDPAYLRG--PFKDVASVRAVQDAPPEPPAF 358

Db 449 GMTVAVKADYEMNRAFMLTWMVSN---QAPLASGIQMSFQSTAGVTISVTDVNEAPYF 504
QY 359 TOAAYH/LTVPENKAPGTLVGQISADUDS-PASPIRYSILPHSDPERCFSIQPEEGTIHT 417
Db 505 PTNKKLIRLEGVPTGTVLTFPSAVDBPDRFMQAVRSKL--SDPANWLNINATNGIIT 562
QY 418 AAPIDREARAWHNLTVLATELGMSWGPGRGWPPLVAFEMSAAPAPPOKSPVGSAGIPOD 477
Db 563 AAVLDRESDYIKNNVYEAT-----FLADNGIIPPA-----SGTGTLO- 599
QY 478 SSAQASRVOVAICTLDENDNAPOLAEPPYDTFVCDSPAAGQLIQVIRALDRDEVGNSSHVS 537
Db 600 -----IYIDINDNAPELL-PKXAOICEK--PNLNVINITTADADIDPNVGPV 645
QY 538 FQGPLGPPDA--NETV 550
Db 646 FELPSVPSAVKKNWTI 661

Search completed: December 8, 2004, 10:27:05
Job time : 52.1417 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 248.512 Seconds
(without alignments)
1435.471 Million cell updates/sec

Title: US-09-788-051-7

Perfect score: 3259

Sequence: 1 CMGRLAAPARAMAGSRHPC.....LPSCQLPLGIPALGIYLCAS 620

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0 %

Maximum Match 100 %

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2897.5	88.9	819	1 CAD0_HUMAN	Q86UP0 Homo sapien
2	2511	77.0	781	2 Q6PFK6	Q6PFK6 mus musculu
3	2511	77.0	781	2 AAH57373	AAH57373 mus muscu
4	2291	70.3	493	2 Q96LQ7	Q96LQ7 homo sapien
5	1602	49.2	796	1 CAD8_HUMAN	P55287 homo sapien
6	1601	49.1	796	2 Q96CZ8	Q96CZ8 homo sapien
7	1596	49.0	796	1 CAD8_MOUSE	P55288 mus musculu
8	1595.5	48.6	796	2 Q8C7Q6	Q8C7Q6 mus musculu
9	1582.5	48.6	794	2 Q93264	Q93264 xenopus lae
10	1558	47.8	792	1 CAD8_CHICK	O93319 gallus galli
11	1536.5	47.1	716	2 Q8C449	Q8C449 mus musculu
12	1536.5	47.1	716	2 AAH57581	AAH57581 mus muscu
13	1536.5	47.1	799	1 CAD8_HUMAN	P55286 homo sapien
14	1536.5	47.0	794	2 Q8BRK4	Q8BRK4 mus musculu
15	1530.5	47.0	799	1 CAD8_MOUSE	P57191 mus musculu
16	1528.5	46.9	799	1 CAD8_MOUSE	P57191 mus musculu
17	1528.5	46.8	716	2 Q8C375	Q8C375 mus musculu
18	1486.5	45.6	370	2 Q86T00	Q86T00 homo sapien
19	1446.5	44.4	788	1 CAD4_HUMAN	O9Y648 mus musculu
20	1441.5	44.2	801	1 CAD6_HUMAN	P55280 mus musculu
21	1441	44.2	789	1 CAD6_RAT	P55280 mus musculu
22	1440	44.2	790	1 CAD6_HUMAN	P55285 mus musculu
23	1431.5	44.0	789	1 CAD7_CHICK	O90763 gallus galli
24	1431.5	43.9	785	1 CAD7_CHICK	O90763 gallus galli
25	1430.5	43.9	788	2 Q8V168	Q8V168 mus musculu
26	1429.5	43.9	788	2 Q8W0S7	Q8W0S7 mus musculu
27	1429.5	43.9	788	2 AAH62962	AAH62962 mus muscu
28	1425	43.7	801	2 Q9Z0M3	Q9Z0M3 mus musculu
29	1423	43.7	551	2 Q8AWM2	Q8AWM2 gallus galli
30	1422	43.6	798	2 Q7ZXY7	Q7ZXY7 gallus galli
31	1422	43.6	798	2 Q8GCH3	Q8GCH3 gallus galli

32	1420	43.6	789	1 CAD9_HUMAN	Q9ULB4 homo sapien
33	1415.5	43.4	785	1 CAD7_HUMAN	Q9ULB5 homo sapien
34	1413	43.4	790	1 CAD6_MOUSE	P97326 mus musculu
35	1412.5	43.3	790	1 CAD1_HUMAN	Q13634 homo sapien
36	1412	43.3	630	2 Q81Y78	Q81Y78 mus musculu
37	1407.5	43.2	785	2 Q8BM92	Q8BM92 mus musculu
38	1400	43.0	790	1 CAD6_CHICK	Q90762 gallus galli
39	1395.5	42.8	790	2 Q8W5Z2	Q8W5Z2 mus musculu
40	1389.5	42.6	790	2 Q91838	Q91838 xenopus lae
41	1372.5	42.1	508	2 Q6PAN4	Q6PAN4 mus musculu
42	1372.5	42.1	508	2 AAH60200	AAH60200 mus muscu
43	1372.5	42.1	794	2 Q86UD2	Q86UD2 mus musculu
44	1368.5	42.0	794	1 CAD6_HUMAN	P55289 mus musculu
45	1344	41.2	792	2 Q9DF50	Q9DF50 xenopus lae

ALIGNMENTS

RESULT 1	CAD0_HUMAN	STANDARD	PRT	819 AA.
ID	Q86UP0, Q86UP1, Q9N784;			
AC	Q86UP0, Q86UP1, Q9N784;			
DT	29-MAR-2004 (Rel. 43, Created)			
DT	29-MAR-2004 (Rel. 43, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Cadherin-24 precursor (UNQ2834/PRO34009).			
GN	Name=CDH24; Synonyms=CDH1L;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND INTERACTIONS WITH			
RP	CTENRINS			
RX	MEDLINE=22753805; PubMed=12734196; DOI=10.1074/jbc.M304119200;			
RA	Katagiri B.J., Nieman M.T., Wheelock M.J., Johnson K.R.;			
RT	"Characterization of cadherin-24, a novel alternatively spliced type			
RT	II cadherin.";			
RL	J. Biol. Chem. 278:27513-27519(2003).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RX	MEDLINE=22867296; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA	Eaton D., Fester J., Grimaldi C., Gu Q., Hase P.E., Heidens S.,			
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,			
RA	Seshagiri S., Simons L., Singh J., Smith V., Srinon J., Vagts A.,			
RA	Vandlen R., Watanabe C., Wieland D., Woods K., Xie M.-H., Yansura D.,			
RA	Yi S., Yu G., Yuan J., Zhang X., Zhang Z., Goddard A., Wood W.L.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale			
RT	effort to identify novel human secreted and transmembrane proteins: a			
RT	bioinformatics assessment.";			
RL	Genome Res. 13:2265-2270(2003).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 3).			
RP	TISSUE=Testis;			
RA	Blum H., Bauersachs S., Mewes H.-W., Gassenhuber J., Wiemann S.;			
RA	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.			
CC	- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.			
CC	- They preferentially interact with themselves in a homophilic			
CC	manner in connecting cells; cadherins may thus contribute to the			
CC	cell-cell adhesion.			
CC	- SUBUNIT: Associates with alpha-, beta- and delta-catenins.			
CC	- SUBCELLULAR LOCATION: Type I membrane protein (potential).			
CC	- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=;			
CC	Name=1; Synonyms=long form;			
CC	Isoid=Q86UP0-1; Sequence=displayed;			
CC	Name=2; Synonyms=short form;			

CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL: BC057373; AAH57373.1; -
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR000233; Cadherin_C term.
 DR Pfam: PF00028; Cadherin_5.
 DR Pfam: PF01049; Cadherin_C_1.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SM00112; CAI_4.
 DR PROSITE: PS00232; CADHERIN_1; 2.
 DR PROSITE: PS50268; CADHERIN_2; 5.
 DR KEGG: Calcium-binding; Cell adhesion; Transmembrane.
 KW SEQUENCE 781 AA; 84104 MW; 15996D6EC9835AA CRC64;

Query Match 77.0%; Score 2511; DB 2; Length 781;
 Best Local Similarity 78.6%; Pred. No. 76-148;
 Matches 502; Conservative 24; Mismatches 47; Indels 66; Gaps 7;

QY 1 CMGRILAPARAMAGSREHPGALLTRRSWVWNOFVIEEYAGEPVLIGKLSHDVDRGE 60
 DB 17 CMGRILAPVPMAGSGRHSGLTLTRRSWVWNOFVIEEYSGEPVLIGKLSHDVDRGE 76
 QY 61 GRTYVLTGEGAGTVEIDATGNHVTKSIDREKKAQYVLLAQAVDRASNPPEPSEF 120
 DB 77 GRTYVLTGEGAGTVEIDATGNHVTKSIDREKKAQYVLLAQAVDRASNPPEPSEF 136
 QY 121 IIKGQDINDNPPFLPGPYHATVPEMSNVGTSVITQVTAHADDPSTGNSAKLVYVLDGL 180
 DB 137 IIKVQDINDNPPFLPGPYHATVPEMSNVGTSVITQVTAHADDPSTGNSAKLVYVLDGL 196
 QY 181 PFFSVDPQTGVVTRALPNMDRETOEELVYVIAQDMGGMGSLGSTTVYVLTSDVNDP 240
 DB 197 PFFSVDPQTGVVTRALPNMDRETOEELVYVIAQDMGGMGSLGSTTVYVLTSDVNDP 256
 QY 241 PKPQSLYQFSVETAGTGLVGRLAQDPDLGNALMAYSILDEGSEAFSISTDLQGR 300
 DB 257 PKPQSLYQFSVETAGTGLVGRLAQDPDLGNALMAYSILDEGSEAFSISTDLQGR 316
 QY 301 DGLLTVRKPLDPEFRSSTYFRVEATNTLIDPAYLRGPKFVAVSVYVQDAPPEPAFTQ 360
 DB 317 DGLLTVRKPLDPEFRSSTYFRVEATNTLIDPAYLRGPKFVAVSVYVQDAPPEPAFTQ 376
 QY 361 AAYHLTVPENKAPGTLVQGISAADLSPASPIRYSILPHSDPERCFSIQPEEGTHTAAP 420
 DB 377 AAYHLTVPENKAPGTLVQGISAADLSPASPIRYSILPHSDPERCFSIQPEEGTHTAAP 436
 QY 421 LDREARAHNTLVATLQSGMGPGRGVPLLVAEWSAPAAPQSPVGSANGIPQDSSA 480
 DB 437 LDREARAHNTLVATLQSGMGPGRGVPLLVAEWSAPAAPQSPVGSANGIPQDSSA 496
 QY 481 QASRQVQAISQTLDEMDNAPQLAEPYDTVCDSAAAPGQLIQVIRALDDEVGNSSHYVFG 540
 DB 499 QASRQVQAISQTLDEMDNAPQLAEPYDTVCDSAAAPGQLIQVIRALDDEVGNSSHYVFG 518
 QY 541 PLGPDANFTVQDNRLPAMFPLMASASWLMHPAER-----GNQPSQSKSS 590
 DB 519 PLGPDANFTVQDNRLPAMFPLMASASWLMHPAER-----GNQPSQSKSS 571
 QY 591 -----SLPGRLFGALPSCQL-PLGTPA---LGIYVC 618
 DB 572 VTWSVCRPDGSMASCMPEAQISPTGLSTGALLATVTC 610

RESULT 3
 AAH57373 PRELIMINARY; PRT; 781 AA.
 ID AAH57373;
 AC AAH57373;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Cadherin-like 24.

GN CDH24.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxId=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Martusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M., Buetterfield Y.S.,
 RA Krzywicki M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.;
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RA Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: BC057373; AAH57373.1; -
 DR SEQUENCE 781 AA; 84104 MW; 15996D6EC9835AA CRC64;

Query Match 77.0%; Score 2511; DB 2; Length 781;
 Best Local Similarity 78.6%; Pred. No. 76-148;
 Matches 502; Conservative 24; Mismatches 47; Indels 66; Gaps 7;

QY 1 CMGRILAPARAMAGSREHPGALLTRRSWVWNOFVIEEYAGEPVLIGKLSHDVDRGE 60
 DB 17 CMGRILAPVPMAGSGRHSGLTLTRRSWVWNOFVIEEYSGEPVLIGKLSHDVDRGE 76
 QY 61 GRTYVLTGEGAGTVEIDATGNHVTKSIDREKKAQYVLLAQAVDRASNPPEPSEF 120
 DB 77 GRTYVLTGEGAGTVEIDATGNHVTKSIDREKKAQYVLLAQAVDRASNPPEPSEF 136
 QY 121 IIKGQDINDNPPFLPGPYHATVPEMSNVGTSVITQVTAHADDPSTGNSAKLVYVLDGL 180
 DB 137 IIKVQDINDNPPFLPGPYHATVPEMSNVGTSVITQVTAHADDPSTGNSAKLVYVLDGL 196
 QY 181 PFFSVDPQTGVVTRALPNMDRETOEELVYVIAQDMGGMGSLGSTTVYVLTSDVNDP 240
 DB 197 PFFSVDPQTGVVTRALPNMDRETOEELVYVIAQDMGGMGSLGSTTVYVLTSDVNDP 256
 QY 241 PKPQSLYQFSVETAGTGLVGRLAQDPDLGNALMAYSILDEGSEAFSISTDLQGR 300
 DB 257 PKPQSLYQFSVETAGTGLVGRLAQDPDLGNALMAYSILDEGSEAFSISTDLQGR 316
 QY 301 DGLLTVRKPLDPEFRSSTYFRVEATNTLIDPAYLRGPKFVAVSVYVQDAPPEPAFTQ 360
 DB 317 DGLLTVRKPLDPEFRSSTYFRVEATNTLIDPAYLRGPKFVAVSVYVQDAPPEPAFTQ 376
 QY 361 AAYHLTVPENKAPGTLVQGISAADLSPASPIRYSILPHSDPERCFSIQPEEGTHTAAP 420
 DB 377 AAYHLTVPENKAPGTLVQGISAADLSPASPIRYSILPHSDPERCFSIQPEEGTHTAAP 436
 QY 421 LDREARAHNTLVATLQSGMGPGRGVPLLVAEWSAPAAPQSPVGSANGIPQDSSA 480
 DB 437 LDREARAHNTLVATLQSGMGPGRGVPLLVAEWSAPAAPQSPVGSANGIPQDSSA 496

```

QY 481 QASRQVAIQTLDENDNAPQLAEPYDFVCDSPAAGQGLIQTALDRDEVGNSSHVSG 540
DB 459 QSSNRQVAIQTLDDENDNAPQLAEPYDFVCDSPAAGQGLIQTALDRDEVGNSSHVSG 518
QY 541 PLGGDANFTVDNFDLPWFHPLIMASASSWLMHPAER-----GNQPSQCKSS 550
DB 519 FVGEDANFTVDNFDNDSGA---SLLPSRPA---PFGQAYLPIELMDWGCPALSTAT 571
QY 591 -----SLPCRLPGALPSCQL-PLGIPA---LGIYLC 618
DB 572 VTVSVCRCPDGSYASCMPEAQSLPTGLSTGALLAIVTC 610

RESULT 4
Q96LQ7 PRELIMINARY; PRT; 493 AA.
ID 096LQ7
AC 096LQ7
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein FLJ25193.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RA NCB1_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Thyroid;
RA Nimmiya K., Magatsuma M., Kanda K., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA Nagai K., Isogai T., Sugano S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 4 cadherin domains.
DR HSPB; AK057922; BAB71613.1; -.
DR HSPB; P12830; 106S.
DR Genew; HGNC:14265; CDR24.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007156; F:homophilic cell adhesion; IEA.
DR InterPro; IPR002126; Cadherin.
DR Pfam; PF00028; Cadherin; 4.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SMO0112; CA, 4.
DR PROSITE; PS00232; CADHERIN_1; 2.
DR PROSITE; PS50268; CADHERIN_2; 4.
DR KEGG; K04461; Calcium-binding.
SQ SEQUENCE 493 AA; 53618 MW; 33F10DF63AF09C1E CRC64;

Query Match 70.3%; Score 2291; DB 2; Length 493;
Best Local Similarity 93.3%; Pred. No. 1.9e-134;
Matches 446; Conservative 2; Mismatches 8; Indels 22; Gaps 2;

```

```

DB 257 PKFQSLVQFVETAGGTLVGRRAQDPDLGNALMAVSIILDEGSEAFSISTDLQGR 316
QY 301 DGLLTVRPDLPESRSSTSFVEATNTLIDPAVLRGFRKVAASRAVQDAPEPPAFQ 360
DB 317 DGLLTVRPDLPESRSSTSFVEATNTLIDPAVLRGFRKVAASRAVQDAPEPPAFQ 376
QY 361 AAVHITVENKAPGTLVQGISAADLSPASIRYSIIPHSDFECFISIQPEEGITHPA 420
DB 377 AAVHITVENKAPGTLVQGISAADLSPASIRYSIIPHSDFECFISIQPEEGITHPA 436
QY 421 LDREKARHNTLVLTAEIG-----WSNCPFGWPLVLAEMSA 460
DB 437 LDREKARHNTLVLTAEIGEDSRHAKAAASWSPSCFWV---GMRRLVLAIPSPA 490

RESULT 5
CADB_HUMAN
ID CADB_HUMAN STANDARD; PRT; 796 AA.
AC P55287; Q15065; Q15065; Q9UQ93; Q9UQ94;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-11 precursor (osteoblast-cadherin) (OB-cadherin) (OSF-4).
GN Name=CDH11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RA NCB1_TaxID=9606;
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=95073006; PubMed=7982033;
RA Tanhara H., Sano K., Helmark R.L., St John T., Suzuki S.;
RT "Cloning of five human cadherins clarifies characteristic features of
RT cadherin extracellular domain and provides further evidence for two
RT structurally different types of cadherin.";
RL Cell Adhes. Commun. 2:15-26 (1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Osteosarcoma;
RX MEDLINE=94216322; PubMed=8163513;
RA Okazaki M., Takeshita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,
RA Amano E.;
RT "Molecular cloning and characterization of OB-cadherin, a new member
RT of cadherin family expressed in osteoblasts.";
RL J. Biol. Chem. 269:12092-12098 (1994).
RN [3]
RP SEQUENCE OF 269-796 FROM N.A. (ISOFORM 1).
RC TISSUE=Fetal brain;
RX MEDLINE=91283540; PubMed=2059658;
RA Suzuki S., Sano K., Tanhara H.;
RT "Diversity of the cadherin family: evidence for eight new cadherins in
RT nervous tissue.";
RL Cell Regul. 2:261-270 (1991).
RN [4]
RP SEQUENCE OF 600-668 FROM N.A. (ISOFORMS 1 AND 2).
RA Kooles P.F.J., Hogendoorn P.C.W., Boyce J.V.M.G., Van Roy F.;
RT "Alternative cadherin-11 transcripts encoding truncated adhesion
RT molecules are detectable in both human cancer and normal cells.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P55287-1; Sequence=displayed;
CC Name=2;
CC IsoId=P55287-2; Sequence=VSP_000640, VSP_000641;
CC -1- TISSUE SPECIFICITY: Expressed mainly in brain but also found in
CC other tissues. Expressed in neuroblasts.

```

CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ch/announce/>
 CC or send an email to license@ebi.ebi.ac.uk).

DR EMBL; L34056; AAA3622.1; -
 DR EMBL; D21254; BAA04798.1; -
 DR EMBL; D21255; BAA04799.1; -
 DR EMBL; AF060370; AAD27755.1; -
 DR EMBL; AF060369; AAD27755.1; JOINED.
 DR EMBL; AF060370; AAD27756.1; -
 DR EMBL; AF060369; AAD27756.1; JOINED.
 DR PIR; A38992; A38992.
 DR HSSP; P09803; 117M.
 DR Gene; HGNC:1750; CDH11.
 DR MIM; 600023; -
 DR GO; GO:0016021; C: integral to membrane; NAS.
 DR GO; GO:0007156; P: hemophilic cell adhesion; NAS.
 DR GO; GO:0001503; P: ossification; NAS.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C_term.
 DR Pfam; PF00028; Cadherin_C_5.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM0112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 DR Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 22
 FT PROPEP 23 53
 FT CHAIN 54 796
 FT DOMAIN 54 617 Extracellular (Potential).
 FT TRANSMEM 618 640 Potential.
 FT DOMAIN 641 796 Cytoplasmic (Potential).
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.
 FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 612 Cadherin 5.
 FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 540 540 N-linked (GlcNAc...) (Potential).
 FT VASAPLIC 632 693 VIVVFLVRLRQKKEPLIVEEEDVRNITTYDEGGGEED
 FT TEARDIATNPDKINGPIR -> GCSISLSPSPREDMR
 FT LVIIGFQMLCSYKVRNRRFLLGVFLKPLIVVATESPT
 FT TITSL (in isoform 2).
 FT VASAPLIC 694 796 /FtId=VSP_000640.
 FT VASAPLIC 694 796 /FtId=VSP_000641.
 FT CONFLICT 271 272 RL -> SV (in Ref. 2).
 FT CONFLICT 275 275 M -> I (in Ref. 2).
 FT CONFLICT 340 340 E -> K (in Ref. 2).
 FT CONFLICT 373 373 S -> A (in Ref. 2).
 FT CONFLICT 471 471 Q -> K (in Ref. 2).
 FT SEQUENCE 796 AA; 88049 MW; 2C67044C78ADB22 CRC64;

Query Match 49.2%; Score 1602; DB 1; Length 796;
 Best Local Similarity 50.4%; Pred. No. 3e-91;
 Matches 323; Conservative 98; Mismatches 134; Indels 86; Gaps 10;

QY 1 CMGRLLA-----APAR-----AMAGSRB--HPGALLTRRSWVWNGPFVIEEYAGEPV 47
 DB 13 CIGMLCHSAFAFERGHLRPSFGHHEKKEGCVLQSKGWMWNGPFVIEEYAGDPV 72
 QY 48 LIGKHSVDVREGRTKYLINGEGAGTVFVDEAGNHVTKSLDREKKAQVLLAAYD 107
 DB 73 LVGRLLSDIDSGDKITKYLISGEAGTIFVIDDKSGNHATKTLDRERPAQYTLMAQAVD 132

QY 108 RASNRLEPPSPFEITKQDINDNPEIFPLGPHATVPEMSNVGTSVIQTVAHDADDPESG 167
 DB 133 RQTNRLPEPPSEFFIKVQDINDNPEFLHEHYHANVPSRNVGTSVIQVTSADADDPYSG 192
 QY 168 NSAKLVYTVLQGLPPESVDPQTVVRAIPNNDRTEQEEFLVVIQAKMGHGGISGST 227
 DB 193 NSAKLVYSILSEGQPFYSVEAQGITRIALPNNDRKAEKHVVIQAKMGHGGISGST 252
 QY 228 TVTVLSDVNNPPEFPOSIVQSVFVETAGCTLVGRADDPDIDGVALMAVSLDDEG 287
 DB 253 KVTITLVNDNPPEFQQLVQSVSEAVPEEVEGRVAKADPDIGENGLVYNIIVDGG 312
 QY 288 SEAFISTDLQGRDGLTVRKPLDPESQSRYSFVEATNTLIDPAVLRGSPKDVASRV 347
 DB 313 MSFETITDYEQBEVILKPKVDETERAVSLKYEANVHIDPFISNGPFKQTVTKI 372
 QY 348 AVQDAPEPPAFQAAVHLTVPEPKAPGLVQGISADLDSPASPRYSILHSDPERFS 407
 DB 373 SVEDADPEPPFAPSYIHEVQENAAAGTVYGVVHAKDPDANSPIRYSIDRHTDREFT 432
 QY 408 IQPEEGTITLAPLDRERAMENITVLATELGWSGPERGWPLLVASAPAPPRSP 467
 DB 433 INPEDGFIITTPEDREETAMNITVPAET----- 463
 QY 468 VSAVGIPODSSAQSRVQVAIQLDENDNAPQLAEPIYDTFYCDS---APGQLIQYR 523
 DB 464 -----HNHQEAQVVAIRVLDVNDNPKFAPEGFICESDQTKPLSNQPIVVIS 514
 QY 524 ALDRDVEGNSHVSPQGP--LGPDAVFYQDRDLPA-----WPFILM 565
 DB 515 ADDKQDITAGPRPFTLSPELIIHNENFVDRDRDTAGVYARRGFSRQKQDYLIPVI 574
 QY 566 ASASSWLMWPAERGNQPAQCKSSLP-CG-RLDGALESC 604
 DB 575 -----SDGGIPMSSTNTLTIKVCQDVVAGALLSC 604

RESULT 6
 ID 096C29 PRELIMINARY; PRT; 796 AA.
 AC 096C29;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Cadherin 11, type 2, isoform 1 preproprotein.
 GN Name=CDH11;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schley G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Scheaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang X., Hsieh F.,
 RA Diatchenko L., Matrusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uscid T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.T., Malek U.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Rahy U., Helton E., Kettlemen W., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Kravtchuk M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RA [2] SEQUENCE FROM N.A.

RA Tissue=Brain;

RA Strausberg R.;

RA Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

CC - FUNCTION: Cadherins are calcium dependent cell adhesion proteins

CC (By similarity).

CC - SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC EMBL: BC013609; AAH13609.1; -

DR HSSP: P09803; 117W.

DR GO: GO:0016020; C:membrane; IEA.

DR GO: GO:0005509; F:calcium ion binding; IEA.

DR InterPro: IPR002126; Cadherin.

DR InterPro: IPR002233; Cadherin_C-term.

DR InterPro: IPR001901; SECC.

DR Pfam: PF00028; Cadherin_C; 1.

DR PRINTS: PRO0205; CADHERIN.

DR SMART: SM00112; CA; 5.

DR PROSITE: PS00232; CADHERIN_1; 3.

DR PROSITE: PS50268; CADHERIN_2; 5.

DR PROSITE: PS01067; SECC_SEC61G; UNKNOWN_1.

DR Calcium; Calcium-binding; Cell adhesion; Transmembrane.

RA SEQUENCE 796 AA; 87979 MW; 8497P8B34F7547C CRC64;

Query Match 49.1%; Score 1601; DB 2; Length 796;

Best Local Similarity 50.4%; Pred. NO. 3.5e-91;

Matches 323; Conservative 98; Mismatches 134; Indels 86; Gaps 10;

QY 1 CMGRLA-----APAR-----AWAGSRE--HPGALARTRRSWMNQFVIEEYAGPEV 47

DB 13 CLGMLCHSAFAFERGHLRPSFGHHEKGEQGLORSRGVMWQFVIEEYTPDDV 72

QY 48 LIGLHSDVDGREGRTYTLTGEGAGTVFIDATGINTKSLDSEKQVYLAQAVD 107

DB 73 LVGLHSDIDSGDGNITYLISGEAGTIFVIDKSGIATKTLDEHRRQYLYMAQAVD 132

QY 108 RASRPLEPPESEFFIKQDINDNPPIPLGPHATVPEMNVGTSVYQVTAHDADPSVG 167

DB 133 RDTNRPLEPPESEFFIKQDINDNPPIPLGPHATVPEMNVGTSVYQVTAHDADPSVG 192

QY 168 NSALVTVTVLDGLPFESVDQGVVTAITNMDREFTOEELVVIQAKMGHNGISGST 227

DB 193 NSALVTVSILEGGYFVEAQGTGIRTPALNMDREKEEYHVVIOAKMGHNGISGST 252

QY 228 TVTVTVLSDVNDNPKPFQSLYQFSVETAGPTLVGLRQADPDLDNALMAYSLIDGSG 287

DB 253 KWTITLVDVNDNPKPFQSLYQFSVETAGPTLVGLRQADPDLDNALMAYSLIDGSG 312

QY 288 SEAFSISTDIOGRDGLTVKPKLDFESQSYFRVEATNTLIDPAYLRGPFQDVASVY 347

DB 313 MESEFITTDTYETOGGVTKKPKVDFETKRAVSLKVAANVHIDPKFISNGPEKDTVTKI 372

QY 348 AVQDAPPPAFPTQAAVHLTVENKAPGLTIGQISADLDSPASPIRYSILPHSDPRCS 407

DB 373 AVEADAPPPAFPTQAAVHLTVENKAPGLTIGQISADLDSPASPIRYSILPHSDPRCS 432

QY 408 IQPEEGIIHTAAPLDREARAHNLTVLATELGWSGWERGVVLTVAEWSADAPFORSP 467

DB 433 INEDGKIKTTKPLDRETAHNLTVFAAI----- 463

QY 468 VGSAGVIGPQSSAQSASVQVATOTLDENNAAPQALAPYDTFVDS-----AAGQLQVIR 523

DB 464 -----HNRHOEAAPVPAIRVLDVNDAPKFAAPYEGFICESDQTPKLSNQPVTIS 514

QY 524 ALRDREYGNSSHVSFOGP--LGPDAFTVQDNNDLPA-----WFHPLLM 565

DB 515 ADDKDDTANGRPRIFFSLPEIINHPFTVRDNDNAGVYRARGGSSRQKQDLYLLPIYI 574

QY 566 ASASSMLHWPAPERGNQAPASQSSSLP-CG-RLPGLPSC 604

DB 575 -----SDGAIIPMSSSTNTLTIKVCQDVNGALLSC 604

RESULT 7

AC CADB MOUSE STANDARD; PRT; 796 AA.

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSF-4).

GN Name=Cdh11; Synonyms=Cad-11;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=95269886; PubMed=7750649;

RT Hoffman I.H.; Balling R.;

RT "Cloning and expression analysis of a novel mesodermally expressed

RT cadherin.";

RL Dev. Biol. 169:337-346(1995).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=95269887; PubMed=7750650;

RT Kimura Y.; Matsunami H.; Inoue T.; Shimamura K.; Uchida N.; Ueno T.;

RT Miyazaki T.; Takeichi M.;

RT "Cadherin-11 expressed in association with mesenchymal morphogenesis

RT in the head, somite, and limb bud of early mouse embryos.";

RL Dev. Biol. 169:347-358(1995).

RN [3]

RP SEQUENCE FROM N.A.

RX STRAIN=C57BL/6; TISSUE=Calvaria;

RX MEDLINE=94216322; PubMed=8163513;

RT Okazaki M.; Takeshita S.; Kawai S.; Kikuno R.; Teujimura A.; Kudo A.;

RT Amano E.;

RT "Molecular cloning and characterization of OB-cadherin, a new member

RT of cadherin family expressed in osteoblasts.";

RL J. Biol. Chem. 269:12092-12098(1994).

RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE=Olfactory epithelium;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;

RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;

RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;

RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Heile F.;

RA Diachenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;

RA Stabileton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Schaefer T.E.;

RA Brownstein M.; Ueda T.B.; Yoshiyuki S.; Carninci P.; Prange C.;

RA Rana S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullany S.J.;

RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;

RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;

RA Villalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;

RA Faley J.; Helton E.; Kettman M.; Madan A.; Rodriguez S.; Sanchez A.;

RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;

RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;

RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;

RA Butterfield Y.S.N.; Krzywinski M.I.; Skalak U.; Smalios D.E.;

RA Scherch A.; Schein J.E.; Jones S.J.M.; Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [5]

RP DEVELOPMENTAL STAGE.

RC STRAIN=C57BL/6; TISSUE=Testis;

RX MEDLINE=9703837; PubMed=8879495;

RA Munro S.B.; Blaschuk O.W.;

RT "A comprehensive survey of the cadherins expressed in the testes of

RT fetal, immature, and adult mice utilizing the polymerase chain

RT reaction.";

RL Biol. Reprod. 55:822-827(1996).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Selectively expressed in osteoblastic cell
 CC lines, precursor cell lines of osteoblasts, and primary
 CC osteoblastic cells from calvaria, as well as in lung, testis, and
 CC brain tissues at low levels.
 CC -1- DEVELOPMENTAL STAGE: In the testis, expression is highest in fetal
 CC gonad and decreases 8-fold in newborn.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL curation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; X77557; CAA54674.1; -;
 DR EMBL; D31963; BAA06730.1; -;
 DR EMBL; D21253; BAA04797.1; -;
 DR EMBL; BC046314; AAB46314.1; -;
 DR PIR; A53584; A53584.
 DR PIR; I48277; I48277.
 DR PIR; I49556; I49556.
 DR HSSP; P09803; 117W.
 DR MGD; MG1:99217; Cdh11.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0005866; C:plasma membrane; IDA.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C_term.
 DR Pfam; PF00028; Cadherin_5.
 DR Pfam; PF01049; Cadherin_C_1.
 DR PRINTS; PR00205; CADHERIN.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 DR KEGG; K04468; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 24 Potential.
 FT PROPEP 25 53 Potential.
 FT CHAIN 54 796 Cadherin-11.
 FT DOMAIN 54 617 Extracellular (Potential).
 FT TRANSMEM 618 640 Potential.
 FT DOMAIN 641 796 Cytoplasmic (Potential).
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.
 FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 612 Cadherin 5.
 FT CARBOHYD 455 455 N-linked (GLCNAC...) (Potential).
 FT CARBOHYD 540 540 N-linked (GLCNAC...) (Potential).
 FT CONFLICT 462 462 E -> D (in Ref. 1).
 FT CONFLICT 589 589 T -> L (in Ref. 2).
 FT CONFLICT 655 655 D -> N (in Ref. 2).
 FT CONFLICT 751 751 V -> M (in Ref. 2).
 FT CONFLICT 777 777 P -> Q (in Ref. 2).
 FT CONFLICT 782 782 L -> P (in Ref. 2).
 SQ SEQUENCE 796 AA; 88112 MW; 0D584D24641DD529 CRC64;

Query Match 49.0%; Score 1596; DB 1; Length 796;
 Best Local Similarity 50.7%; Pred. No. 7, 1e-91;
 Matches 317; Mismatches 97; Mismatches 127; Indels 84; Gaps 8;

DB 29 SHLHSPFHGHKEKGGVYLQSKRGWVWVNFVEIEETGDPVTVGSLHSDIDSGDNT 88
 15 SREHP-----GRLALTRRSWVNOGFVEEYVAGPEPTVLGLTHSDVDRGERT 63
 64 KYLLTGEGAGTVFVDEATGNHVTKSLDREKKAQVYLLAQNVAASNRPLEPSEFIK 123

DB 89 KYLLTGEGAGTVFVDDKSGNHNATKTLDRERAAQYTLMAQAVDRDTRPLEPSEFIK 148
 QY 124 GQDINDNPIPEPLGEYHATVPEMSNVGTSVIQVTAHADDPYGNASAKLYTVTDGPEF 183
 DB 149 VQDINDNPEELHEIYHANVPEPSNVGTSVIQVTAHADDPYGNASAKLYTVTDGPEF 208
 QY 184 SYDPQGVVTRTIPMMDSEIQEELVYQADMGGMGSLGSTVTVTLSPDVNPNPKF 243
 DB 209 SEAGTGLIRLPMWDEAKAEHVYVQAQMGSGMGLSGTTVITLIDVNDPKF 268
 QY 244 POSLYQFSVETAGPGLTVGRLLRAQDPDLGNALMAVSYLDGEGSEAFSITDLOGDGL 303
 DB 269 POSVQMSVSEAAVGEVGRVAKADPOIGENGLVTVYVQDGLFEITDYEYTDQGV 328
 QY 304 LTVKRPDLPESSQSSIFRVEATNTLIDPAYLRGPFKQVAVRVAVQAPPEPQAY 363
 DB 329 VTKKRPVFEETKRAVSLKEANVHIDKFLSNGFKQVTVKLSVEDAPPEFLAPSY 388
 QY 364 HLTVPENKAPGLVGOISAAUDSPASPIRYSILPHSDPERCFSIQPEEGTHTAPADR 423
 DB 389 IHVQENMAAGTVGVGRVAKQDPAANSPIRYSIDHTLDFFTINPEDGFIKTKPLDR 448
 QY 424 EAPAHNLTVLATELGMSWGPBGRVPLLVAEWSAPAPQSSPVGSAVGIPOSSAQS 483
 DB 449 EETAMINISVFAAEI-----NHRQET 470
 QY 484 RYQVAIQTLDENDNA POLAEPYDFVCDSPAAP---GOLIOYRALDRDEVSSHVSFO 539
 DB 471 KQPVARLVQVNDNA PKFAPEGTCESDHPKALSNQPIVVSADDDDTNNGRFLFS 530
 QY 540 GP--LGPDAFTVQDNRDLPA-----WFHPLMASASSWHLWPAERGN 581
 DB 531 LPPEIMHNPFTVRBDRNTAGVYARRGFSRQKDFYLLPIVI-----SDGI 579
 QY 582 QPASQKSSSLP-CG-RLPGALPSC 604
 DB 580 PMSSTNTLTITKVCQDVAGALLSC 604

RESULT 8
 Q8CTG6 PRELIMINARY; PRT; 796 AA.
 AC Q8CTG6;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length
 DE enriched library, clone:C530015F15 product:cadherin 11, full insert
 DE sequence.
 GN Name=Cdh11;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=spinal cord;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RT Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=spinal cord;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RT Nature 409:685-690(2001).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=spinal cord;
 RA the FANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;

"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs." Nature 420:563-573(2002).

SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Spinal cord;
MEDLINE=20493974; PubMed=11042159;
Carlini P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).

SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Spinal cord;
MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carlini P.,
Kono H., Akiyama J., Nishi K., Kizunai T., Tashiro H., Itoh M.,
Suni N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsuyama T., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujitake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).

SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Spinal cord;
Adechi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carlini P.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hoti F., Imocani K., Ishi Y., Itoh M., Kagawa I., Kasubawa T.,
Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
Kurihara K., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tasawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
(by similarity).

-1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).

-1- SIMILARITY: Contains 5 cadherin domains.

EMBL: AK049652; BAC33860.1; -
HSSP: P09803; 117W.
MGD: MGI:99217; Cdh11.
GO: GO:0005737; C:cytoplasm; IDA.
GO: GO:0005886; C:plasma membrane; IDA.
InterPro: IPR002126; Cadherin.
InterPro: IPR002233; Cadherin_C-term.
pfam: PF00028; Cadherin_5.
PRINTS: PF01049; Cadherin_C_1.
PRINTS: PR00205; CADHERIN.
SMART: SM00112; CA_5.
PROSITE: PS00233; CADHERIN_1; 3.
PROSITE: PS50268; CADHERIN_2; 5.
Kw: Calcium-binding; Cell adhesion; Transmembrane.
SEQUENCE 796 AA; 88126 MW; 71963374B21B329 CRC64;

Query Match 49.0%; Score 1595.5; DB 2; Length 796;
Best Local Similarity 51.6%; Pred. No. 7.6e-91;
Matches 314; Conservative 97; Mismatches 125; Indels 73; Gaps 7;

QY 20 GPALLRRSRWNNQFVIEVAGPPEVYLGKHSVDGEGTGYLLTGEGAGTYFVVD 79
DB 45 GQVLOKSKGMVWQFVIEVAGPPEVYLGKHSVDGEGTGYLLTGEGAGTYFVVD 104
QY 80 EATGNHVTXSLDREKAYQVYLLAQAVDRASNRLPPESEFLIKGQDINDNPPIFLGPY 139
DB 105 DKSGNIHATKTLDRERAPAYTLMAQAVDRVNRNPLPPESEFLIKVQDINDNPPIFLHET 164

QY 140 HATVEMSNVGTSTVQTAHADDPVSGNSAKVYTVLDSLPFSPVDPQGVATPMM 199
DB 165 HANVPSNVGTSTVQTAHADDPVSGNSAKVYTVLDSLPFSPVDPQGVATPMM 224
QY 200 DEETQEEFLVVIQANDMGHMGGLSGSTTVTLTSDVNDNPKPEPOSTLYPSVVEIAPG 259
DB 225 DEAEKEHYVVIQANDMGHMGGLSGSTTVTLTSDVNDNPKPEPOSTLYPSVVEIAPG 284
QY 260 TLVGLRQDPPDIGNALMAVSIIDGEGSEAFSTLDQSGDGLITRKPIEDFSQSSYS 319
DB 285 EEWGRVKAADPDIGENGLVTNIVDGGIELEFETTDYETDGVKKLPVDFETKQAYS 344
QY 320 FFEVATNTLIDPAYLRGSPFDVAVSVVAVDAPPEPAFTQAAVHLTPENKAPGLTVGQ 379
DB 345 LKIEAANVHIDPKFISNPFQDVTWKISVEDADEPPEFLAPSYIHEQENAAAGTVGR 404
QY 380 ISALDLPSPAPRISILIPSDPERCSIQEESTITPAALDEBARAHNLTVALTELG 439
DB 405 VAAKQDPAKSPRISIDRATDLRFPFINDEDFIKTKPLDEETAMINI SVPAEI- 463
QY 440 MSWGERGMVPLVEMGAPAPAPQSPVSGAVGIPQDSSAQASRVOVAIOTLDENAP 499
DB 464 -----HNHQETKVVAIRVLDVNDNAP 486
QY 500 QLAEPYDFVDSAP-----GQLIQVTRALDRDEVGSSHVSFGCP--LGPDAFTVQDN 553
DB 487 KFAAYEGFICSDHPKALSNOPIVTVASADQDDTANGPPIFELPEIMHNPFTVRDN 546
QY 554 RDLPA-----WPHPLMASASVLMHPAPERGQNPASQGSSTLP-CG- 595
DB 547 RDNHGVYARCGGSRKQKDYLLPIVI-----SDGGIPMSSNTLITIKVCCG 595
QY 596 RLPGALPSC 604
DB 596 DVNGALLSC 604

RESULT 9
ID O93264 PRELIMINARY; PRT; 794 AA.
AC O93264;
DT 01-NOV-1998 (TREMblrel. 08. Created)
DT 01-NOV-1998 (TREMblrel. 08. Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26. Last annotation update)
DE Cadherin precursor.
GN Name=Xcad-11;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=Zygote;
RX MEDLINE=98202517; PubMed=9533956;
RA Hadeball B., Borchers A., Wiedlich D.;
"Xenopus cadherin-11 (Xcadherin-11) expression requires the Wg/Wnt
signal.";
Mol. Cell. Dev. 72:101-113(1998).
RL -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
(by similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
CC -1- SIMILARITY: Contains 5 cadherin domains.
EMBL: AF002983; AAC28073.1; -
HSSP: P09803; 117W.
GO: GO:0016020; C:membrane; IEA.
GO: GO:0005509; F:calcium ion binding; IEA.
GO: GO:0007156; F:homophilic cell adhesion; IEA.
InterPro: IPR002126; Cadherin.
InterPro: IPR002233; Cadherin_C-term.
pfam: PF00028; Cadherin_5.
PRINTS: PF01049; Cadherin_C_1.
PRINTS: PR00205; CADHERIN.

DR SMART; SMO0112; CA: 5
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 KM Calcium; Calcium-binding; Cell adhesion; Signal; Transmembrane.
 FT SIGNAL 1 53 potential.
 FT CHAIN 54 794 cadherin.
 SQ SEQUENCE 794 AA; 88302 MW; 7221AD4CEA719DB CRC64;
 Query Match 48.6%; Score 1582.5; DB 2; Length 794;
 Best Local Similarity 50.4%; Pred. No. 4,9e-90;
 Matches 310; Conservative 97; Mismatches 133; Indels 75; Gaps 5;
 QY 20 GPALLRTRRSWMNQFVIEEYAGEPEVLLIGKLSHSDVDRGGRGRTKYLITGEGAGTFFVID 79
 DB 45 GQVLRHRSKRWVWVNFVIEEYGPDPVYVGRHSDVDSQDWIKIKYLISGEGAGTFFVID 104
 QY 80 EATGNHVTKSLDREKKAQVYLLAQAADRASNRPLEPSEFFIKGQDINDNPFIFPLGPFY 139
 DB 105 DKSQNHATKTLDEERAAQYTLMAQAVDRETNKPLEPSEFFIKVQDINDNPFIFLHENY 164
 QY 140 HATVPEMSNVGTSVIQVTAHADDDPSYGNASAKLYVTLDGLPFPSVDPQGVVRAIPM 199
 DB 165 HANVPENSVNGTSVIQVTAHADDDPTGNSAKLYSLLEGQYFVSFAQSGIIRTAIPM 224
 QY 200 DRETQEEFLVVIQAKDMGGMGSLGSTVTVTLSDVNDNPKPQSGLYQFSVETAGPG 259
 DB 225 DRAKEEYHVVIQAKDMGGMGSLGSTTKVTITLTDVNDNPKPQSGLYQFSVETAGPG 284
 QY 260 TLVGRLAQDPDLGDNALMAYSITLDGEGSEAFSITDLOGRDGLTVRKPLDFESQSY 319
 DB 285 EEVERIRAKDPDIEGNGIKRILIEGDAEFELTAYTVQEGVVKLKVVADVEIKKFS 344
 QY 320 FRVETATLLDPAALRGRPFEDVAVRVAQDAPEPPAQTAAVHLTVPENKAPGLTVQ 379
 DB 345 MKVAANVHIDRRLSRGPFEDTATKISVEDPEPEPIFERSYTLEVENASDVTGVR 404
 QY 380 ISAADLSPASPIRYSTILPHSDPERCSIQPEEETITAAPLDREAAAMNLTVALTEL 439
 DB 405 VHAQDPRAANSPIRYSIDRHTDLDRFSPINPEDVITTKGLDREESPMENISIAEV- 463
 QY 440 WSWGPERGWVLLVAEMSAPAPQSRPVSAGVIGPQSSAQSARVOVAIQTLDENDAP 499
 DB 464 -----HNRIHERVVALKVLDKDNAP 486
 QY 500 QLAPEYDTFVCDAAFGQLIQVIRALDRDEVGSSHVSFGQP--LGPDAFTVQDNRL 556
 DB 487 EFAPKFAFVCEANPINOEFITITAVKCDTANGLRFLFSPPEIIVHPNPFITIDREDN 546
 QY 557 PA-----WFHPLMASASSWLHWPAPR-----GNPQASQ 586
 DB 547 TASIRVGRGVFSRKKDLYLVIVISDGS---PWSSTVTLTVSRICNSDGSQSLCN 602
 QY 587 GKSSSLPCGRULPGAL 601
 DB 603 AEPQSLNAGLSTAL 617
 RESULT 10
 CADB_CHICK STANDARD; PRT; 792 AA.
 AC 093319;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-11 precursor.
 GN Name=CDH11;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN [1]

RC STRAIN-White leghorn;
 RA Wei J., Dong X.R., Topouzis S., Zimmer W.E., Broders F., Thüery J.P.,
 RA Kotelnitsky V., Majesky M.W.,
 RT "Molecular cloning of chick cadherin 11 and its expression during
 RT smooth muscle differentiation and formation of the tunica media";
 RL Submitted (Mar-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-stb.ch/announce/>
 CC or send an email to license@isb-stb.ch).
 CC EMBL; AF053342; AAC33675.1; -
 DR HSSP; P09803; 117M.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR002123; Cadherin_C-term.
 DR Pfam; PFO0028; Cadherin_5.
 DR Pfam; PFO1049; Cadherin_C/1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SMO0112; CA: 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 KM Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 22
 FT PROPEP 23 53
 FT CHAIN 54 792
 FT DOMAIN 54 613
 FT TRANSMEM 614 634
 FT DOMAIN 635 792
 FT DOMAIN 792 834
 FT DOMAIN 835 859
 FT DOMAIN 860 883
 FT DOMAIN 884 908
 FT DOMAIN 909 933
 FT DOMAIN 934 958
 FT CARBOHYD 455 485
 FT CARBOHYD 536 556
 FT CARBOHYD 594 594
 SQ SEQUENCE 792 AA; 87572 MW; 3E34880686731AB CRC64;
 Query Match 47.8%; Score 1558; DB 1; Length 792;
 Best Local Similarity 55.0%; Pred. No. 1.6e-88;
 Matches 296; Conservative 86; Mismatches 116; Indels 40; Gaps 2;
 QY 20 GPALLRTRRSWMNQFVIEEYAGEPEVLLIGKLSHSDVDRGGRGRTKYLITGEGAGTFFVID 79
 DB 45 GQVLRHRSKRWVWVNFVIEEYGPDPVYVGRHSDVDSQDWIKIKYLISGEGAGTFFVID 104
 QY 80 EATGNHVTKSLDREKKAQVYLLAQAADRASNRPLEPSEFFIKGQDINDNPFIFPLGPFY 139
 DB 105 DKSQNHATKTLDEERAAQYTLMAQAVDRETNKPLEPSEFFIKVQDINDNPFIFLHENY 164
 QY 140 HATVPEMSNVGTSVIQVTAHADDDPSYGNASAKLYVTLDGLPFPSVDPQGVVRAIPM 199
 DB 165 HANVPENSVNGTSVIQVTAHADDDPTGNSAKLYSLLEGQYFVSFAQSGIIRTAIPM 224
 QY 200 DRETQEEFLVVIQAKDMGGMGSLGSTVTVTLSDVNDNPKPQSGLYQFSVETAGPG 259
 DB 225 DRAKEEYHVVIQAKDMGGMGSLGSTTKVTITLTDVNDNPKPQSGLYQFSVETAGPG 284
 QY 260 TLVGRLAQDPDLGDNALMAYSITLDGEGSEAFSITDLOGRDGLTVRKPLDFESQSY 319
 DB 285 EEVERIRAKDPDIEGNGIKRILIEGDAEFELTAYTVQEGVVKLKVVADVEIKKFS 344

QY 320 FRVETNTLLDPAVLRGPEKDVASVAVQADAEPAFTOAAVHLVPEKAPGLNG 379
 Db 345 LKVEANVHIDPKISNGPFDDTYVKTIVEDADEPVPFKPSTIFEVQSNASGVVVK 404
 QY 380 ISAADLDSPPASPIRYSILPHSDPERCSIQPEEGTHTAPLDREARAWNTLVATLGL 439
 Db 405 VHADPDPAANSASIRYSIDRHTDLERYFTINADDNITIALDRREELAMENISVPAVEV 463
 QY 440 WSKPEEGWVPLVLAEMSAPAPQBSVPQSAVCIPODSSAQSRVVAIQTIDENDNAP 499
 Db 464 -----HKHQQAKVPAVKVVDVNDAP 486
 QY 500 QLAPEYDTFVCDSPAAPGLQIVITRALDRDEVGNSSHVSFGCP--LIGDANFTVQDRD 555
 Db 487 KFAAAYEAFVCEMARNRNOQFTISADKXDSANGPRITFSLPEIITHNPFSLRDND 544
 RESULT 11
 ID Q8C449 PRELIMINARY; PRT; 716 AA.
 AC Q8C449;
 DT 01-MAR-2003 (Tremblrel, 23, Created)
 DT 01-MAR-2003 (Tremblrel, 28, Last sequence update)
 DT 01-OCT-2004 (Tremblrel, 28, Last annotation update)
 DB Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched
 DE library, clone: C630002D14 product: cadherin 8, full insert sequence
 DE (Cdh8 protein).
 GN Name=Cdh8;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.";
 RL Mech. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:585-590(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA The FANTOM Consortium.
 RA RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=20493374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama Y., Nishii K., Katsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishimi T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujisake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA Aichi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kasegawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shitaki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeya Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marstein K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton W., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein W.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonfield G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skaleja U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (by similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
 DR EMBL; AK083082; BAC38758.1; -;
 DR EMBL; BC057581; AAH57581.1; -;
 DR HSP; P15116; INCT.
 DR MGD; MGI:107434; Cdh8.
 DR GO; GO:0016020; C:membrane; IEA;
 DR GO; GO:0005509; F:calcium ion binding; IEA;
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR002233; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin_C; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 KW Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 716 AA; 79145 MW; 976PF5D845F938BD CRC64;
 QY Query Match 47.1%; Score 1536.5; DB 2; Length 716;
 Best Local Similarity 48.1%; Pred. No. 31e-87;
 Matches 301; Conservative 109; Mismatches 135; Indels 81; Gaps 9;
 23 LKTRRSWNOQFVIEEYAGBPVLIGLHSDVDGEGRTKXLLTGAGAGTVFIDEAT 82

Dh	56	LSNSKRGWVNNQNFVLEBPSGPELIVGRLHTDLDPGSKIKYILSGGASTIQLQINDIT	11.5
Qy	83	GNHVTKSLDREKQAQVYLIAQVDPASRPLEPPESEFIKQODINDPPLFPGPHAT	14.2
Dh	116	GDHIAIRLDREKAEVETTLQAQVDEETKPLEPPESEFIKQODINDPAEFLNGPYHAT	17.7
Qy	143	VPEMSNGTGVIVYOTAHMDADPSGYSASKLYVTVDGLPEFVEDDPQTVSTALPNMDRE	20.2
Dh	176	VPEMSLIGTSVTVNVTATDADDPYGNASAKLYVLSLEGQYPSIEBETMIITALPNMDRE	23.5
Qy	203	TOSEFVLVYIAKMGHMGGLSGSTVTYVTLSDVNDNPPKPFQOSLYQSVVETAPGTLV	26.2
Dh	236	AKSEYLVVYIAKMGHSGGLSGSTVTLTVTLVDVNDNPPKPFQOSLYHVSVEDVILGTAI	29.5
Qy	263	GLRLAOPDLDGNALAAVSTLDGEGSEAFSISTDQGRGLTVKPLDPFESORSYGFV	32.2
Dh	296	GRVYANDQDIGNAQQSSYDILDSGDALTEITSDAQOAGVIRLKLKPLDPEFTKSYTLKV	35.5
Qy	323	EATNTLIDPAYLRRGPPKVAVSVRAVQDAPEPPAFTQAYHLYTVENKAPGTLVQOISA	38.2
Dh	356	EAANIHIDPFSSSGPEKDTATKIVIEDADEPVPFSSPTYLLEHENAALNSYIGQVTA	41.5
Qy	383	ADLDSPASPRYSITLPLSPDERCFSTOPEEGTHTNAPLDREARAHNLTLYALTELGSMW	44.4
Dh	416	RDPITTSPTSPRLSDRTDLDEROPFNINADGKITLATPLDRLSVWHNTITIAHEI----	47.1
Qy	443	GPERGWVPLLVAMSAAPAPBPQRSVGSAAVGIPQSSAQASVQVAYIQTLDENDAPOLA	50.2
Dh	472	-----RNHSQISSTVPAIKVLLVDNNADEFA	49.7
Qy	503	EPYDTPVCDAAAPGGLIQVTRALDRDRENGSSHSVQSGPLGPD---ANFTVQDNRD---	55.5
Dh	498	SEYBAFLCENKRGQVYIQVYASNDKDDPKNGHFLYSLPEPMANNPFIKKEDNSL	55.5
Qy	556	-----LPAMFPLMLASASSLWHPPAERGNQPASQCKSSSL-PCG-RLPGA	60.0
Dh	556	SLIAKHNGFNRQKQOEYVLLPIV-----SPSGNPPPLSSTSTVTLIRVCGQSDNGV	60.4
Qy	601	LPSCQ-----LPGLI---PALGVLG	61.8
Dh	605	VQSCNVAIVPLIGLSKGLIALIILAC	63.0
RESULT 12			
AAH57581 PRELIMINARY; PRG; 716 AA.			
AP	AAH57581	SEQUENCE FROM N.A.	
RC	STRAIN=CS7BL/6; TISSUE=Brain;		
RX	MEDLINE=23368257; PubMed=12477932;		
RA	Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.C.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Sculler G.D.,		
DS	Alschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,		
OS	Cdh8 protein.		
OC	Mus musculus (Mouse).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RA	RAH57581	SEQUENCE FROM N.A.	
RC	STRAIN=CS7BL/6; TISSUE=Brain;		
RX	MEDLINE=23368257; PubMed=12477932;		
RA	Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.C.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Sculler G.D.,		
DS	Alschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,		
OS	Cdh8 protein.		
OC	Mus musculus (Mouse).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RA	RAH57581	SEQUENCE FROM N.A.	
RC	STRAIN=CS7BL/6; TISSUE=Brain;		
RX	MEDLINE=23368257; PubMed=12477932;		
RA	Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.C.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Sculler G.D.,		
DS	Alschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,		
OS	Cdh8 protein.		
OC	Mus musculus (Mouse).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RA	RAH57581	SEQUENCE FROM N.A.	
RC	STRAIN=CS7BL/6; TISSUE=Brain;		
RX	MEDLINE=23368257; PubMed=12477932;		
RA	Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.C.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Sculler G.D.,		
DS	Alschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,		
OS	Cdh8 protein.		
OC	Mus musculus (Mouse).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RA	RAH57581	SEQUENCE FROM N.A.	
RC	STRAIN=CS7BL/6; TISSUE=Brain;		
RX	MEDLINE=23368257; PubMed=12477932;		
RA	Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.C.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Sculler G.D.,		
DS	Alschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,		
OS	Cdh8 protein.		
OC	Mus musculus (Mouse).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RA	RAH57581	SEQUENCE FROM N.A.	
RC	STRAIN=CS7BL/6; TISSUE=Brain;		
RX	MEDLINE=23368257; PubMed=12477932;		
RA	Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.C.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Sculler G.D.,		
DS	Alschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,		
OS	Cdh8 protein.		
OC	Mus		

Query	Subject	Score	Length	Matches	Conservative	Mismatches	Indels	Gaps
1	RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S., Kravynets M.I., Skalska U., Smallie D.E., Schnerch A., Schein J.E., Jones S.V., Maira M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	47.1%	Score 1536.5; DB 2; Length 716;	301	109	135	81	9
2	RA Strauberg R., Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases. DR SEQUENCE 716 AA; 79145 MW; 976F5D845F938BD CRC64;	48.1%	Pred. No. 3,18-87;	301	109	135	81	9
3	DB LNRTRSWTANQPFPIIEYAGPEPLVTKGLHSDVDREBGRKYLIGEGAGTVFVDEAT	82						
4	DB LRSKSKGWANWQMFVLEERSGEPILVRLHTDLPSSKIKYILSGDGGITFQINDIT	115						
5	QY GNHVTKSLDREKKQVYLAAQVDRAPNRLEPSEFFIKGQDINNPRIPLGYPVHAT	142						
6	DB GDTHAIKRLDREKKAYTLTAQVDFENRKLPEPSEFIKQVDINDMAEFINGVYHAT	175						
7	QY VPMNSVNGTSVQTVAHDADDPSSYGNSAKLYVTVLDELPPSVDPCQTGVTRKLPNNDR	202						
8	DB VPMNSITLGTSVNVNATADDPVYGNSAKLYVSLBQPFPSIEPEFAIITKLPNNDR	235						
9	QY TOSEFIVVIAQADMGHMGSGSTTVTLSDVNDNPKPEPQSLYQSFVETAPGTLV	262						
10	DB AKREYLVVIAQADMGHSGSGSLTTLVTLTDVNDNPKPEFAGSLYHFSVDEVLGTAI	295						
11	QY GRLAODPPLGNALMAVSIIDGEGSEAFISTDLQGRDGLTVRKPLDPESQRTSFRY	322						
12	DB GRVAKADODIGENAGSYDIIDGDTALFELTSAQADQGVIRLKRKLDEYKSYTLKV	355						
13	QY EATNTLIDAVYVRGPFQKVASVRAVODADEPAFTQAAHILVPEPKAPGLTVQOISA	382						
14	DB EANNHTIDPFSGRPFKDTATVKIVADDAPEPVFSPTLYLEHNAALNSVITQVNA	415						
15	QY ADIDSPASPIRYSILPHSDPERCFSTIQEESGTHTAAPLDREAPAMNLTVALTELGMW	442						
16	DB RDEDITSSPIRFSIRHNTDLERQFINADDKIFLAPFLRRLSVMNITITATEI	471						
17	QY GPRGWVPLLVAMWSAPAPQGRSPVGSAAVGIPODSSAQASRYOVAIQTLDENDNAPOLA	502						
18	DB RNSQISRPVAAIKVLVDVNDABERA	497						
19	QY EPYDTFVCDSPAAPGQLIQVTRALDREYGNSSHWSPQGLGPD--ANFTVDNRD--	555						
20	DB SEYEALCEIENGRPGQVITQVSAMDQDQKNGHF--FLVSLPFEVANNPNPTIKKENNSL	585						
21	QY -----LPAWHPLILMASASSWLMWPAEAGNQPASQGRSSSI-PG-RLPGA	600						
22	DB SILAKNGENRQKQEVYLLPIYI-----SDSGNPPLSSTLTITRVCGCSNDGV	604						
23	QY 601 LPSCQ-----LPLGI---PALGIYLC 618							
24	DB 605 VQSCNVEAYVLEIGLSMGALITLILAC 630							
25	RESULT 13							
26	CAD8_HUMAN STANDARD; PRT; 799 AA.							
27	AC P55286; Q9UBA2;							
28	DT 01-OCT-1996 (Rel. 34, Created)							
29	DT 16-OCT-2001 (Rel. 40, Last sequence update)							
30	DT 05-JUN-2004 (Rel. 44, Last annotation update)							
31	DE Cadherin-8 precursor.							
32	NAME CDH8							

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed:10861224;
RA Shimoyama Y., Teujimoto G., Kitajima M., Natori M.,
RT "Identification of three human type-II classic cadherins and frequent
RT heterophilic interactions between different subclasses of type-II
RT classic cadherins."
RL Biochem. J. 349:159-167 (2000).
RN [2]
RP SEQUENCE OF 7-799 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95073006; PubMed=7982033;
RA Tanihara H., Sano K., Heilmann R.L., St John T., Suzuki S.,
RT "Cloning of five human cadherins clarifies characteristic features of
RT cadherin extracellular domain and provides further evidence for two
RT structurally different types of cadherin."
RL Cell Adhes. Commun. 2:15-26 (1994).
RN [3]
RP SEQUENCE OF 294-799 FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=91283540; PubMed=2059658;
RA Suzuki S., Sano K., Tanihara H.,
RT "Diversity of the cadherin family: evidence for eight new cadherins in
RT nervous tissue."
RL Regul. Cell. 2:261-270 (1991).
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Mainly expressed in brain. Found in certain
CC nerve cell lines, such as retinoblasts, glioma cells and
CC neuroblasts.
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL, custodian
CC of the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AB035305; BA87419.1; -;
DR EMBL; L34060; AAA35628.1; ALT_INTT.
DR HSBP; P09803; 117W.
DR Genew; HGNC:1767; CDH8.
DR MIM; 603008; -;
DR GO; GO:0007155; P:cell adhesion; TAS.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR000233; Cadherin_C_term.
DR Pfam; PF00028; Cadherin_5.
DR Pfam; PF01049; Cadherin_C_1.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SMO0112; CA; 5.
DR PROSITE; PS00232; CADHERIN_1; 3.
DR PROSITE; PS00268; CADHERIN_2; 5.
KW Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 61 Potential.
FT CHAIN 62 799 Cadherin-8.
FT DOMAIN 62 621 Extracellular (Potential).
FT TRANSMEM 622 642 Potential.
FT DOMAIN 643 799 Cytoplasmic (Potential).
FT DOMAIN 643 167 Cadherin 1.
FT DOMAIN 168 276 Cadherin 2.
FT DOMAIN 277 391 Cadherin 3.
FT DOMAIN 392 494 Cadherin 4.

FT DOMAIN 495 616 Cadherin 5.
FT CARBOHYD 33 33 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 57 57 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 188 188 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 473 473 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 544 544 N-linked (GlcNAc...) (Potential).
FT CONFLICT 355 355 V -> D (in Ref. 2 and 3).
FT CONFLICT 647 647 H -> HQ (in Ref. 2 and 3).
SQ SEQUENCE 799 AA; 88253 MW; 9B119B86039C6A0A CRC64;

Query Match 47.1%; Score 1536.5; DB 1; Length 799;
Best Local Similarity 47.9%; Pred. No. 3.6e-87;
Matches 300; Conservative 111; Mismatches 134; Indels 81; Gaps 9;

QY 23 LLTRRSWVWVNFVIEEYAGPEVYLGKHSVDVREGRTKYLITSEAGTVFVIDEAT 82
DB 56 LNRSGRWVWVNFVIEEYAGPEVYLGKHSVDVREGRTKYLITSEAGTVFVIDEAT 115
QY 83 GNHTKSLDREERAGVYLAQVDRASNRLPEPSEFIKGGDINNPPFPFGPHAT 142
DB 116 GDHAIKLDREERAGVYLAQVDRASNRLPEPSEFIKGGDINNPPFPFGPHAT 175
QY 143 VPEMSNVGTSVIOVTAHDADDPYGSNAKLYVTVLDGLPPEVSDPOTGVRTAIPNDRE 202
DB 176 VPEMSILGTSVNTVATDADDPYGSNAKLYVTVLDGLPPEVSDPOTGVRTAIPNDRE 235
QY 203 TOEFLLVYIOAKMGKMGKSGSTTVYVLSVNDNPKRPGSLYQPSVETKPGTLV 262
DB 236 AKEEVLVYIOAKMGKMGKSGSTTVYVLSVNDNPKRPGSLYQPSVETKPGTLV 295
QY 263 GLRQADPDLDMALMAYSLDGESEAFSISTDQGRDGLTVRKPLDFESQSYGFRV 322
DB 296 GRVANKDDIDENNQSSVDIIDGGTALFETSAQAGDGIIRKRLDETKSKYLVK 355
QY 323 EATNTLIDPAYLRGPFQDVASVNAVQADPEPPAFYQAAHYLTVPENKAPGLVQISA 382
DB 356 EAAVNHIDPRSGGPFQDTATKIVEDDEPVPFSPTLLEVENALNSVIGQVTA 415
QY 383 ADLSPASPIYSILPHSDPERCFSDPEEGTHTAALDPEARAWNTLVATELGMSW 442
DB 416 RDPDITSPILPSIDREHDLERQFNINADDKITLAPLDELSWNTITINET 471
QY 443 GPERGWVLLVAEWSAPAPAPQSPVGSANGIPDSSAQAQRVOVAIQTLDENADQLA 502
DB 472 -----RNHSQISRVVAIKVLDVNDNADEFA 497
QY 503 EPIYDFVCDAAAPGOLIOVTRALDRDEVGNSSHVSPGPIGPD-----ANFTVQDNRD 555
DB 498 SEYEFVLCENKPGQVQIVTASAMKDDPKNGHY--FLYSLPEVNNPNFTIKNEPNSL 555
QY 556 -----LPWFHPLMASASGKWTMPAERGNOPASQSGSSL-PCG-RUPGA 600
DB 556 SILAKHNGFNKQKQEVLLPILI-----SDSGNPPLSSTLTTRVCCSNDGV 604
QY 601 LPSCQ-----LPDGI---PALGIYLC 618
DB 605 VQSCNVEAYVPLIGLSMGALTAIILAC 630

RESULT 14
ID Q8BRK4 PRELIMINARY; PRT; 754 AA.
AC Q8BRK4;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched
DE library, clone:A830083p13 product:cadherin 8, full insert
DE sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxId=10090;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=2108566; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RA The FANTOM Consortium;
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [4]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=20499374; PubMed=11042259;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Komori H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:157-163(2000).
RN [5]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Komori H., Akiyama U., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujisake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa Y., Tanaka T., Matsura S., Kawai U.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
RN [6]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RA Adachi U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imochi K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Komori H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sato H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akashita S., Takeda Y., Tanaka T.,
RA Toganu A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 5 cadherin domains.
DR HMBP; P15116; INCU.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro; IPR002126; Cadherin.
DR RefSeq; NP_030023.3; Cadherin_C_term.

Query	March	47.0%	Score 1532.5	DB 2	Length 754
Best Local Similarity	47.9%	Pred. No. 6e-87			
Matches 300	Conservative 110	Mismatches 155	Indels 81	Gaps 9	
Dr Pfam: PF01049; Cadherin C, 1.					
DR PRINTS: PR00205; CADHERIN.					
DR SMART: SM00112; CA: 5.					
DR PROSITE: PS00222; CADHERIN_1; 3.					
DR PROSITE: PS0268; CADHERIN_2; 5.					
DR Calcium: Calcium-binding; Cell adhesion; Transmembrane.					
SW Sequence: 754 AA: 83624 MW: 149037003F21568 CRC64.					
Query March	47.0%	Score 1532.5	DB 2	Length 754	
Best Local Similarity	47.9%	Pred. No. 6e-87			
Matches 300	Conservative 110	Mismatches 155	Indels 81	Gaps 9	
Dr Pfam: PF01049; Cadherin C, 1.					
DR PRINTS: PR00205; CADHERIN.					
DR SMART: SM00112; CA: 5.					
DR PROSITE: PS00222; CADHERIN_1; 3.					
DR PROSITE: PS0268; CADHERIN_2; 5.					
DR Calcium: Calcium-binding; Cell adhesion; Transmembrane.					
SW Sequence: 754 AA: 83624 MW: 149037003F21568 CRC64.					

RX MEDLINE=99190518; PubMed=9521872;
 RA Kido M., Obata S., Tanihara H., Rochelle J.M., Seidlin M.F.,
 RA Taketani S., Suzuki S.T.;
 RT "Molecular properties and chromosomal location of cadherin-8.";
 RL Genomics 48:186-194(1998).
 CC
 CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Name=1;
 CC IsoId=O54800-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O54800-2; Sequence=VSP_000638, VSP_000639;
 CC -!- SIMILARITY: Contains 5 cadherin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AB010436; BAA24452.1; -
 CC EMBL; AB010437; BAA24453.1; -
 CC HSSP; P09803; 117W.
 CC RCD; 69286; Cdh8.
 CC InterPro; IPR002126; Cadherin.
 CC InterPro; IPR000233; Cadherin_C_term.
 CC Pfam; PF00028; Cadherin; 5.
 CC Pfam; PF01049; Cadherin_C; 1.
 CC PRINTS; PR00205; CADHERIN.
 CC SMART; SM00112; CA; 5.
 CC PROSITE; PS00232; CADHERIN_1; 3.
 CC PROSITE; PS50268; CADHERIN_2; 5.
 CC KW Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
 KW Repeat; signal; Transmembrane.
 FT SIGNAL 1 29 Potential.
 FT PROPEP 30 61 Potential.
 FT CHAIN 62 799 Cadherin-8.
 FT DOMAIN 62 621 Extracellular (Potential).
 FT TRANSMEM 622 642 Potential.
 FT DOMAIN 643 799 Cytoplasmic (Potential).
 FT DOMAIN 643 167 Cadherin 1.
 FT DOMAIN 168 276 Cadherin 2.
 FT DOMAIN 277 391 Cadherin 3.
 FT DOMAIN 392 494 Cadherin 4.
 FT DOMAIN 495 616 Cadherin 5.
 FT CARBOHYD 188 188 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 473 473 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 544 544 N-linked (GlcNAc...) (Potential).
 FT VARSPIC 514 532 IGVSAADKDDPNKGHFL -> NISMLILNMFVNCFLV
 FT N (in isoform 2).
 FT /FTId=VSP_000638.
 FT /FTId=VSP_000639.
 FT VARSPIC 533 799 Missing (in isoform 2).
 FT SEQUENCE 799 AA; 88332 MW; F01D45R80966CB6 CRC64;
 Query Match 47.0%; Score 1530.5; DB 1; Length 799;
 Best Local Similarity 47.9%; Pred. No. 8.6e-87;
 Matches 300; Conservative 110; Mismatches 135; Indels 81; Gaps 9;
 QY 23 LILTRPSWVNOFFVIEYVAPVILGKLSHSDVDGEGSTKYLTEGSGATVIVDEAT 82
 DB 56 LNSKSGWVWVQVLEFSGPPIVGRHTLDLPSSKKIKIISGDGSGITIFQINDIT 115
 QY 83 GNTHVTKSLDREKKAQYVLLAQAVDRASNRPLEPSPSEFTIKGQDINDNPPIPLGPYAT 142
 DB 116 GDTHAIKRLDREKKAQYVLLAQAVDRASNRPLEPSPSEFTIKGQDINDNPPIPLGPYAT 175

QY 143 VEMSGVTSVIOVTAHADDPSYGNASAKLYVTVLDGLPFPSVDPQGVVTAIPNDRE 202
 DB 176 VEMSGVTSVIOVTAHADDPSYGNASAKLYVTVLDGLPFPSVDPQGVVTAIPNDRE 235
 QY 203 TOEFLLVYIOAKDNGGNGGSGSTTVTVLSDVNDNPKPQGLYQPSVETAGPGLV 262
 DB 236 AAEFLVYIOAKDNGGNGGSGSTTVTVLSDVNDNPKPQGLYQPSVETAGPGLV 295
 QY 263 GRLAQQDPLDGNALMAVSIIDEGSEAFSISTLOGDGLLTVRKPLDFPSQSSYFRV 322
 DB 296 GRLAQQDPLDGNALMAVSIIDEGSEAFSISTLOGDGLLTVRKPLDFPSQSSYFRV 355
 QY 323 EATNTLIDPAYLRGPFKDVASVRVAVQDAPEPAFTQAAVYHTVPENKAPGLTVGOISA 382
 DB 356 EATNTLIDPAYLRGPFKDVASVRVAVQDAPEPAFTQAAVYHTVPENKAPGLTVGOISA 415
 QY 383 ADLSPAPRIVSLPHSDPERCSIOPEBGTHTTAAPLDEARAHNTLYLATELGMSW 442
 DB 416 RDPDTSSPIRSDIRHTLDERQFVNADSKITLAPLDRELSVWHVHSITATEI 471
 QY 443 GPERGVPLLVAEWSAPAPAPQSPVGSVAVGIPDSSAQAASRVOVAIQTDENDAPOLA 502
 DB 472 GPERGVPLLVAEWSAPAPAPQSPVGSVAVGIPDSSAQAASRVOVAIQTDENDAPOLA 497
 QY 503 ERYDTFVCDSPAAPGQIIQVITALDRDEVGNSHVSFGQPLGPD 555
 DB 498 SEYENFLCENKPGQVIOVSAAMDKDPKNGH 555
 QY 556 LPAWHPPLMASASASWLMPPAERGNOFASQKSSSL-PCG-RLPGA 600
 DB 556 LPAWHPPLMASASASWLMPPAERGNOFASQKSSSL-PCG-RLPGA 604
 QY 601 LPSCQ-----LPLGI---PALGIYLC 618
 DB 605 VQSCNVEPYVLPILGSMGALTAIILAC 630

Search completed: December 8, 2004, 10:24:37
 Job time : 250.512 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 256.564 Seconds
(without alignments)
866.886 Million cell updates/sec

Title: US-09-788-051-7
3259
Perfect score: 1 CMGRLLAARAWAGSRHPG.....LPSCQLPLGIPALGIVLCAS 620
Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Genesep23Sep04:*
2: genesep21980s:*
3: genesep21990s:*
4: genesep2000s:*
5: genesep2001s:*
6: genesep2002s:*
7: genesep2003s:*
8: genesep2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3259	100.0	620	7	ADD29448 Human cad
2	3259	100.0	636	7	ADD29445 Human cad
3	2651.5	81.4	781	5	ABBS3296 Human pol
4	2651.5	81.4	781	5	AAM48736 Human pol
5	2651.5	81.4	781	5	ABG34078 Human cel
6	2651.5	81.4	781	6	ABR40114 Human cel
7	2651.5	81.4	781	6	ADK01366 Human PRO
8	2651.5	81.4	781	6	ADA43795 Human sec
9	2651.5	81.4	781	6	ADA43563 Human sec
10	2651.5	81.4	781	6	ADA01238 Human PRO
11	2651.5	81.4	781	6	ADA01122 Human sec
12	2651.5	81.4	781	7	ADA06941 Human sec
13	2651.5	81.4	781	7	ADA08429 Human PRO
14	2651.5	81.4	781	7	ADA08429 Human PRO
15	2651.5	81.4	781	7	ADB99722 Human PRO
16	2651.5	81.4	781	7	ADB87005 Human PRO
17	2651.5	81.4	781	7	ADB66160 Human sec
18	2651.5	81.4	781	7	ADB99838 Human PRO
19	2651.5	81.4	781	7	ADB99493 Novel hum
20	2651.5	81.4	781	7	ADB66044 Human sec
21	2651.5	81.4	781	7	ADC23442 Human tta
22	2651.5	81.4	781	7	ADC26135 Human PRO
23	2651.5	81.4	781	7	ADC04962 Human PRO
24	2651.5	81.4	781	7	ADG11268 Human PRO
25	2651.5	81.4	781	7	ADD88199 Human PRO

26	2651.5	81.4	781	7	ADD95494 Human sec
27	2651.5	81.4	781	7	ADD06424 Human PRO
28	2651.5	81.4	781	7	ADD83199 Human PRO
29	2651.5	81.4	781	7	ADD88315 Human PRO
30	2651.5	81.4	781	7	ADD90896 Human sec
31	2651.5	81.4	781	7	ADP99451 Human PRO
32	2651.5	81.4	781	7	ADG06544 Human PRO
33	2651.5	81.4	781	7	ADG05495 Human PRO
34	2651.5	81.4	781	7	ADG82496 Human PRO
35	2651.5	81.4	781	8	ADG51749 Human sec
36	2651.5	81.4	781	8	ADG51865 Human sec
37	2651.5	81.4	781	8	ADG37723 Human sec
38	2651.5	81.4	781	8	ADG37607 Human sec
39	2651.5	81.4	781	8	ADG95378 Human PRO
40	2651.5	81.4	781	8	ADG38078 Human PRO
41	2651.5	81.4	781	8	ADG76167 Human PRO
42	2651.5	81.4	781	8	ADG39490 Human PRO
43	2651.5	81.4	781	8	ADG04294 Human PRO
44	2651.5	81.4	781	8	ADG39891 Human PRO
45	2651.5	81.4	781	8	ADG19756 Human PRO

ALIGNMENTS

RESULT 1
ADD29448
ID ADD29448 standard; protein; 620 AA.
XX
AC ADD29448;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human cadherin-like mature protein.
XX
KW cadherin-like protein; transmembrane protein; cadherin domain;
KW homotypic cell-cell adhesion; cytosolic; osteopontin; cancer;
KW osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
KW metastatic tumour; human.
XX
OS Homo sapiens.
XX
PN US200314491-A1.
XX
PD 31-JUL-2003.
XX
PF 16-FEB-2001; 2001US-00788051.
XX
PR 03-FEB-2000; 2000US-00496914.
XX
PR 27-APR-2000; 2000US-00560875.
XX
PA (GODR/) GODBOLE S D.
PA (KUOC/) KUO C.
PA (ARTE/) ARTERBURN M C.
PA (YEUN/) YEUNG G.
PA (PALE/) PALENCIA S.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (DRMA/) DRMANAC R T.
XX
PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;
PI Liu C, Drmanac RT;
XX
XX WPI; 2003-829799/77.
XX
XX Novel isolated human secreted cadherin-like polypeptide useful for
XX treating diseases such as cancers, osteoporosis, Paget's disease,
XX osteomalacia, hyperostosis, osteopetrosis.
XX
XX Claim 11, SEQ ID NO 7, 63pp; English.
XX
XX This invention relates to a novel isolated human secreted cadherin-like
XX protein and the DNA sequence which encodes it. Cadherins are a family of

transmembrane proteins which share a common cadherin domain in their extracellular region. The extracellular portion mediates homotypic cell-cell adhesion that is calcium dependent. Modulators of the protein of the invention may have cytostatic or osteopathic activity. The invention may allow development of therapeutics useful for the treatment of diseases such as cancers, osteoporosis, Paget's disease, osteomalacia, hyperostosis and osteopetrosis. The protein and DNA sequence of the invention may also be useful as markers for prognosis of metastatic tumours. The present sequence is that of the mature human secreted cadherin-like protein which was used during the exemplification of the invention.

Sequence 620 AA;

Query Match 100.0%; Score 3259; DB 7; Length 620;
Best Local Similarity 100.0%; Pred. No. 3.8e-270;
Matches 620; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CMGRLLAARARAWASRRHPGALRLTRRSWVWNOFVIEBYAGBEPYLICKLHSDVDGR 60
1 CMGRLLAARARAWASRRHPGALRLTRRSWVWNOFVIEBYAGBEPYLICKLHSDVDGR 60
61 GRTKYLITGBGAGVFVIDEATGNHHTKSLDREKQYVLLAQAVDRASNRPLEPSEF 120
61 GRTKYLITGBGAGVFVIDEATGNHHTKSLDREKQYVLLAQAVDRASNRPLEPSEF 120
121 IIKQDINDNPPILPGPHATVEMSNVGTSVIQVTAHADDPSSYNSAKLYTVYLDGL 180
121 IIKQDINDNPPILPGPHATVEMSNVGTSVIQVTAHADDPSSYNSAKLYTVYLDGL 180
121 IIKQDINDNPPILPGPHATVEMSNVGTSVIQVTAHADDPSSYNSAKLYTVYLDGL 180
181 PFESVDPTGVVTRTAIPNMDRETOEBFLVIOAKDMGSHGSLSGSTTVVTLSDVNDP 240
181 PFESVDPTGVVTRTAIPNMDRETOEBFLVIOAKDMGSHGSLSGSTTVVTLSDVNDP 240
241 PKFQSLYQSFVETAGRGTLVGRLLAQQDPLDGNALMAYSLDGESEAFSISTDLQGR 300
241 PKFQSLYQSFVETAGRGTLVGRLLAQQDPLDGNALMAYSLDGESEAFSISTDLQGR 300
241 PKFQSLYQSFVETAGRGTLVGRLLAQQDPLDGNALMAYSLDGESEAFSISTDLQGR 300
301 DGLITVKKPLDFESQSRYSFRVETNTLIDPAYLRSPFDVAVVAQDAEPAPFTQ 360
301 DGLITVKKPLDFESQSRYSFRVETNTLIDPAYLRSPFDVAVVAQDAEPAPFTQ 360
361 AAYHLTVENKAPGTLVGOISADLDSPASPIRSLIHSDEPERCSIQEEGTITTAAP 420
361 AAYHLTVENKAPGTLVGOISADLDSPASPIRSLIHSDEPERCSIQEEGTITTAAP 420
421 LDRARARHNLTVLATELGMSWGPBGRWVPLVAEMSAAPAPQSRPVGSAGVCPDSSA 480
421 LDRARARHNLTVLATELGMSWGPBGRWVPLVAEMSAAPAPQSRPVGSAGVCPDSSA 480
481 QASRVOVAIQTLIDENDNAFQALAEYDFTVCDASAPGQLIVIPALRDDEVGNSHVSFQG 540
481 QASRVOVAIQTLIDENDNAFQALAEYDFTVCDASAPGQLIVIPALRDDEVGNSHVSFQG 540
541 PLGPDANFTVQDNNDLPAMFHPILMASASWLMHPAERGNQASQKSSSLPCGRLLPGA 600
541 PLGPDANFTVQDNNDLPAMFHPILMASASWLMHPAERGNQASQKSSSLPCGRLLPGA 600
601 LPSCQLPLGIPALGIVLCAS 620
601 LPSCQLPLGIPALGIVLCAS 620

RESULT 2
ADD29445
ADD29445 standard; protein; 636 AA.

AC ADD29445;
DE 15-JAN-2004 (first entry)
XX Human cadherin-like protein amino acid sequence.

cadherin-like protein; transmembrane protein; cadherin domain; homotypic cell-cell adhesion; cytostatic; osteopathic; cancer; osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis; metastatic tumour; human.

Homo sapiens.

Key Location/Qualifiers
FT Peptide 1..16
FT /label=Signal_peptide
FT Protein 17..636
FT /label=Mature_human_cadherin-like_protein

US2003144491-A1.

31-JUL-2003.

16-FEB-2001; 2001US-00788051.

03-FEB-2000; 2000US-00456914.

27-APR-2000; 2000US-00560875.

(GODB/) GODBOLE S D.

(KUDC/) KUD C.

(ARTE/) ARTERBURN M C.

(YEUN/) YEUNG G.

(PALE/) PALENCIA S.

(TANG/) TANG Y T.

(LIUC/) LIU C.

(DRMA/) DRMANAC R T.

Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT, Liu C, Drmanac RT;

WPI, 2003-829799/77.

N-PSDB; ADD29461, ADD29446.

Novel isolated human secreted cadherin-like polypeptide useful for treating diseases such as cancers, osteoporosis, Paget's disease, osteomalacia, hyperostosis, osteopetrosis.

Claim 11; SEQ ID NO 4; 636p; English.

This invention relates to a novel isolated human secreted cadherin-like protein and the DNA sequence which encodes it. Cadherins are a family of transmembrane proteins which share a common cadherin domain in their extracellular region. The extracellular portion mediates homotypic cell-cell adhesion that is calcium dependent. Modulators of the protein of the invention may have cytostatic or osteopathic activity. The invention may allow development of therapeutics useful for the treatment of diseases such as cancers, osteoporosis, Paget's disease, osteomalacia, hyperostosis and osteopetrosis. The protein and DNA sequence of the invention may also be useful as markers for prognosis of metastatic tumours. The present sequence is that of the human secreted cadherin-like protein of the invention.

Sequence 636 AA;

Query Match 100.0%; Score 3259; DB 7; Length 636;
Best Local Similarity 100.0%; Pred. No. 4e-270;
Matches 620; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CMGRLLAARARAWASRRHPGALRLTRRSWVWNOFVIEBYAGBEPYLICKLHSDVDGR 60
17 CMGRLLAARARAWASRRHPGALRLTRRSWVWNOFVIEBYAGBEPYLICKLHSDVDGR 76
61 GRTKYLITGBGAGVFVIDEATGNHHTKSLDREKQYVLLAQAVDRASNRPLEPSEF 120
77 GRTKYLITGBGAGVFVIDEATGNHHTKSLDREKQYVLLAQAVDRASNRPLEPSEF 136
121 IIKQDINDNPPILPGPHATVEMSNVGTSVIQVTAHADDPSSYNSAKLYTVYLDGL 180
137 IIKQDINDNPPILPGPHATVEMSNVGTSVIQVTAHADDPSSYNSAKLYTVYLDGL 196

QY 181 PFFSVDPQTGVVRTAIPNMDETGEFLVVIQAKMGHMGGLSGSTTVTLSDVNDP 240
 DB 197 PFFSVDPQTGVVRTAIPNMDETGEFLVVIQAKMGHMGGLSGSTTVTLSDVNDP 256
 QY 241 PKFPOSILYQFSVETAGPGLTVGRRAODPDIGNMAVSTLDEGSEAFSTLDQGR 300
 DB 257 PKFPOSILYQFSVETAGPGLTVGRRAODPDIGNMAVSTLDEGSEAFSTLDQGR 316
 QY 301 DGLTVRKPLDPEESQSRYSFVEATNTLIDPAYLRGPFKDVASVRAVQDAPEPPAFQ 360
 DB 317 DGLTVRKPLDPEESQSRYSFVEATNTLIDPAYLRGPFKDVASVRAVQDAPEPPAFQ 376
 QY 361 AAHVLTPENKAPGTLVGOISADLDSPASIRYSILPHSDPERCFSTIOEEGTHTAAP 420
 DB 377 AAHVLTPENKAPGTLVGOISADLDSPASIRYSILPHSDPERCFSTIOEEGTHTAAP 436
 QY 421 LDREARAHNLTVALTELGMGMPERGWPPLVAVEMGAPAAPQSRSPVGSANGIPQDSSA 480
 DB 437 LDREARAHNLTVALTELGMGMPERGWPPLVAVEMGAPAAPQSRSPVGSANGIPQDSSA 496
 QY 481 QASRVQVAIQTLDENDNAPQLAEPYDTFVCDSPAAGQLIQVIRALDRDEVGNSHVSFOG 540
 DB 497 QASRVQVAIQTLDENDNAPQLAEPYDTFVCDSPAAGQLIQVIRALDRDEVGNSHVSFOG 556
 QY 541 PLGPDAPFTVQDNEDLPAMFHPPLMASASSWLMHPAPERGQAPASQKSSSLPCGRLEGA 600
 DB 557 PLGPDAPFTVQDNEDLPAMFHPPLMASASSWLMHPAPERGQAPASQKSSSLPCGRLEGA 616
 QY 601 LPSCQLPLGIPALGIVLCAS 620
 DB 617 LPSCQLPLGIPALGIVLCAS 636

RESULT 3
 ABB53296
 ID ABB53296 standard; protein; 781 AA.
 AC ABB53296;
 XX 12-FEB-2002 (first entry)
 DT Human polypeptide #36.
 DE Human;
 XX Human; noctropic; neuroprotective; anticonvulsant; antidepressant;
 KM neuroleptic; tranquilizer; antiarrhythmic; cardiact; antidiabetic;
 KM antiinflammatory; antilipidemic; hepatotropic; virucide; antidiabetic;
 KM neuropeptide; anorectic; cytotactic; vaccine; neurological disease;
 KM cardiovascular disease; respiratory disease; liver disease;
 KM renal disease; skeletal muscle disease; gastrointestinal disease;
 KM placental disease; testicular cancer; male fertility; pancreatic disease.
 XX Homo sapiens.
 OS WO200181363-A1.
 EN 01-NOV-2001.
 XX 26-APR-2001; 2001WO-US013360.
 PF 27-APR-2000; 2000US-0199963P.
 ER 11-MAY-2000; 2000US-0203338P.
 PR 25-MAY-2000; 2000US-0207087P.
 PR 26-MAY-2000; 2000US-0207546P.
 XX (SMIK) SMITHLINE BEECHAM CORP.
 PA (SMIK) SMITHLINE BEECHAM PLC.
 XX Agarwal P, Murdock PR, Rizvi SK, Smith RF, Xiang Z, Kabanick KS;
 PI Lai Y, Xie Q;
 XX WPI, 2002-041392/05.
 DR N-PDSB; ABA90361.

XX Novel polypeptides and polynucleotides useful as a vaccine for preventing
 PT and treating diseases associated the polypeptide, e.g. Alzheimer's
 PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.
 XX
 PS Claim 1; Page 108-109; 116pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising a 277, 480,
 CC 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
 CC 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,
 CC 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
 CC given in the specification. The polypeptides, modulators of the
 CC polypeptides and antibodies against the polypeptides are useful for
 CC treating diseases such as neurological and psychiatric diseases including
 CC Alzheimer's, parapranuclear palsy, Huntington's disease, myotonic
 CC dystrophy, anorexia and depression; cardiovascular diseases including;
 CC congestive heart failure, Hodgkin's disease and myocardial infarction;
 CC respiratory diseases including asthma, chronic obstructive pulmonary
 CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
 CC diseases including hypercholesterolemia, cirrhosis, viral and nonviral
 CC hepatitis, type II diabetes mellitus, acute tubular necrosis and
 CC renal disease including renal failure, acute tubular necrosis and
 CC glomerulonephritis; skeletal muscle diseases including Eulenburg's
 CC disease, hypoglycaemia and obesity; gastrointestinal diseases including
 CC myotonia congenita and intestinal obstruction; lymph diseases including
 CC lymphagiectasia; diseases of placenta including chorioangioma; diseases
 CC of testes including testicular cancer, male reproductive diseases
 CC including low testosterone and male infertility; and disease of pancreas
 CC including low testostosterone and Type 1 and 2 diabetes and obesity. The
 CC present sequence is a polypeptide of the invention
 CC
 XX
 SQ Sequence 781 AA;
 Query Match 81.4%; Score 2651.5; DB 5; Length 781;
 Best Local Similarity 84.5%; Pred. No. 76-218;
 Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;
 QY 1 CMGRLAPARAWAGREHPALTRTRSWWNQCFVIEVAGPEPVILGKLSVDRCGE 60
 DB 17 CMGRLAPARAWAGREHPALTRTRSWWNQCFVIEVAGPEPVILGKLSVDRCGE 76
 QY 61 GRTKYLITGEGAGTVFVIDEATGNTHVTKSLDREKAQVLLAQVDRASNPPLPPSEF 120
 DB 77 GRTKYLITGEGAGTVFVIDEATGNTHVTKSLDREKAQVLLAQVDRASNPPLPPSEF 136
 QY 121 IIRKQDINDNPPIPLGPHATVPMSNVGTSVIOVTAHADDPDPSYSAKLVTVLQDL 180
 DB 137 IIRKQDINDNPPIPLGPHATVPMSNVGTSVIOVTAHADDPDPSYSAKLVTVLQDL 196
 QY 181 PFFSVDPQTGVVRTAIPNMDETGEFLVVIQAKMGHMGGLSGSTTVTLSDVNDP 240
 DB 197 PFFSVDPQTGVVRTAIPNMDETGEFLVVIQAKMGHMGGLSGSTTVTLSDVNDP 256
 QY 241 PKFPOSILYQFSVETAGPGLTVGRRAODPDIGNMAVSTLDEGSEAFSTLDQGR 300
 DB 257 PKFPOSILYQFSVETAGPGLTVGRRAODPDIGNMAVSTLDEGSEAFSTLDQGR 316
 QY 301 DGLTVRKPLDPEESQSRYSFVEATNTLIDPAYLRGPFKDVASVRAVQDAPEPPAFQ 360
 DB 317 DGLTVRKPLDPEESQSRYSFVEATNTLIDPAYLRGPFKDVASVRAVQDAPEPPAFQ 376
 QY 361 AAHVLTPENKAPGTLVGOISADLDSPASIRYSILPHSDPERCFSTIOEEGTHTAAP 420
 DB 377 AAHVLTPENKAPGTLVGOISADLDSPASIRYSILPHSDPERCFSTIOEEGTHTAAP 436
 QY 421 LDREARAHNLTVALTELGMGMPERGWPPLVAVEMGAPAAPQSRSPVGSANGIPQDSSA 480
 DB 437 LDREARAHNLTVALTELGMGMPERGWPPLVAVEMGAPAAPQSRSPVGSANGIPQDSSA 496
 QY 481 QASRVQVAIQTLDENDNAPQLAEPYDTFVCDSPAAGQLIQVIRALDRDEVGNSHVSFOG 540
 DB 497 QASRVQVAIQTLDENDNAPQLAEPYDTFVCDSPAAGQLIQVIRALDRDEVGNSHVSFOG 556

QY 541 PLGPDANFTVDNRD-----LPA-----WFHPLMASASSMLH--- 573
 DB 519 PLGPDANFTVDNRDGSASLLPSPRPAPRHPAPVLPVLELMDWQPALSTATVTVSVCR 578
 QY 574 -----WPPAERGNQAPASQ 587
 DB 579 QPDSGVASCPWEAHLASAAGLSTG 602
 RESULT 4
 AAM48736
 ID AAM48736 standard; protein: 781 AA.
 AC AAM48736;
 XX
 DT 28-MAR-2002 (first entry)
 XX
 DE Human cadherin family member 57805 protein SEQ ID NO 2.
 XX
 KW Human; cadherin 57805; osteopathic; hepatotropic; antibacterial;
 KW antidiabetic; neuroprotective; antiarthritic; antineuritic;
 KW dermatological; immunosuppressive; antiinflammatory; antiporiatic;
 KW antiaesthetic; antiallergic; antileptotic; haemostatic; antipruritic;
 KW anorectic; hypotensive; antierosclerotic; cardiant; antiarhythmic;
 KW anorectic; immunomodulatory; vasotropic; virucide; cytostatic; liver;
 KW thrombolytic; analgesic; anabolic; immune disorder; cardiovascular;
 KW vital; pain; metabolism; osteoporosis; diabetes mellitus; arthritis;
 KW osteoarthritis; multiple sclerosis; Crohn's disease; asthma; allergy;
 KW thrombus; inflammation; infection; ischaemia; irritable bowel syndrome;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 EN WO200190145-A2.
 XX
 PD 29-NOV-2001.
 XX
 PE 18-MAY-2001; 2001WO-US016013.
 XX
 PR 19-MAY-2000; 2000US-0205674P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Curtis RAD;
 XX
 DR WPI; 2002-083082/11.
 XX
 DR N-PSDB; ABA96406, ABA96407.
 XX
 PT New human cadherin family protein and polynucleotides, useful for
 PT diagnosing and treating disorders e.g. obstructive jaundice, multiple
 PT sclerosis, encephalomyelitis and atherosclerosis and to identify
 PT modulators of therapeutic use.
 XX
 XX Claim 9; Page 105; 119pp; English.
 XX
 PS The invention relates to human cadherin family polypeptide designated
 CC 57805 with osteopathic, hepatotropic, antibacterial, antidiabetic,
 CC neuroprotective, antiarthritic, antineuritic, dermatological,
 CC immunosuppressive, antiinflammatory, antiporiatic, antiaesthetic,
 CC antiallergic, antileptotic, haemostatic, antipruritic, antiaesthetic,
 CC hypotensive, antierosclerotic, cardiant, antiarhythmic, anorectic,
 CC immunomodulatory, vasotropic, virucide, cytostatic, thrombolytic,
 CC analgesic and anabolic activity. The 57805 molecules are useful for
 CC diagnosing and treating disorders which include disorders associated with
 CC bone metabolism, immune disorders, cardiovascular disorders, liver
 CC disorders, viral diseases, pain or metabolic disorders. Especially bone
 CC metabolism including osteoporosis, rickets, osteosclerosis, cirrhosis;
 CC immune disorders including autoimmune disease including diabetes mellitus
 CC arthritis, including rheumatoid arthritis and osteoarthritis, multiple
 CC sclerosis, systemic lupus, dermatitis, psoriasis, Crohn's disease,
 CC asthma, thrombocytopenia, Graves' disease, graft-versus-host disease,
 CC allergy; cardiovascular disorders, thrombus, hypertension,
 CC atherosclerosis, arrhythmias and cardiomyopathy; liver disorders,

CC glycogen storage disease, vascular disorders, chronic heart failure,
 CC portal vein thrombosis; viral diseases; metabolic or pain disorders
 CC include obesity, anorexia nervosa and diabetes, inflammation, infection
 CC and ischaemia, irritable bowel syndrome. The polynucleotides are also
 CC useful in gene therapy
 CC
 CC Sequence 781 AA;
 SQ
 Query Match 81.4%; Score 2651.5; DB 5; Length 781;
 Best Local Similarity 84.5%; Pred. No. 7e-218;
 Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;
 QY 1 CMGRILAPARAWAGREHHPALLTRRSWYVWNGFVIEEYAGEPYVIGKHSVDVRGE 60
 DB 17 CMGRILAPARAWAGREHHPALLTRRSWYVWNGFVIEEYAGEPYVIGKHSVDVRGE 76
 QY 61 GRTKYLFBGAGTVFVDEATGNHHTKSIDREKXQYLLAAQVARSRLPEPSEF 120
 DB 77 GRTKYLFBGAGTVFVDEATGNHHTKSIDREKXQYLLAAQVARSRLPEPSEF 136
 QY 121 IIKGQDINDNPPFPLGPHATVEMSNVGTSVIQTVAHADDPDSYNSAKLVYTVLDGL 180
 DB 137 IIKVQDINDNPPFPLGPHATVEMSNVGTSVIQTVAHADDPDSYNSAKLVYTVLDGL 196
 QY 181 PFFSYDPQTGYVTRAIIPMDRETOEELVVIQAQDMGHHGSLGSTTVTVLSDVNDP 240
 DB 197 PFFSYDPQTGYVTRAIIPMDRETOEELVVIQAQDMGHHGSLGSTTVTVLSDVNDP 256
 QY 241 PKFPOSIVQFVETAGTGLVGRRAODPDLGNALMAVSIIDGSESEAFSISTDQGR 300
 DB 257 PKFPOSIVQFVETAGTGLVGRRAODPDLGNALMAVSIIDGSESEAFSISTDQGR 316
 QY 301 DGLLTVRKPLDPESQSYSPFEVETNTLIDPAYLRGPFQDVASVAVADAPPPAFQ 360
 DB 317 DGLLTVRKPLDPESQSYSPFEVETNTLIDPAYLRGPFQDVASVAVADAPPPAFQ 376
 QY 361 AAYHLTVENKAPGLVQGISAADLDSPPASIRYSIIPSPDECFISOPEEGITHAAP 420
 DB 377 AAYHLTVENKAPGLVQGISAADLDSPPASIRYSIIPSPDECFISOPEEGITHAAP 436
 QY 421 LDREARAWNTLVATLEIGMSWGERGVPLVLAEMSAAPAPQSPVGAAGVIGDSSA 480
 DB 437 LDREARAWNTLVATLEIGMSWGERGVPLVLAEMSAAPAPQSPVGAAGVIGDSSA 498
 QY 481 QASRQVVALIOTLDENDNAPOLAEEDYDFVCDASAPGOLIOVIRALDRDEVGNSSHVSFOG 540
 DB 459 QASRQVVALIOTLDENDNAPOLAEEDYDFVCDASAPGOLIOVIRALDRDEVGNSSHVSFOG 518
 QY 541 PLGPDANFTVDNRD-----LPA-----WFHPLMASASSMLH--- 573
 DB 519 PLGPDANFTVDNRDGSASLLPSPRPAPRHPAPVLPVLELMDWQPALSTATVTVSVCR 578
 QY 574 -----WPPAERGNQAPASQ 587
 DB 579 QPDSGVASCPWEAHLASAAGLSTG 602
 RESULT 5
 ABG34078
 ID ABG34078 standard; protein: 781 AA.
 AC ABG34078;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Human Pro peptide #45.
 XX
 KW Human; PRO; secreted protein; transmembrane protein; genetic disorder;
 KW tumour; cancer.
 XX
 OS Homo sapiens.
 XX
 EN WO200224888-A2.

XX 28-MAR-2002.
 PD 29-AUG-2001; 2001WO-US027099.
 XX 01-SEP-2000; 2000US-0229896P.
 PR 05-SEP-2000; 2000US-0230621P.
 PR 22-SEP-2000; 2000US-0235147P.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 12-JAN-2001; 2001US-0261878P.
 PR 16-JAN-2001; 2001US-0261910P.
 PR 16-JAN-2001; 2001US-0261939P.
 PR 16-JAN-2001; 2001US-0262150P.
 PR 25-JAN-2001; 2001US-0264395P.
 PR 02-FEB-2001; 2001US-0264421P.
 PR 09-FEB-2001; 2001US-0267623P.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 09-MAR-2001; 2001US-0274399P.
 PR 03-APR-2001; 2001US-0280982P.
 PR 04-APR-2001; 2001US-0282128P.
 PR 04-APR-2001; 2001US-0282198P.
 PR 09-MAY-2001; 2001US-0290589P.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 XX (SETH) GENENTECH INC.
 PA Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;
 PI Fong S;
 XX WPI; 2002-362426/39.
 DR N-PSDB; ABR70009.
 XX New PRO polypeptides and polynucleotides encoding the polypeptides,
 PT useful in gene therapy, chromosome identification, tissue typing, or for
 PT genetic analysis of individuals with genetic disorders.
 XX Claim 11, Fig 98; 218pp; English.
 PS This invention relates to the cDNA and protein sequences of novel
 CC secreted and transmembrane polypeptides PRO polypeptides. The invention
 CC also comprises a method for producing the proteins of the invention by
 CC recombinant means and antibodies specific for the protein of the
 CC invention. The antibody may be used for detecting the PRO proteins of the
 CC invention and may be used to modify their activity. polynucleotides may
 CC be used as hybridisation probes for a cDNA library to isolate the full-
 CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation
 CC probes for mapping the gene which encodes that PRO and for genetic
 CC analysis of individuals with genetic disorders, in assays to identify
 CC other proteins or molecules involved in binding reaction, to generate
 CC transgenic animals or knock-out animals which in turn are useful in the
 CC development and screening of therapeutically useful reagents, for
 CC chromosome identification, and tissue typing. The PRO polypeptides are
 CC useful in gene therapy, and as molecular weight markers for protein
 CC electrophoresis purposes. The sequences may also be used to detect
 CC overexpression on PRO polypeptides in cancerous tumours and for screening
 CC for differentially expressed genes using microarray technology. The
 CC present sequence represents a human PRO protein of the invention
 XX
 XX Sequence 781 AA;
 SQ

Query Match: 81.4%; Score 2651.5; DB 5; Length 781;
 Best Local Similarity 84.5%; Pred. No. 7e-218;
 Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 CNGRLAAPRAVAGSTEHGEPALLTRRSWVNOGFVLEEVAGPEPVVIGLHSDVDGCE 60
 DB 17 CNGRLAAPRAVAGSTEHGEPALLTRRSWVNOGFVLEEVAGPEPVVIGLHSDVDGCE 76

QY 61 GRTKYLITGEAGCTVFIDEATGNHHTKSLDREKAQYVLLAQAVDASNRPLEPSEF 120
 DB 77 GRTKYLITGEAGCTVFIDEATGNHHTKSLDREKAQYVLLAQAVDASNRPLEPSEF 136
 QY 121 IIKGODINDNPPIFPLGPGYHATVPMSNVGTSGVIOVTAHADDPSSYGNASAKLYVTVDGL 180
 DB 137 IIKGODINDNPPIFPLGPGYHATVPMSNVGTSGVIOVTAHADDPSSYGNASAKLYVTVDGL 196
 QY 181 PFFSVDPQGVVTRTIPMWDRETQEEFLVYVQAKMGGMGLSGSTTVTLTSPVNNP 240
 DB 197 PFFSVDPQGVVTRTIPMWDRETQEEFLVYVQAKMGGMGLSGSTTVTLTSPVNNP 256
 QY 241 PFFSVDPQGVVTRTIPMWDRETQEEFLVYVQAKMGGMGLSGSTTVTLTSPVNNP 300
 DB 257 PFFSVDPQGVVTRTIPMWDRETQEEFLVYVQAKMGGMGLSGSTTVTLTSPVNNP 316
 QY 301 DGLITVRKPLDPSQSYSEFVEATNTLIDPAYLRGFPKYVASVRYVQAPPEPATQ 360
 DB 317 DGLITVRKPLDPSQSYSEFVEATNTLIDPAYLRGFPKYVASVRYVQAPPEPATQ 376
 QY 361 AAYHLLVPEKAPGTLVQGISAADLSPASPIRYSILHSDPERCFSTIOPEEGTHTAP 420
 DB 377 AAYHLLVPEKAPGTLVQGISAADLSPASPIRYSILHSDPERCFSTIOPEEGTHTAP 436
 QY 421 LDREARAMNLTVLATELGMSWGPGRGVPLVLAEMSAFADPORSFVGSAYGIDQSSA 480
 DB 437 LDREARAMNLTVLATELGMSWGPGRGVPLVLAEMSAFADPORSFVGSAYGIDQSSA 496
 QY 481 QASRVQVATQTDENDNAPQLAPEPTFYCDSSAABGOLIOVTRALDREVGSSHYVSG 540
 DB 499 QASRVQVATQTDENDNAPQLAPEPTFYCDSSAABGOLIOVTRALDREVGSSHYVSG 518
 QY 541 PLGPDANFTVQDNRD-----LPA-----WFPPLMASASWMLH--- 573
 DB 519 PLGPDANFTVQDNRDSSASLLPSRAPPRHAPVLPFIEMDMGQPALSTATVTSVCR 578
 QY 574 -----WPAERGNQPASOG 587
 DB 579 CQPDGSVASCWPEAHLSAAGISTG 602

RESULT 6
 ABR40114
 ID ABR40114 standard; protein; 781 AA.
 AC ABR40114;
 XX
 DT 04-JUL-2003 (first entry)
 DE Human cell adhesion and extracellular matrix protein, CADECW-11.
 XX Human; anti-HIV; antiallergic; cerebroprotective; antiparkinsonian;
 XX anticonvulsant; nootropic; neuroprotective; immunosuppressive;
 XX dermatological; anti-inflammatory; cyostatic; antiarteriosclerotic;
 KW gene therapy; cell adhesion; extracellular matrix; CADPCM;
 KW immune system disorder; AIDS; allergy; neurological disorder; stroke;
 KW Parkinson's disease; epilepsy; developmental disorder; Down's syndrome;
 KW cerebral palsy; connective tissue disorder; systemic lupus erythematosus;
 KW genetic disorder; Alport's syndrome; cell proliferative disorder; cancer;
 KW atherosclerosis.
 XX
 OS Homo sapiens.
 XX
 EN W02003027230-A2.
 XX
 PD 03-APR-2003.
 XX
 PF 02-AUG-2002; 2002WO-US024649.
 XX
 PR 03-AUG-2001; 2001US-0309964P.
 PR 03-AUG-2001; 2001US-03100119P.
 PR 17-AUG-2001; 2001US-0313091P.
 PR 31-AUG-2001; 2001US-0316771P.

07-SEP-2001; 2001US-0317896P.
 PR 21-SEP-2001; 2001US-0324781P.
 PR 05-OCT-2001; 2001US-0327606P.
 PR 12-OCT-2001; 2001US-0328960P.
 PR 09-NOV-2001; 2001US-0344471P.
 PR 17-MAY-2002; 2002US-0381291P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Burford N, Warren BA, Duggan BW, Mason EM, Richardson TW, Yue H;
 PI Forsythe JF, Elliott VS, Griffin JA, Gotvad AE, Azimzal Y,
 PI Kallik DA, Xu Y, Honchell CD, Baughn MR, Gietzen KJ, Lee S;
 PI Walla NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Ramkumar J;
 XX
 DR WPI; 2003-354645/33.
 DR N-PSDB; ACC00402.
 XX
 PT New human cell adhesion and extracellular matrix proteins (CADECM),
 PT useful for diagnosing, treating or preventing disorders associated with
 PT aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies
 PT or stroke.
 XX
 PS Claim 1; Page 192-194; 234pp; English.
 XX
 CC The present invention relates to novel human cell adhesion and
 CC extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding
 CC sequences (ACC00392-ACC00413 and ABR40104-ABR40125). The coding sequences
 CC and proteins are useful in diagnosing, treating and preventing disorders
 CC associated with aberrant expression of CADECM, such as immune system
 CC disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,
 CC Parkinson's disease or epilepsy), developmental disorders (e.g. Down's
 CC syndrome or cerebral palsy), connective tissue disorders (e.g. systemic
 CC lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell
 CC proliferative disorders (e.g. cancer or atherosclerosis)
 CC
 SQ Sequence 781 AA;
 Query Match 81.4%; Score 2651.5; DB 6; Length 781;
 Best Local Similarity 84.5%; Pred. No. 7e-218;
 Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;
 QY 1 CMGRILAPARAMAGSRHPPGALTRRSWMNQFVIEEYAGPEPILICKLSDDVDRG 60
 DB 17 CMGRILAPARAMAGSRHPPGALTRRSWMNQFVIEEYAGPEPILICKLSDDVDRG 76
 QY 61 GRTKYLLTGSGAGVFIYDEATGNHVTKSLDREKQAYVLLAQAVDRASNPRLPEPSEF 120
 DB 77 GRTKYLLTGSGAGVFIYDEATGNHVTKSLDREKQAYVLLAQAVDRASNPRLPEPSEF 136
 QY 121 IIRGODINDNPPIPLGPYHATVPENSVGTSVIOWTAHADDPVGNASKVYTTLDGL 180
 DB 137 IIRGODINDNPPIPLGPYHATVPENSVGTSVIOWTAHADDPVGNASKVYTTLDGL 196
 QY 181 PFESVDPQTGVRTAIPNMDRETOEELVVIQAKDQGHGSLGSGTIVVTLSDVDNP 240
 DB 197 PFESVDPQTGVRTAIPNMDRETOEELVVIQAKDQGHGSLGSGTIVVTLSDVDNP 256
 QY 241 PKPEQSLYQSFVETAPGTLVGRILRAQDPDLGNMLMAVSIIDGSGSAFISTDLQR 300
 DB 257 PKPEQSLYQSFVETAPGTLVGRILRAQDPDLGNMLMAVSIIDGSGSAFISTDLQR 316
 QY 301 DGLITVAKPLDFESQSFVETATNLLIDPAVLRGPFQDVASVVAQDAPEPAFTQ 360
 DB 317 DGLITVAKPLDFESQSFVETATNLLIDPAVLRGPFQDVASVVAQDAPEPAFTQ 376
 QY 361 AAHHLTVENKARGLTVGOISADLSPASPPIRYSLIPHSDFPRCSIOPESGTHTAAP 420
 DB 377 AAHHLTVENKARGLTVGOISADLSPASPPIRYSLIPHSDFPRCSIOPESGTHTAAP 436
 QY 421 LDSEARAHNLTVLATELGMWGPGRGWVPLVAEWSAPAPQSPVGSAGVIGODSSA 480
 DB 437 LDSEARAHNLTVLATELGMWGPGRGWVPLVAEWSAPAPQSPVGSAGVIGODSSA 480
 DSA 458

QY 481 QASRYOVAIOTLDENDNAPOLAEFYDTVCSSAARGCIIQVIRALDRDENSSHSVFG 540
 DB 459 QASRYOVAIOTLDENDNAPOLAEFYDTVCSSAARGCIIQVIRALDRDENSSHSVFG 518
 QY 541 PLGPDANFTVQDNRD-----LPA-----WPHLLMASASSWTH--- 573
 DB 519 PLGPDANFTVQDNRGSGASILLPSRRAPRRHAPVPIELMDKQGPALSSRTATVSVCR 578
 QY 574 -----WPPARGNOPASQG 587
 DB 579 COPDGSVASCWPEAHLISAAGLSTG 602
 RESULT 7
 ID ADA01366 standard; protein; 781 AA.
 XX
 AC ADA01366;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human PRO polypeptide #49.
 XX
 KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
 KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
 KW microvascular endothelial cell; endothelial cell tube formation;
 KW sports-related joint problem; articular cartilage defect; osteoarthritis;
 KW rheumatoid arthritis; osteopathic; anti-rheumatic; antiarthritic.
 XX
 OS Homo sapiens.
 XX
 PN US2003068779-A1.
 XX
 PD 10-APR-2003.
 XX
 PZ 16-SEP-2002; 2002US-00245107.
 XX
 PR 09-MAY-2001; 2001US-0230589P.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WJ, Zhang Z,
 PI Fong S;
 XX
 DR WPI; 2003-625484/59.
 DR N-PSDB; ADA01365.
 XX
 PT Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
 PT stimulating proliferation of human microvascular endothelial cells, and
 PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
 PT cells.
 XX
 PS Claim 11; Fig 98; 307pp; English.
 XX
 CC The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
 CC colon, breast, prostate, rectal, cervical and liver tumours). The
 CC polynucleotides are useful in molecular biology, including uses as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
 CC be used in preparing PRO polypeptides by recombinant techniques and in
 CC generating either transgenic animals or knock-out animals which are
 CC useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides or antibodies are used in preparing a

medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for inducing endothelial cell tube formation and for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence represents a human PRO polypeptide of the invention.

Sequence 781 AA:

Query Match 81.4%; Score 2651.5; DB 6; Length 781;
Best Local Similarity 84.5%; Pred. No. 7e-218;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

```

QY 1 CMGRLAAPARAMAGSREHPGALLRTRRSWVMNQFVIEEYAGEPVLIGKLSVDVDRGE 60
DB 17 CMGRLAAPARAMAGSREHPGALLRTRRSWVMNQFVIEEYAGEPVLIGKLSVDVDRGE 76
QY 61 GRTKYLLTGEGAGTIVIDEATGNIHVTKSLDREERKQVYLLAQAVDRASNPLEPSEF 120
DB 77 GRTKYLLTGEGAGTIVIDEATGNIHVTKSLDREERKQVYLLAQAVDRASNPLEPSEF 136
QY 121 IIKGQDINDNPPIPLGPHYATPEMSNVGTSVIOVTAHDADDSYGSNAKLVYTVLDGL 180
DB 137 IIKGQDINDNPPIPLGPHYATPEMSNVGTSVIOVTAHDADDSYGSNAKLVYTVLDGL 196
QY 181 PPFISVDPTGVYRTAIPNMDRETQEEFLVITQAKDMGSHMGSLSGSTTVYTVLSDVNDP 240
DB 197 PPFISVDPTGVYRTAIPNMDRETQEEFLVITQAKDMGSHMGSLSGSTTVYTVLSDVNDP 256
QY 241 PKFPOSILQFSVETAGPGLVGRRAQDPDIGNALMAYSILDEGESEAFSISTDQGR 300
DB 257 PKFPOSILQFSVETAGPGLVGRRAQDPDIGNALMAYSILDEGESEAFSISTDQGR 316
QY 301 DGLTVRKPLDPEESQSYSPFEVATNTLIDPAYLRGPKFQVAVRVAVQDAPSPAPFTQ 360
DB 317 DGLTVRKPLDPEESQSYSPFEVATNTLIDPAYLRGPKFQVAVRVAVQDAPSPAPFTQ 376
QY 361 AAHYHTVENKAPGLTNGOISAADDSBPSPRYSIILPHSPCECFSTIOPEEGTHTAAR 420
DB 377 AAHYHTVENKAPGLTNGOISAADDSBPSPRYSIILPHSPCECFSTIOPEEGTHTAAR 436
QY 421 LDREARAHNLTVLATELGMSGMPERGVPLLVAMSNAPAPQSPVGSAAVGIPODSSA 480
DB 437 LDREARAHNLTVLATEL-----DSSA 458
QY 461 QASRQVAIQTLDENDNAPQLAEPYDTVCDSAPAGQIIQVTRALDREVNSSSHVFCG 540
DB 459 QASRQVAIQTLDENDNAPQLAEPYDTVCDSAPAGQIIQVTRALDREVNSSSHVFCG 518
QY 541 PLGPPANTVQDNRD-----LPA-----WFPHILMASASMLH--- 573
DB 519 PLGPPANTVQDNRDGSGASLLPSRPAPRRAPYVIEIEMDQGPALSTRTATVAVCR 578
QY 574 -----WPPAERGNQPASQG 587
DB 579 COPDGSVASCWPEAHLSSAAGLSTG 602

```

XX Homo sapiens.
XX US2003064474-A1.
XX 03-APR-2003.
XX 16-SEP-2002; 2002US-00245859.
XX 29-AUG-2001; 2001WO-US027099.
XX 18-JUL-2002; 2002US-00197942.
XX (GENTH) GENENTECH INC.
XX Baker KP, Eaton DL, Filvaroff E, Grimaldi JC,
XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
XX Fong S;
XX WPI; 2003-605867/57.
XX N-PDSB; ADA43794.
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
XX PRO21383, useful in molecular biology, chromosome and gene mapping, in
XX generating antisense RNA and DNA, and in gene therapy.

Claim 11; Fig 98; 308bp; English.

The invention relates to an isolated secreted/transmembrane (PRO) polypeptide, having at least 80% sequence identity to a sequence selected from any one of the 57 amino acid sequences given in specification, or to a sequence encoded by a nucleic acid molecule selected from any one of the nucleic acid sequences deposited under any of the ATCC accession numbers given in specification, or a sequence having at least 80% identity to PRO lacking its associated signal peptide, an extracellular domain of PRO with or without its associated signal peptide. Also included are vectors, transformed host cells, anti-PRO antibodies, the nucleic acids encoding PRO, PRO fusion proteins, inducing endothelial cell tube formation (by administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and an oligonucleotide probe derived from any one of the above nucleotide sequences. PRO6018 polypeptide is useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080 and PRO21383 polypeptides are useful for stimulating the proliferation of human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006 polypeptides are useful for inhibiting the proliferation of human microvascular endothelial cells. PRO polypeptides are useful for detecting the presence of tumour in a mammal, including tumours of lung, colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and PRO34274 polypeptides are useful for inducing endothelial cell tube formation. PRO or the antibody are useful in the preparation of a medicament for treating a condition responsive to PRO polypeptide. The oligonucleotide probes are useful for isolating genomic and cDNA nucleotide sequences, for measuring or detecting the expression of an associated gene, and as antisense probes. PRO nucleic acid is useful as a hybridisation probe, in chromosome and gene mapping, in the generation of antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The present sequence represents a PRO protein.

Sequence 781 AA:

Query Match 81.4%; Score 2651.5; DB 6; Length 781;
Best Local Similarity 84.5%; Pred. No. 7e-218;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

```

QY 1 CMGRLAAPARAMAGSREHPGALLRTRRSWVMNQFVIEEYAGEPVLIGKLSVDVDRGE 60
DB 17 CMGRLAAPARAMAGSREHPGALLRTRRSWVMNQFVIEEYAGEPVLIGKLSVDVDRGE 76
QY 61 GRTKYLLTGEGAGTIVIDEATGNIHVTKSLDREERKQVYLLAQAVDRASNPLEPSEF 120
DB 77 GRTKYLLTGEGAGTIVIDEATGNIHVTKSLDREERKQVYLLAQAVDRASNPLEPSEF 136

```

QY 121 IIKGQDINDNPPILPGFYHATVEMSNVGTSTVIQVTAHADDDPSYGNASKLVYTVLDGL 180
 DB 137 IIKVQDINDNPPILPGFYHATVEMSNVGTSTVIQVTAHADDDPSYGNASKLVYTVLDGL 196
 QY 181 PFFSVDPQTGVVTRAIEMMDRETOEFLVYIQAKDNGHNGSGSTTVYTVLSDVNDP 240
 DB 197 PFFSVDPQTGVVTRAIEMMDRETOEFLVYIQAKDNGHNGSGSTTVYTVLSDVNDP 256
 QY 241 PKFPQSLYQFSVETAGPGLVGRRAQDDPDLGNALMAYSIIDGSESAFSTIDLOGR 300
 DB 257 PKFPQSLYQFSVETAGPGLVGRRAQDDPDLGNALMAYSIIDGSESAFSTIDLOGR 316
 QY 301 DGLTVRKPLDPEQORSYFRVEATNTLIDPAYLRGPFQDVASVYAVODAPPPAFTQ 360
 DB 317 DGLTVRKPLDPEQORSYFRVEATNTLIDPAYLRGPFQDVASVYAVODAPPPAFTQ 376
 QY 361 AAYHLTVENKAPGTLVGOISADLDSPPASPIRYSILPHSDPERCFIOPEEGTHTAAP 420
 DB 377 AAYHLTVENKAPGTLVGOISADLDSPPASPIRYSILPHSDPERCFIOPEEGTHTAAP 436
 QY 421 LDRBARAHNLTVALTELIGMSWGERGVPLLVAMSAAPAPQRSFVGSAGIIPDSSA 480
 DB 437 LDRBARAHNLTVALTELIGMSWGERGVPLLVAMSAAPAPQRSFVGSAGIIPDSSA 458
 QY 481 QASRYOVAIOTLDENDNAPOLAEPRYDFVCDASAPGQLIQVIRALDRDEYGNSSHYSPG 540
 DB 459 QASRYOVAIOTLDENDNAPOLAEPRYDFVCDASAPGQLIQVIRALDRDEYGNSSHYSPG 518
 QY 541 PLGPDANFTVQDNED-----LPA-----WFHPLMASASSWLH--- 573
 DB 519 PLGPDANFTVQDNEDGASALLPSRAPPRHAPYLVPIELMDWGQPLSTATVTVSVCR 578
 QY 574 -----WPPAERGNQAPASG 587
 DB 579 CQPDGVSVAWCWPEAHLSAAGLSTG 602

RESULT 9
 ADA43563
 ID ADA43563 standard; protein: 781 AA.
 AC ADA43563;
 XX
 XX 20-NOV-2003 (first entry)
 DT
 XX
 XX Human secreted/transmembrane polypeptide PRO34009.
 DE
 XX Human; PRO; secreted protein; transmembrane protein;
 KM endothelial cell tube formation; chondrocyte cell differentiation;
 KM microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KM breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KM liver tumour; cytostatic; vaccine.
 XX
 OS Homo sapiens.
 XX
 XX US2003073196-A1.
 FN
 XX
 PD 17-APR-2003.
 PD
 XX
 PF 18-SEP-2002; 2002US-00246210.
 PF
 XX
 PR 04-APR-2001; 2001US-0282199P.
 PR 28-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 PR
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI, Zhang Z,
 PI Feng S,
 XX WPI; 2003-743814/70.

DR N-PSDB; ADA43562.
 XX
 PT New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
 PT PRO21383 useful for stimulating the proliferation or differentiation of
 PT chondrocyte cells and detecting the presence of a tumor in a mammal.
 PS
 XX Claim 11; Fig 98; 307pp; English.
 CC The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acids deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide. Also included are vectors,
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
 CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
 CC and PRO21383 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumour in a mammal, including tumours of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence represents a PRO protein.
 XX
 XX Sequence 781 AA;
 SQ
 Query Match 81.4%; Score 2651.5; DB 6; Length 781;
 Best Local Similarity 84.4%; Pred. No. 7e-218;
 Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;
 QY 1 CMGRLAAPARAWAGSRHHPGALIRTRRSWVWNOFVIEEYAGEPYLIKLSHDVDRGE 60
 DB 17 CMGRLAAPARAWAGSRHHPGALIRTRRSWVWNOFVIEEYAGEPYLIKLSHDVDRGE 76
 QY 61 GRTYVLLTGEAGVAFVIDEATGNVHTKSLDRETKQVYLLAQAVRASNPPEPSEF 120
 DB 77 GRTYVLLTGEAGVAFVIDEATGNVHTKSLDRETKQVYLLAQAVRASNPPEPSEF 136
 QY 121 IIKGQDINDNPPILPGFYHATVEMSNVGTSTVIQVTAHADDDPSYGNASKLVYTVLDGL 180
 DB 137 IIKVQDINDNPPILPGFYHATVEMSNVGTSTVIQVTAHADDDPSYGNASKLVYTVLDGL 196
 QY 181 PFFSVDPQTGVVTRAIEMMDRETOEFLVYIQAKDNGHNGSGSTTVYTVLSDVNDP 240
 DB 197 PFFSVDPQTGVVTRAIEMMDRETOEFLVYIQAKDNGHNGSGSTTVYTVLSDVNDP 256
 QY 241 PKFPQSLYQFSVETAGPGLVGRRAQDDPDLGNALMAYSIIDGSESAFSTIDLOGR 300
 DB 257 PKFPQSLYQFSVETAGPGLVGRRAQDDPDLGNALMAYSIIDGSESAFSTIDLOGR 316
 QY 301 DGLTVRKPLDPEQORSYFRVEATNTLIDPAYLRGPFQDVASVYAVODAPPPAFTQ 360
 DB 317 DGLTVRKPLDPEQORSYFRVEATNTLIDPAYLRGPFQDVASVYAVODAPPPAFTQ 376
 QY 361 AAYHLTVENKAPGTLVGOISADLDSPPASPIRYSILPHSDPERCFIOPEEGTHTAAP 420

Db 377 AAYHLTPENKAPGTLVGQISADLDSPASPIRYSILPHSDPERCFSIQPEEGTHTAAP 436
 Qy 421 LDRBARAMHNLTVATLTELGMKSGPERGWPVLVAMENSAAPAPQPSRVASGAVGIPDDSSA 480
 Db 437 LDRBARAMHNLTVATLTEL-----DSSA 458
 Qy 481 QASRVQVAIQTLDDENNAPQLAEPYDTFVCDSPAAPGQLIQVIRALDRDEVGNSHVSFOG 540
 Db 459 QASRVQVAIQTLDDENNAPQLAEPYDTFVCDSPAAPGQLIQVIRALDRDEVGNSHVSFOG 518
 Qy 541 PLGPDANFTVQDNRD-----LPA-----WFHPLMASASSWLH--- 573
 Db 519 PLGPDANFTVQDNRDGASALLPSRPAPPRHAPYLVPILMDWGQPALSTATVTVSVCR 578
 Qy 574 -----WPAERGNQPASOG 587
 Db 579 CQPDGVSASCPWPAHLSAAGLSTG 602

RESULT 10

ADA01238 ID ADA01238 standard; protein; 781 AA.

AC ADA01238;

DT 06-NOV-2003 (first entry)

DE Human PRO polypeptide #49.

XX Human; PRO, secreted polypeptide; transmembrane polypeptide;
 XX tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
 XX cancer; lung; colon; breast; prostate; rectum; kidney; liver;
 XX microvascular endothelial cell; endothelial cell tube formation.
 OS Homo sapiens.

PN US2003068782-A1.

PD 10-APR-2003.

PF 16-SEP-2002; 2002US-00245851.

PR 27-APR-1999; 99US-0131271P.

PR 29-OCT-1999; 99US-0162506P.

PR 02-DEC-1999; 99MO-08028551.

PR 29-AUG-2001; 2001MO-08027099.

PR 18-JUL-2002; 2002US-00197942.

XX (GETH) GENENTECH INC.

PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,

PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,

PI Fong S;

XX MPI; 2003-625487/59.

DR N-PESDB; ADA01237.

XX Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the

CC preparation of a medicament for treating a condition responsive to PRO

CC polypeptide, and as therapeutic agents e.g. vaccines.

CC Claim 11; Fig 98; 308pp; English.

CC The invention relates to isolated human PRO polypeptides (secreted and

CC gene therapy. The polynucleotides may also be used in preparing PRO
 CC polypeptides by recombinant techniques and in generating either
 CC transgenic animals or knock-out animals which are useful in the
 CC development and screening of therapeutically useful reagents. The PRO
 CC polypeptides or antibodies are used in preparing a medicament for
 CC treating a condition responsive to the polypeptides or antibodies, such
 CC as tumours, for stimulating and inhibiting proliferation of human
 CC microvascular endothelial cells and for inducing endothelial cell tube
 CC formation. This sequence represents a human PRO polypeptide of the
 CC invention.

XX Sequence 781 AA;

SQ Query Match 81.4%; Score 2651.5; DB 6; Length 781;

Best Local Similarity 84.5%; Pred. No. 7e-218;

Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

Qy 1 CMGRLAAPARAGSREHCPALLTRRSWVNOGFVEEYAGPEPVILGKLSVDVDRGE 60
 Db 17 CMGRLAAPARAGSREHCPALLTRRSWVNOGFVEEYAGPEPVILGKLSVDVDRGE 76
 Qy 61 GRTKYLLTGEAGTGFVIDEATGNHVTKSLDREKAQYVLLAQAVIDRASNPPLPPESEF 120
 Db 77 GRTKYLLTGEAGTGFVIDEATGNHVTKSLDREKAQYVLLAQAVIDRASNPPLPPESEF 136
 Qy 121 IIKGQDINNPPFLPGFYHATVPKMSNGTGVIVQTAHDADDPGNGSAKIYTVYLDGL 180
 Db 137 IIKGQDINNPPFLPGFYHATVPKMSNGTGVIVQTAHDADDPGNGSAKIYTVYLDGL 196
 Qy 181 PFFSVPOGTGVYRTAIPMDRETOEEFLVIOAKMGGMGSLGSGTIVTSLDVNDNP 240
 Db 197 PFFSVPOGTGVYRTAIPMDRETOEEFLVIOAKMGGMGSLGSGTIVTSLDVNDNP 256
 Qy 241 PKFPOSLYQPSVETATGPGTIVGRLARQDPDIGNALMAYSLIDGSEAFSISTDLQGR 300
 Db 257 PKFPOSLYQPSVETATGPGTIVGRLARQDPDIGNALMAYSLIDGSEAFSISTDLQGR 316
 Qy 301 DGLITRKRLDPESQSYSFVEATNTLIDPAYLRGPKDYASVAVQAQAPPEPAFTQ 360
 Db 317 DGLITRKRLDPESQSYSFVEATNTLIDPAYLRGPKDYASVAVQAQAPPEPAFTQ 376
 Qy 361 AAYHLTPENKAPGTLVGQISADLDSPASPIRYSILPHSDPERCFSIQPEEGTHTAAP 420
 Db 377 AAYHLTPENKAPGTLVGQISADLDSPASPIRYSILPHSDPERCFSIQPEEGTHTAAP 436
 Qy 421 LDRBARAMHNLTVATLTELGMKSGPERGWPVLVAMENSAAPAPQPSRVASGAVGIPDDSSA 480
 Db 437 LDRBARAMHNLTVATLTEL-----DSSA 458
 Qy 481 QASRVQVAIQTLDDENNAPQLAEPYDTFVCDSPAAPGQLIQVIRALDRDEVGNSHVSFOG 540
 Db 459 QASRVQVAIQTLDDENNAPQLAEPYDTFVCDSPAAPGQLIQVIRALDRDEVGNSHVSFOG 518
 Qy 541 PLGPDANFTVQDNRD-----LPA-----WFHPLMASASSWLH--- 573
 Db 519 PLGPDANFTVQDNRDGASALLPSRPAPPRHAPYLVPILMDWGQPALSTATVTVSVCR 578
 Qy 574 -----WPAERGNQPASOG 587
 Db 579 CQPDGVSASCPWPAHLSAAGLSTG 602

RESULT 11

ADA01122 ID ADA01122 standard; protein; 781 AA.

AC ADA01122;

DT 06-NOV-2003 (first entry)

DE Human secreted/transmembrane polypeptide PRO34009.

XX Human; PRO, secreted protein; transmembrane protein;

KM endothelial cell tube formation; chondrocyte cell differentiation;
 KM microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KM breast; prostate tumour; rectal tumour; kidney tumour;
 KM liver tumour; cytostatic; vaccine.
 OS Homo sapiens.
 XX
 XX US2003068780-A1.
 XX
 PD 10-APR-2003.
 XX
 PF 16-SEP-2002; 2002US-00245143.
 XX
 PR 02-AUG-2000; 2000US-0222695P.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S;
 DR WPI; 2003-625485/59.
 DR N-PSDB; ADA01121.
 XX
 PT Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
 PT preparation of a medicament for treating a condition responsive to PRO
 PT polypeptide, and as therapeutic agents e.g. vaccines.
 PT
 PS
 PS Claim 11; Fig 98; 307pp; English.
 XX
 XX The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acids deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide, also included are vectors,
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
 CC PRO10275, PRO10207, PRO20933 or PRO34274 polypeptide or its agonist) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO133, PRO20080
 CC and PRO21383 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumour in a mammal, including tumours of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO10207, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence represents a PRO protein.
 CC
 XX
 XX Sequence 781 AA:
 Query Match 81.4%; Score 2651.5; DB 7; Length 781;
 Best Local Similarity 84.5%; Pred. No. 7e-218;
 Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;
 QY 1 CMGRLAAPARAWGSRHHPGALLTRRSWVWVQFVIEEYAGPEPVILGKLHSDVDGE 60

DB |||||
 17 CMGRLAAPARAWGSRHHPGALLTRRSWVWVQFVIEEYAGPEPVILGKLHSDVDGE 76
 QY |||||
 61 GRTKLLGEGAGTGVFIDEATGNHYTKSLDREKAYVLLAAYVDAASRLPEPSEF 120
 DB |||||
 77 GRTKLLGEGAGTGVFIDEATGNHYTKSLDREKAYVLLAAYVDAASRLPEPSEF 136
 QY |||||
 121 IIKQDINDNPEIPLGEPYHATVPEMSNVGTSVIGTVAHADDSYGSAXLYTVTDGL 180
 DB |||||
 137 IIKQDINDNPEIPLGEPYHATVPEMSNVGTSVIGTVAHADDSYGSAXLYTVTDGL 196
 QY |||||
 181 PFEVSVDPOGVVTRTAPMMDRETOEFLVLIQAKDMGGMGLSGSTTVTLSDVNDP 240
 DB |||||
 197 PFEVSVDPOGVVTRTAPMMDRETOEFLVLIQAKDMGGMGLSGSTTVTLSDVNDP 256
 QY |||||
 241 PKEPQSLVQSVETAGTGLVGRAPDPLGDMALMAYSLIDEGSEAFSISTDQGR 300
 DB |||||
 257 PKEPQSLVQSVETAGTGLVGRAPDPLGDMALMAYSLIDEGSEAFSISTDQGR 316
 QY |||||
 301 DGLITVRKPLDPESGRSISFRVEATNTLIDPAYLRGPFKQVAVRVAVODAPPPAF 360
 DB |||||
 317 DGLITVRKPLDPESGRSISFRVEATNTLIDPAYLRGPFKQVAVRVAVODAPPPAF 376
 QY |||||
 361 AAYHLTVENKAPGLVQGISAADLSPASPIRSILPHSDPESCFSIQPEEGITHRAAP 420
 DB |||||
 377 AAYHLTVENKAPGLVQGISAADLSPASPIRSILPHSDPESCFSIQPEEGITHRAAP 436
 QY |||||
 421 LDREARAHNTLTATBELGMSWGPREGVPLVAEWSAPAAPQSPVGAAGIPOS 480
 DB |||||
 437 LDREARAHNTLTATBELGMSWGPREGVPLVAEWSAPAAPQSPVGAAGIPOS 458
 QY |||||
 481 QASRYQVAILQTLDENNDNAPOLAEYDPFVCSAPGOLIVTRALDSDEVGSSHVFOG 540
 DB |||||
 489 QASRYQVAILQTLDENNDNAPOLAEYDPFVCSAPGOLIVTRALDSDEVGSSHVFOG 518
 QY |||||
 541 PLGPDANFTVQDNRD-----LPA-----MFHPLMASASSWLH--- 573
 DB |||||
 519 PLGPDANFTVQDNRDGASLLPSRPAPPRHAPVLPVIELMDQGPALSSATVTVSVC 578
 QY |||||
 574 -----WPPARNGQPPASOG 587
 DB |||||
 579 QDPGVSASCPPEALHSAALSTG 602
 RESULT 12
 ADA43679
 ID ADA43679 standard; protein. 781 AA.
 XX
 AC ADA43679;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted/transmembrane polypeptide PRO34009.
 XX
 KM Human, PRO; secreted protein; transmembrane protein;
 KM endothelial cell tube formation; chondrocyte cell differentiation;
 KM microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KM breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KM liver tumour; cytostatic; vaccine.
 XX
 OS Homo sapiens.
 XX
 XX US2003073190-A1.
 XX
 PD 17-APR-2003.
 XX
 PF 09-SEP-2002; 2002US-00238283.
 XX
 PR 01-JUL-1998; 98US-0091358P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 20-JUL-1999; 99US-0144758P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 25-AUG-1999; 99US-00380137.

30-MAR-2000; 2000MOW-US008439.
02-JUN-2000; 2000MOW-US015264.
PR 29-AUG-2001; 2001MOW-US027099.
PR 18-JUL-2002; 2002US-00197942.

XX
XX PA (GENTH) GENENTECH INC.
XX PA Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI Guney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
PI Fong S,
DR WPJ; 2003-585304/55.
DR N-PSDB; ADA43678.

XX
XX PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.

PS
PS Claim 11; Fig 98; 352pp: English.

XX
XX The invention relates to an isolated secreted/transmembrane (PRO)
CC polypeptide, having at least 80% sequence identity to a sequence selected
CC from any one of the 57 amino acid sequences given in specification, or to
CC a sequence encoded by a nucleic acid molecule selected from any one of
CC the nucleic acids deposited under any of the ATCC accession numbers given
CC in specification, or a sequence having at least 80% identity to PRO
CC lacking its associated signal peptide, an extracellular domain of PRO
CC with or without its associated signal peptide. Also included are vectors,
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC administering PRO281, PRO2810, PRO189, PRO4499, PRO6308, PRO6000,
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC an oligonucleotide probe derived from any one of the above nucleotide
CC sequences. PRO6008 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC and PRO21383 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4497 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumour in a mammal, including tumours of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and CDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence represents a PRO protein.

XX
XX Sequence 781 AA;

Query Match 81.4%; Score 2651.5; DB 7; Length 781;
Best Local Similarity 84.5%; Pred. No. 7e+218;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4

Dy 1 CMGRLAAPARAAGSREHPGALLTRRSWNNQFVEIEVAGPEVLIGKLSVDVRGE 60
17 CMGRLLAAPPARAAGSEHPGALLTRRSWNNQFVEIEVAGPEVLIGKLSVDVRGE 76
Dy 61 GRTKYILLTGEGAGTVFVIDEAGNIHYTSLDREEAQYVLLAQAVDRASNPRLPPSPF 120
77 GRTKYILLTGEGAGTVFVIDEAGNIHYTSLDREEAQYVLLAQAVDRASNPRLPPSPF 136
Dy 121 IIKGGDINNPFIPLGPYHAATVPENSNVTSTVCTAHADADPSSYGNSAKIYYTLDEL 180
137 IIKGGDINNPFIPLGPYHAATVPENSNVTSTVCTAHADADPSSYGNSAKIYYTLDEL 196
Dy 181 PEPSPDPQCVCVTAIPNMDRETQEERFLVIYIAKMGNHGSGISTTYTNLSDPNRP 240

Db	19	PFPSVDQGVVTRT	A1PNNVDETRTEEF	LVVIQAKDMGSHMGJSGSTTVTLISDVNDNP	256				
Qy	241	KRFPSGLYQSFVETNAGCTT	VGRLRADDPDPLGNLMAVS	ILDEGSEAFSISTDLOQR	300				
Db	257	KRFPSGLYQSFVETNAGCTT	VGRLRADDPDPLGNLMAVS	ILDEGSEAFSISTDLOQR	316				
Qy	301	DGLLTVRKRLDEDSQSRYS	FRVEATNTLLIDPAYLRRGCFKQ	VASRVAVODADPEPPAFQ	360				
Db	317	DGLLTVRKRLDEDSQSRYS	FRVEATNTLLIDPAYLRRGCFKQ	VASRVAVODADPEPPAFQ	376				
Qy	361	AAHLTVPENKAPGLU	NGOISAADSDSPSIRSTII	PHSDPERCFSTIOPEEGTHTAAR	420				
Db	377	AAHLTVPENKAPGLU	NGOISAADSDSPSIRSTII	PHSDPERCFSTIOPEEGTHTAAR	436				
Qy	421	LDRERAPAMNLTVLAT	ELGWSWGPBGVPLLVAEWSAPAA	PQRSFVSGAVGIPDSSA	480				
Db	437	LDRERAPAMNLTVLAT	ELGWSWGPBGVPLLVAEWSAPAA	PQRSFVSGAVGIPDSSA	458				
Qy	481	QASRVQVALCTD	ENDNAPQIAEPYDTEVCDSAA	PGQLIQYIRALDRDEVGNSHSVFG	540				
Db	459	QASRVQVALCTD	ENDNAPQIAEPYDTEVCDSAA	PGQLIQYIRALDRDEVGNSHSVFG	518				
Qy	541	PLPGDANFTYQDNRD	-----LPA-----	WFHPLIMASASSWLH---	573				
Db	519	PLPGDANFTYQDNRD	SGASILLPSRPAPRPHAPVLP	PIELWMOGQFALSSATATVAVCR	578				
Qy	574	-----WPPAEKGNP	ASQSG	587					
Db	579	CQPDGVSASCP	FEAHLASAAGISTG	602					
RESULT 13									
ID	ADA06941	standard; protein; 781 AA.							
AC	ADA06941;								
DT	06-NOV-2003	(first entry)							
DE	Human PRO polypeptide #49.								
XX	Human; PRO; secreted polypeptide; transmembrane polypeptide;								
KW	tumour neurosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour								
KW	adrenal; lung; colon; breast; prostate; rectum; cervix; liver;								
KW	microvascular endothelial cell; endothelial cell tube formation;								
KW	bone disorder; cartilage disorder; sports injury; proteoglycan;								
KW	cartilage; sports-related joint problem; articular cartilage defect;								
KW	osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder;								
KW	thalassaemia; immune system cell infiltration; cancer; vulnery;								
KW	antianemic; osteopathic; antirheumatic; antirheumatic.								
XX	Homo sapiens.								
OS	US2003068781-A1.								
PN	10-APR-2003.								
PD	16-SEP-2002; 2002US-00245771.								
PF	03-AUG-1999; 99US-0146843P.								
PR	15-MAY-2000; 2000MO-US013158.								
PR	29-AUG-2001; 2001MO-US020799.								
PR	18-JUL-2002; 2002US-00197942.								
XX	(GETH) GENENTECH INC.								
PA	Baker KP, Baton DL, Filvaroff E, Goddard A, Grimaldi JC;								
PI	Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;								
PI	Fong S;								
XX	MPI; 2003-625486/59.								
DR	N-PSDB; ADA06940.								
XX									

PT Novel secreted and transmembrane polypeptides, PRO polypeptides useful
PT for stimulating proliferation or differentiation of chondrocyte cells and
PT inducing endothelial cell tube formation.

XX Claim 11; Fig 98; 307pp; English.

CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptide or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for inducing endothelial cell
CC tube formation and for treating various bone and/or cartilage disorders
CC such as sports injuries and arthritis. PRO polypeptides which stimulate
CC the release of proteoglycans from cartilage are useful for treating
CC sports-related joint problems, articular cartilage defects, osteoarthritis
CC and rheumatoid arthritis. PRO polypeptides are also useful
CC for treating various mammalian haemoglobin-associated disorders such as
CC various thalassaemias and conditions which may benefit from enhanced
CC local immune system cell infiltration. This sequence represents a human
CC PRO polypeptide of the invention.

XX Sequence 781 AA:

Query Match 81.4%; Score 2651.5; DB 7; Length 781;
Best Local Similarity 84.5%; Pred. No. 7e-218;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 CMGSLAPAPAMGSRHPPALLRTRRSMVWVNOFVTEYAGPEEVLIGKHSVDREE 60
DB 17 CMGRILAPAPAMGSRHPPALLRTRRSMVWVNOFVTEYAGPEEVLIGKHSVDREE 76
QY 61 GRKYLLTGAGTGVFVDEATGNHVTSLDREKAQVYLAQAVDRASNPLEPPSEF 120
DB 77 GRKYLLTGAGTGVFVDEATGNHVTSLDREKAQVYLAQAVDRASNPLEPPSEF 136
QY 121 IINGODINDNPPFPIGPRVATVPEMSNGTSTVIOVTAHDADPSGNSAKIVYVLDGL 180
DB 137 IIXQDINDNPPFPIGPRVATVPEMSNGTSTVIOVTAHDADPSGNSAKIVYVLDGL 196
QY 181 PFSVDPQTSVGTALPNDRETQBEFLVVIQAKDMGGMGSGSTVTVTLSDVNDP 240
DB 197 PFSVDPQTSVGTALPNDRETQBEFLVVIQAKDMGGMGSGSTVTVTLSDVNDP 256
QY 241 PKFPQSLYQSVVETGPGTLVGRLAQDPDLGNALMAYSLIDGSGEAFSITDLOGR 300
DB 257 PKFPQSLYQSVVETGPGTLVGRLAQDPDLGNALMAYSLIDGSGEAFSITDLOGR 316
QY 301 DGLLTVRKPLDFESQSYFRVETATLIDPATLRGPFQDVASVVAQDAPPEPAFTQ 360
DB 317 DGLLTVRKPLDFESQSYFRVETATLIDPATLRGPFQDVASVVAQDAPPEPAFTQ 376
QY 361 AAHHLVPEKAGTLVGOISADLDSPASPIRYSILPHSDPERCFSTQPEEGTHTAP 420
DB 377 AAHHLVPEKAGTLVGOISADLDSPASPIRYSILPHSDPERCFSTQPEEGTHTAP 436
QY 421 LDREAPAMHLVTLATELGWSGPERGWVLLVAEMSAAPAPQSPVGSANGIQDSSA 480
DB 437 LDREAPAMHLVTLATELGWSGPERGWVLLVAEMSAAPAPQSPVGSANGIQDSSA 498
QY 481 QASRVOVAIQTLDENNDNAPQALAEPYDTFVCDASAPGQILQVTRALDRDEVGNSHVSFQG 540

DB 459 QASRVOVAIQTLDENNDNAPQALAEPYDTFVCDASAPGQILQVTRALDRDEVGNSHVSFQG 518
QY 541 PLGPDANFTVQDNRGASLLPSPRAPPRAPIVPIELMDWGPALSTATVTVSVC 573
DB 519 PLGPDANFTVQDNRGASLLPSPRAPPRAPIVPIELMDWGPALSTATVTVSVC 578
QY 574 -----WPPAERGQNPASOG 587
DB 579 COPDGSVASCPWEAHLISAAGLSTG 602

RESULT 14
ADA08429
ID ADA08429 standard; protein, 781 AA.
XX
AC ADA08429;
DT 06-NOV-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO34009.
XX
KW osteopathic; anti-rheumatic; anti-arthritis; gene therapy;
KW cell proliferation stimulator;
KW chondrocyte cell differentiation stimulator;
KW secreted and transmembrane protein; PRO; human; PRO1313; PRO20080;
KW PRO1383; human microvascular endothelial cell proliferation; PRO6071;
KW PRO4487; PRO6006; PRO240; PRO256; PRO659; PRO1002; PRO4316; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour;
KW sports-related joint problem; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; tissue typing.
XX
OS Homo sapiens.
XX
EN US2003068783-A1.
XX
PD 10-APR-2003.
XX
PF 16-SEP-2002; 2002US-00245883.
XX
PR 09-MAY-2001; 2001US-0290589P.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
PA (GENTH) GENENTECH INC.
XX
PI Baker KP, Baton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WT, Zhang Z,
PI Fong S;
XX
DR MPI; 2003-625488/59.
DR N-PSDB; ADA08428.
XX
PT Novel isolated PRO1313, PRO20080 or PRO2183 polypeptide useful for
PT stimulating proliferation of human microvascular endothelial cells, and
PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
PT cells.

XX Claim 11; Fig 98; 308pp; English.

CC The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide (I). PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080,
CC or PRO2183 polypeptide is useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487, or PRO6006
CC polypeptide is useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides such as PRO240, PRO256,
CC PRO699, PRO1002, PRO4316, etc., are useful for detecting the presence of
CC tumour in a mammal which involves comparing the level of expression of
CC the above mentioned polypeptides in a test sample of cells taken from the
CC mammal, and a control sample of normal cells of the same cell type, where
CC a higher level of expression of the PRO polypeptide in the test sample as

compared to the control sample is indicative of the presence of tumour in the mammal, the tumour being adrenal tumour, lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour, cervical tumour or liver tumour. PRO6018 polypeptide is useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis, or rheumatoid arthritis. PRO polypeptides are useful as molecular weight markers for protein electrophoresis. (I) is also useful for screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). The polynucleotide (II) encoding (I) is useful as hybridisation probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. PRO nucleic acid is also be useful for the preparation of PRO polypeptides. The full-length native sequence of PRO gene or its portions may be used as hybridisation probes for a cDNA library to isolate the full-length PRO cDNA or to isolate still other cDNAs. Nucleotide sequences encoding PRO can also be used to construct hybridisation probes for mapping the gene which encodes that PRO and for the genetic analysis of individuals with genetic disorders. (II) encoding (I) or its modified forms can also be used to generate either transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful reagents. (II) encoding PRO polypeptides are also useful in gene therapy techniques to treat conditions associated with aberrant expression or activity of (I). The PRO polypeptides and nucleic acid molecules are useful for tissue typing. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide.

Sequence 781 AA;

Query Match	81.4%;	Score 2651.5;	DB 7;	Length 781;
Best Local Similarity	84.5%;	Pred. No. 7e-218;		
Matches 527; Conservative	5;	Mismatches 17;	Indels 75;	Gaps 4;

```

OY 1 CMGRILAAPARMAWAGSREHPGRLALTTRRSWMMNOCFVLEEYAGPEPVILIGLHSDVDC 60
Db 17 CMGRILAAPARMAWAGSREHPGRLALTTRRSWMMNOCFVLEEYAGPEPVILIGLHSDVDC 76
OY 61 GRTKLLTGEAGATFVFIIDEATGNHVTXSLDREKAQYVLLAQAVDRASRPLPEPSEF 120
Db 77 GRTKLLTGEAGATFVFIIDEATGNHVTXSLDREKAQYVLLAQAVDRASRPLPEPSEF 136
OY 121 IIKGODINDNPPFELGPYHATVPMSNVGTSIVIOATHADDPBSYNSAKLVYTVLDGL 180
Db 137 IIKVQDINDNPPFELGPYHATVPMSNVGTSIVIOATHADDPBSYNSAKLVYTVLDGL 196
OY 181 PEFSDVDPQTGVARTIIPMMDETQEEFLVYIAKMGHMGSLGSSITVYVTLSPVNNP 240
Db 197 PEFSDVDPQTGVARTIIPMMDETQEEFLVYIAKMGHMGSLGSSITVYVTLSPVNNP 256
OY 241 PKFPOSTIQFSVETAGPGLVGRFACDPDLDGNALMAYSILDEGEAIFSITDLOGR 300
Db 257 PKFPOSTIQFSVETAGPGLVGRFACDPDLDGNALMAYSILDEGEAIFSITDLOGR 316
OY 301 DGLLTVRKRLDEQSORSYSFRVEATNTLIDPAYLRGPCKDVASVRVAVODAPBPAPFTQ 360
Db 317 DGLLTVRKRLDEQSORSYSFRVEATNTLIDPAYLRGPCKDVASVRVAVODAPBPAPFTQ 376
OY 361 AAYHULTVENKAPGTLVGOISAADLDPSPASPIRYSILPHSDDERCFSTLOPEGTHTTAP 420
Db 377 AAYHULTVENKAPGTLVGOISAADLDPSPASPIRYSILPHSDDERCFSTLOPEGTHTTAP 436
OY 421 LDREBARAHNLTVLTELGMSWGPBERGWVLLVAEWSABAPAPQSSPVGSAVGIPODSSA 480
Db 437 LDREBARAHNLTVLTELGMSWGPBERGWVLLVAEWSABAPAPQSSPVGSAVGIPODSSA 496
OY 481 QASRYOVAIQTILDENDNAPQLAEFYDTFVCDSPAAPQOLIQVIRALDRDEVGNSSHVSFOG 540
Db 459 QASRYOVAIQTILDENDNAPQLAEFYDTFVCDSPAAPQOLIQVIRALDRDEVGNSSHVSFOG 518
OY 541 PLGPDANFTYQDNED-----LPA-----WFHPLMASSSMWLH--- 573
Db 519 PLGPDANFTYQDNEDDSSAILPFSRBPAPRHAYLVFIELMDWGOPALSTIAITVVSVC 578

```

Db 579 CQPDGSVASCWPEAHLISAAGLSTG 602

RESULT 15

ID ADB99722 standard; protein; 781 AA.

AC ADB99722;

DT 04-DEC-2003 (first entry)

DE Human PRO polypeptide SEQ ID 98.

KM Human; PEO; secreted polypeptide; transmembrane polypeptide;
KM tumour necrosis factor- α ; TNF- α ; blood; chondrocyte cell; tumour
KM adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
KM microvascular endothelial cell; endothelial cell tube formation;
KM sports-related joint problem; articular cartilage disease; osteoarthritis
KM rheumatoid arthritis; osteoporotic; antirheumatic; antiarthritic.

Homo sapiens.

PN US2003082728-A1.

PD 01-MAY-2003

PF 16-SEP-2002; 2002US-00245185.

PR 07-JUL-1998; 98US-0091978P.

PR 25-AUG-1999; 99US-00380137.

PR 18-JUL-2002; 2002US-00197942.

PA (GETH) GENENTECH INC.

PI Baker KP, Eaton DL, Filvarco

PI Fong S;

DR WPT; 2003-743898/70.

XX
XX

PT acids, useful for diagnosing, preventing and/or creating tumors, such as lung, colon, breast, prostate, rectal, kidney or liver tumors.

XX
PS
Claim 11: Fied 98: 308pp: English.

XX The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptides or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for inducing endothelial cell
CC tube formation and for treating sports-related joint problems, articular
CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
CC represents a human PRO polypeptide of the invention.

xx
xx
Sequence 781 AA

Query Match 81.4%; Score 2651.5; DB 7; Length 781;
Best Local Similarity 84.5%; Pred. No. 7e-218;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

```
QY 1 CMGRLAAPARAWAGREHPGALLRTRSWWNOFVIEEYASGPETLIGLHSDVDGE 60
   |||
Db 17 CMGRLAAPARAWAGREHPGALLRTRSWWNOFVIEEYASGPETLIGLHSDVDGE 76
   |||
QY 61 GRTKYLITGEGAGTVFVIDEATGNIVHTKSLDREKAYVLLAQAVDRASNRPLEPSEF 120
   |||
Db 77 GRTKYLITGEGAGTVFVIDEATGNIVHTKSLDREKAYVLLAQAVDRASNRPLEPSEF 136
   |||
QY 121 IIKGODINDNPFIFPLGPHATPEMNGSVTQVTAHADDPSTYGNSAKLYTVLDGL 180
   |||
Db 137 IIKVODINDNPFIFPLGPHATPEMNGSVTQVTAHADDPSTYGNSAKLYTVLDGL 196
   |||
QY 181 PFFSVDPQTGVYRTAIPMDRETOEEFLVVIQAKDMGSHNGSLGSTTVTLSDVNDP 240
   |||
Db 197 PFFSVDPQTGVYRTAIPMDRETOEEFLVVIQAKDMGSHNGSLGSTTVTLSDVNDP 256
   |||
QY 241 PKFPOSILYQFSVETAGGTLVGRRAQDPDLGNALMAYSILDGEGSEAFSISTDLQGR 300
   |||
Db 257 PKFPOSILYQFSVETAGGTLVGRRAQDPDLGNALMAYSILDGEGSEAFSISTDLQGR 316
   |||
QY 301 DGLLTVRKPLDFESQASYSFVEATNTLIDPAYLRGPFKDVASVRVAVODAPEPPAFQ 360
   |||
Db 317 DGLLTVRKPLDFESQASYSFVEATNTLIDPAYLRGPFKDVASVRVAVODAPEPPAFQ 376
   |||
QY 361 AAHLYTVENKAPGTLVGOISADLDSPPASPIRYSILPHSDPERCFISIQPEEGTIHTAP 420
   |||
Db 377 AAHLYTVENKAPGTLVGOISADLDSPPASPIRYSILPHSDPERCFISIQPEEGTIHTAP 436
   |||
QY 421 LDRERAMHNLTVLATELGMSWGPGRGVPLVAEMGAPAPAPQRPVSAGVIRQDSSA 480
   |||
Db 437 LDRERAMHNLTVLATEL-----DSSA 458
   |||
QY 481 QASRVQVAIOTLDENDNAPOLAEPYDTFVQDSAPGQLIQVIRALDRDEVGNSSHYVFOG 540
   |||
Db 459 QASRVQVAIOTLDENDNAPOLAEPYDTFVQDSAPGQLIQVIRALDRDEVGNSSHYVFOG 518
   |||
QY 541 PLGPDANFTVQDNRD-----LPA-----WFHPLMASASSWLH--- 573
   |||
Db 519 PLGPDANFTVQDNRDGASLLPSRPAFPRHAPYLVIEIWDWGQPALSTATVTVSVGR 578
   |||
QY 574 -----WPPAERGNQAPASOG 587
   |||
Db 579 COPDGSVASCWPEAHLASAAGLSTG 602
   |||
```

Search completed: December 8, 2004, 10:13:04
Job time : 257.564 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 10:13:18 ; Search time 633.542 Seconds
(Without alignments)
349.544 Million cell updates/sec

Title: US-09-788-051-7
Perfect score: 3259
Sequence: 1 CMGRAPARAWAGREHPG.....LPSCQPLGIPALGIVLCAS 620

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

1:	/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2:	/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5:	/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6:	/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7:	/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8:	/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9:	/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10:	/cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11:	/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12:	/cgn2_6/ptodata/1/pubpaa/US09C_NEW_PUB.pep:*
13:	/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
14:	/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15:	/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16:	/cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17:	/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
18:	/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
------------	-------	-------------	--------	-------	-------------

1	3259	100.0	620	10	US-09-788-051-7
2	3259	100.0	636	10	US-09-788-051-4
3	2651.5	81.4	781	9	US-09-860-866-2
4	2651.5	81.4	781	14	US-10-245-752-98
5	2651.5	81.4	781	14	US-10-245-659-98
6	2651.5	81.4	781	14	US-10-245-103-98
7	2651.5	81.4	781	14	US-10-245-107-98
8	2651.5	81.4	781	14	US-10-245-143-98
9	2651.5	81.4	781	14	US-10-245-771-98
10	2651.5	81.4	781	14	US-10-245-851-98
11	2651.5	81.4	781	14	US-10-245-883-98
12	2651.5	81.4	781	14	US-10-237-535-98

14	2651.5	81.4	781	14	US-10-238-283-98	Sequence 98, Appl
15	2651.5	81.4	781	14	US-10-238-370-98	Sequence 98, Appl
16	2651.5	81.4	781	14	US-10-245-055-98	Sequence 98, Appl
17	2651.5	81.4	781	14	US-10-245-147-98	Sequence 98, Appl
18	2651.5	81.4	781	14	US-10-245-730-98	Sequence 98, Appl
19	2651.5	81.4	781	14	US-10-245-739-98	Sequence 98, Appl
20	2651.5	81.4	781	14	US-10-246-210-98	Sequence 98, Appl
21	2651.5	81.4	781	14	US-10-239-196-98	Sequence 98, Appl
22	2651.5	81.4	781	14	US-10-243-024-98	Sequence 98, Appl
23	2651.5	81.4	781	14	US-10-243-409-98	Sequence 98, Appl
24	2651.5	81.4	781	14	US-10-245-821-98	Sequence 98, Appl
25	2651.5	81.4	781	14	US-10-245-880-98	Sequence 98, Appl
26	2651.5	81.4	781	14	US-10-245-033-98	Sequence 98, Appl
27	2651.5	81.4	781	14	US-10-243-095-98	Sequence 98, Appl
28	2651.5	81.4	781	14	US-10-245-185-98	Sequence 98, Appl
29	2651.5	81.4	781	14	US-10-245-427-98	Sequence 98, Appl
30	2651.5	81.4	781	14	US-10-245-473-98	Sequence 98, Appl
31	2651.5	81.4	781	14	US-10-245-770-98	Sequence 98, Appl
32	2651.5	81.4	781	14	US-10-245-877-98	Sequence 98, Appl
33	2651.5	81.4	781	14	US-10-246-976-98	Sequence 98, Appl
34	2651.5	81.4	781	14	US-10-243-320-98	Sequence 98, Appl
35	2651.5	81.4	781	14	US-10-162-435-13	Sequence 98, Appl
36	2651.5	81.4	781	14	US-10-242-743-98	Sequence 98, Appl
37	2651.5	81.4	781	14	US-10-237-636-98	Sequence 98, Appl
38	2651.5	81.4	781	14	US-10-238-325-98	Sequence 98, Appl
39	2651.5	81.4	781	14	US-10-238-346-98	Sequence 98, Appl
40	2651.5	81.4	781	14	US-10-238-411-98	Sequence 98, Appl
41	2651.5	81.4	781	14	US-10-243-124-98	Sequence 98, Appl
42	2651.5	81.4	781	14	US-10-243-425-98	Sequence 98, Appl
43	2651.5	81.4	781	14	US-10-243-446-98	Sequence 98, Appl
44	2651.5	81.4	781	14	US-10-245-874-98	Sequence 98, Appl
45	2651.5	81.4	781	14	US-10-245-874-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-09-788-051-7
; Sequence 7, Application US/09788051
; Publication No. US20030144491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dmanac, Radolje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES A
; FILE REFERENCE: HYS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 100.0%; Score 3259; DB 10; Length 620;
Best Local Similarity 100.0%; Pred. No. 8.3e-233; Indels 0; Gaps 0;
Matches 620; Conservative 0; Mismatches 0;
CY 1 CMGRAPARAWAGREHPALTRRRSMWVNFVIEYAGPEPVLLIGKLSVDVDRSE 60

Db 1 CMGRILAAPARAMAGSREHHPGALLTRRSWVWNOFVIEEYAGEPVLIGKLSHDVDRGE 60
 Qy 61 GRTKYLITGEGAGTVFVIDEATGNIHVTKSLDREKQAYVLLAQAVDASNRPLEPSEF 120
 Db 61 GRTKYLITGEGAGTVFVIDEATGNIHVTKSLDREKQAYVLLAQAVDASNRPLEPSEF 120
 Qy 121 IIKGODINDNPPILFPGYHATVEMSVGTSVQVTAHADDDPSYGNASLYTVVDGL 180
 Db 121 IIKGODINDNPPILFPGYHATVEMSVGTSVQVTAHADDDPSYGNASLYTVVDGL 180
 Qy 181 PFFSVDPOTGVVTRTALPMMDRETOEEFLVVIQAADMGGHGGSGSTTVTLSDVNDP 240
 Db 181 PFFSVDPOTGVVTRTALPMMDRETOEEFLVVIQAADMGGHGGSGSTTVTLSDVNDP 240
 Qy 241 PKFPOSLYQFSVETAGGTLVGRRAQDDPLGNALMAYSILDGEGSEAFSISTDLQGR 300
 Db 241 PKFPOSLYQFSVETAGGTLVGRRAQDDPLGNALMAYSILDGEGSEAFSISTDLQGR 300
 Qy 301 DGLTVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFVDVASVRAVODAPPAFTQ 360
 Db 301 DGLTVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFVDVASVRAVODAPPAFTQ 360
 Qy 361 AAHLTVENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSTIOEEGTHTAAP 420
 Db 361 AAHLTVENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSTIOEEGTHTAAP 420
 Qy 421 LDREARAHNLTVLATELGMSWGERGMVPLVAEMSAAPAPORSFVGSAGVIGPOSSA 480
 Db 421 LDREARAHNLTVLATELGMSWGERGMVPLVAEMSAAPAPORSFVGSAGVIGPOSSA 480
 Qy 481 QASRVOVAIQTLDENNDAPOLAEFYDTFVCDASAPGQLIVIRALDRDEVGNSSHVSFOG 540
 Db 481 QASRVOVAIQTLDENNDAPOLAEFYDTFVCDASAPGQLIVIRALDRDEVGNSSHVSFOG 540
 Qy 541 PLGPDANFTVODNDLDAWHPHPLMASASSWLHMPERGNOPASOGKSSSLPCGRLPGA 600
 Db 541 PLGPDANFTVODNDLDAWHPHPLMASASSWLHMPERGNOPASOGKSSSLPCGRLPGA 600
 Qy 601 LPSCQLPLGIPALGIVLCAS 620
 Db 601 LPSCQLPLGIPALGIVLCAS 620

RESULT 2
 US-09-788-051-4
 ; Sequence 4, Application US/09788051
 ; Publication No. US20030144491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Godbole, Shubhada D
 ; APPLICANT: Kuo, Chiaoyn
 ; APPLICANT: Ateeburn, Matthew C
 ; APPLICANT: Yeung, George
 ; APPLICANT: Palencia, Servando
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Liu, Chenchua
 ; APPLICANT: Dramac, Radoje T
 ; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN
 ; FILE REFERENCE: HYS-39
 ; CURRENT APPLICATION NUMBER: US/09/788,051
 ; PRIOR FILING DATE: 2001-02-16
 ; PRIOR APPLICATION NUMBER: US 09/560,875
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: US 09/496,914
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 636
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-788-051-4

Query Match 100.0%; Score 3259; DB 10; Length 636;
 Best Local Similarity 100.0%; Pred. No. 8,7e-233;
 Matches 620; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMGRILAAPARAMAGSREHHPGALLTRRSWVWNOFVIEEYAGEPVLIGKLSHDVDRGE 60
 Db 17 CMGRILAAPARAMAGSREHHPGALLTRRSWVWNOFVIEEYAGEPVLIGKLSHDVDRGE 76
 Qy 61 GRTKYLITGEGAGTVFVIDEATGNIHVTKSLDREKQAYVLLAQAVDASNRPLEPSEF 120
 Db 77 GRTKYLITGEGAGTVFVIDEATGNIHVTKSLDREKQAYVLLAQAVDASNRPLEPSEF 136
 Qy 121 IIKGODINDNPPILFPGYHATVEMSVGTSVQVTAHADDDPSYGNASLYTVVDGL 180
 Db 137 IIKGODINDNPPILFPGYHATVEMSVGTSVQVTAHADDDPSYGNASLYTVVDGL 196
 Qy 181 PFFSVDPOTGVVTRTALPMMDRETOEEFLVVIQAADMGGHGGSGSTTVTLSDVNDP 240
 Db 197 PFFSVDPOTGVVTRTALPMMDRETOEEFLVVIQAADMGGHGGSGSTTVTLSDVNDP 256
 Qy 241 PKFPOSLYQFSVETAGGTLVGRRAQDDPLGNALMAYSILDGEGSEAFSISTDLQGR 300
 Db 257 PKFPOSLYQFSVETAGGTLVGRRAQDDPLGNALMAYSILDGEGSEAFSISTDLQGR 316
 Qy 301 DGLTVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFVDVASVRAVODAPPAFTQ 360
 Db 317 DGLTVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFVDVASVRAVODAPPAFTQ 376
 Qy 361 AAHLTVENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSTIOEEGTHTAAP 420
 Db 377 AAHLTVENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSTIOEEGTHTAAP 436
 Qy 421 LDREARAHNLTVLATELGMSWGERGMVPLVAEMSAAPAPORSFVGSAGVIGPOSSA 480
 Db 437 LDREARAHNLTVLATELGMSWGERGMVPLVAEMSAAPAPORSFVGSAGVIGPOSSA 496
 Qy 481 QASRVOVAIQTLDENNDAPOLAEFYDTFVCDASAPGQLIVIRALDRDEVGNSSHVSFOG 540
 Db 497 QASRVOVAIQTLDENNDAPOLAEFYDTFVCDASAPGQLIVIRALDRDEVGNSSHVSFOG 556
 Qy 541 PLGPDANFTVODNDLDAWHPHPLMASASSWLHMPERGNOPASOGKSSSLPCGRLPGA 600
 Db 557 PLGPDANFTVODNDLDAWHPHPLMASASSWLHMPERGNOPASOGKSSSLPCGRLPGA 616
 Qy 601 LPSCQLPLGIPALGIVLCAS 620
 Db 617 LPSCQLPLGIPALGIVLCAS 636

RESULT 3
 US-09-860-868-2
 ; Sequence 2, Application US/09860868
 ; Patent No. US20020076757A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Curtis, Roy A. J.
 ; TITLE OF INVENTION: 57805, A NOVEL HUMAN CADHERIN FAMILY
 ; FILE REFERENCE: 10448-050001
 ; CURRENT APPLICATION NUMBER: US/09/860,868
 ; PRIOR FILING DATE: 2001-05-18
 ; PRIOR APPLICATION NUMBER: 60/205,674
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 781
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-860-868-2

Query Match 81.4%; Score 2651.5; DB 9; Length 781;
 Best Local Similarity 84.5%; Pred. No. 1.3e-187;
 Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

```
QY 1 CMGRLAAPARAWAGSREHGPALLTRRSWVWNOFFVIEEYAPPEVILIGLHSDVDGE 60
DB 17 CMGRLAAPARAWAGSREHGPALLTRRSWVWNOFFVIEEYAPPEVILIGLHSDVDGE 76
QY 61 GRTKYLLTGEAGTAVFIDEATGNHVTXSLDREKAQVYLLAQVDRASNRPLEPSEF 120
DB 77 GRTKYLLTGEAGTAVFIDEATGNHVTXSLDREKAQVYLLAQVDRASNRPLEPSEF 136
QY 121 IIKGODINDNPIFELGPHATVPEMSNVGTSVIOVTAHADDPSSYNSAKLYVTLDDGL 180
DB 137 IIKVODINDNPIFELGPHATVPEMSNVGTSVIOVTAHADDPSSYNSAKLYVTLDDGL 196
QY 181 PFESVDPQGTGVRTAIPNMDRETOEELVYIOAKMGHMGGLSGSTTVTLSDVNDNF 240
DB 197 PFESVDPQGTGVRTAIPNMDRETOEELVYIOAKMGHMGGLSGSTTVTLSDVNDNF 256
QY 241 PKFPOSIVQFSVETAGPGLVGRLAQDPDLGNALMAYSLDGESEAFSISTDLQGR 300
DB 257 PKFPOSIVQFSVETAGPGLVGRLAQDPDLGNALMAYSLDGESEAFSISTDLQGR 316
QY 301 DGLITVRKPLDPESSQSYSEFVEATNTLIDPAYLRGPFXDVASVRVAVODAEPPAFIQ 360
DB 317 DGLITVRKPLDPESSQSYSEFVEATNTLIDPAYLRGPFXDVASVRVAVODAEPPAFIQ 376
QY 361 AAYHITVPEKAPGLTVGOISADLDSPASPIRYSILPHSDPERCFSIOPEEGTHTAAP 420
DB 377 AAYHITVPEKAPGLTVGOISADLDSPASPIRYSILPHSDPERCFSIOPEEGTHTAAP 436
QY 421 LDREARAHNLTVALTELGMWGMPERGVPFLVLAEMSAAPAPQPSVAGSIVGIPDSSA 480
DB 437 LDREARAHNLTVALTELGMWGMPERGVPFLVLAEMSAAPAPQPSVAGSIVGIPDSSA 496
QY 481 QASRVOVAIOTLDENNAPOLAEPYDTFVCDSPAAGQIQTIVRALDDEVGNSSHVSFOG 540
DB 499 QASRVOVAIOTLDENNAPOLAEPYDTFVCDSPAAGQIQTIVRALDDEVGNSSHVSFOG 558
QY 541 PLGPDANTVQDND-----LPA-----WFHPLMASASSMLH--- 573
DB 519 PLGPDANTVQDNDGASALLPSRPAPRHAPVLPVLEIMWQGPALSTATVTVSVCR 578
QY 574 -----WPPAERGNOPASOG 587
DB 579 QCPDGSVASCWPEAHLSAAGLSTG 602

RESULT 4
US-10-245-752-98
; Sequence 98, Application US/10245752
; Publication No. US20030064473A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watande, Collin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630RJC66
; CURRENT APPLICATION NUMBER: US/10/245,752
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
```

```
QY 1 CMGRLAAPARAWAGSREHGPALLTRRSWVWNOFFVIEEYAPPEVILIGLHSDVDGE 60
DB 17 CMGRLAAPARAWAGSREHGPALLTRRSWVWNOFFVIEEYAPPEVILIGLHSDVDGE 76
QY 61 GRTKYLLTGEAGTAVFIDEATGNHVTXSLDREKAQVYLLAQVDRASNRPLEPSEF 120
DB 77 GRTKYLLTGEAGTAVFIDEATGNHVTXSLDREKAQVYLLAQVDRASNRPLEPSEF 136
QY 121 IIKGODINDNPIFELGPHATVPEMSNVGTSVIOVTAHADDPSSYNSAKLYVTLDDGL 180
DB 137 IIKVODINDNPIFELGPHATVPEMSNVGTSVIOVTAHADDPSSYNSAKLYVTLDDGL 196
QY 181 PFESVDPQGTGVRTAIPNMDRETOEELVYIOAKMGHMGGLSGSTTVTLSDVNDNF 240
DB 197 PFESVDPQGTGVRTAIPNMDRETOEELVYIOAKMGHMGGLSGSTTVTLSDVNDNF 256
QY 241 PKFPOSIVQFSVETAGPGLVGRLAQDPDLGNALMAYSLDGESEAFSISTDLQGR 300
DB 257 PKFPOSIVQFSVETAGPGLVGRLAQDPDLGNALMAYSLDGESEAFSISTDLQGR 316
QY 301 DGLITVRKPLDPESSQSYSEFVEATNTLIDPAYLRGPFXDVASVRVAVODAEPPAFIQ 360
DB 317 DGLITVRKPLDPESSQSYSEFVEATNTLIDPAYLRGPFXDVASVRVAVODAEPPAFIQ 376
QY 361 AAYHITVPEKAPGLTVGOISADLDSPASPIRYSILPHSDPERCFSIOPEEGTHTAAP 420
DB 377 AAYHITVPEKAPGLTVGOISADLDSPASPIRYSILPHSDPERCFSIOPEEGTHTAAP 436
QY 421 LDREARAHNLTVALTELGMWGMPERGVPFLVLAEMSAAPAPQPSVAGSIVGIPDSSA 480
DB 437 LDREARAHNLTVALTELGMWGMPERGVPFLVLAEMSAAPAPQPSVAGSIVGIPDSSA 496
QY 481 QASRVOVAIOTLDENNAPOLAEPYDTFVCDSPAAGQIQTIVRALDDEVGNSSHVSFOG 540
DB 499 QASRVOVAIOTLDENNAPOLAEPYDTFVCDSPAAGQIQTIVRALDDEVGNSSHVSFOG 558
QY 541 PLGPDANTVQDND-----LPA-----WFHPLMASASSMLH--- 573
DB 519 PLGPDANTVQDNDGASALLPSRPAPRHAPVLPVLEIMWQGPALSTATVTVSVCR 578
QY 574 -----WPPAERGNOPASOG 587
DB 579 QCPDGSVASCWPEAHLSAAGLSTG 602

RESULT 5
US-10-245-752-98
Query Match 81.4%; Score 2651.5; DB 14; Length 781;
Best Local Similarity 84.5%; Pred. No. 1.3e-187;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
;
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
;
; US-10-245-752-98
```

US-10-245-859-98
; Sequence 98, Application US/10245859
; Publication No. US20030064474A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Macanbe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C78
; CURRENT APPLICATION NUMBER: US/10/245, 859
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/066478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-859-98

Query Match 81.4%; Score 2651.5; DB 14; Length 781;
Best Local Similarity 84.5%; Pred. No. 1.3e-187;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 CMGRLAARAMAGSRHPPALLRTRRSMVNNQFVIERAGPEVLLGKLSHDVDRGE 60
DB 17 CMGRLAARAMAGSRHPPALLRTRRSMVNNQFVIERAGPEVLLGKLSHDVDRGE 76
QY 61 GRTKYLITGEGAGTVEIDEATGNIVHTKSLDSEERKAQVLLAQAADRASNRPLEPSEPF 120
DB 77 GRTKYLITGEGAGTVEIDEATGNIVHTKSLDSEERKAQVLLAQAADRASNRPLEPSEPF 136
QY 121 IIRGQDINDNPPFPLGPHYATVPEMSNGTSTVQTAHADDDPSYGNSAKIYTVLDEL 180
DB 137 IIRGQDINDNPPFPLGPHYATVPEMSNGTSTVQTAHADDDPSYGNSAKIYTVLDEL 196
QY 181 PFESVDPQTSVATAPNMDRETQEEFLVVIQAKMGKMGAGLSSGTTVTTLSDVNMP 240
DB 197 PFESVDPQTSVATAPNMDRETQEEFLVVIQAKMGKMGAGLSSGTTVTTLSDVNMP 256
QY 241 PKPFSQIYQPSVETVAGPGLVGRRAQDPDLDGNALMAYSLDGESEAFSISTDLOGR 300
DB 257 PKPFSQIYQPSVETVAGPGLVGRRAQDPDLDGNALMAYSLDGESEAFSISTDLOGR 316

QY 301 DGLITVRKLPDESORSYFRYEATNTLLIDPAYLRKGFVKQVAVRVAODAPPPATQ 360
DB 317 DGLITVRKLPDESORSYFRYEATNTLLIDPAYLRKGFVKQVAVRVAODAPPPATQ 376
QY 361 AAYHLTVENKAPGLVQOISADIDSPASPIRYSILPHSDPERCFSIQPEEGTHTAP 420
DB 377 AAYHLTVENKAPGLVQOISADIDSPASPIRYSILPHSDPERCFSIQPEEGTHTAP 436
QY 421 LDREARAWNTLVLTATELGWMSGPGRGVPLLVNEMSAFAPRQSPVGSVAVGIPQSSA 480
DB 437 LDREARAWNTLVLTATELGWMSGPGRGVPLLVNEMSAFAPRQSPVGSVAVGIPQSSA 458
QY 481 QASRVOVAIOTLIDENDNAPOLAEPYDTFVCDAAFGOLIQVIRALDRDEVGNSSHVSFOG 540
DB 459 QASRVOVAIOTLIDENDNAPOLAEPYDTFVCDAAFGOLIQVIRALDRDEVGNSSHVSFOG 518
QY 541 PEGPANTVQDNRP-----LPA-----WPHPLMASASSMHL--- 573
DB 519 PEGPANTVQDNRPQSGASLLPSPAPRHAFLVPIELMDWQOPALSTATVTSYCR 578
QY 574 -----WPPARGNQPPASOG 587
DB 579 CQPDGSVASCPPEAHLASAAGLSTG 602

RESULT 6
US-10-245-103-98
; Sequence 98, Application US/10245103
; Publication No. US20030068778A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Macanbe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C12
; CURRENT APPLICATION NUMBER: US/10/245, 103
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien

Wed Dec 8 11:46:33 2004

us-09-788-051-7.rapb

US-10-245-103-98

Query Match 81.4%; Score 2651.5; DB 14; Length 781;
Best Local Similarity 84.5%; Pred. No. 1.3e-187;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 CMGRLAAPARAWAGSREHPGALLTRRSVMWNOFVIEEYAGPEPVILGKLSVDVDRGE 60
DB 17 CMGRLAAPARAWAGSREHPGALLTRRSVMWNOFVIEEYAGPEPVILGKLSVDVDRGE 76
QY 61 GRTKYLLTGEAGATVVIDEATGNHVTKSLDREKQYVLLAQVDRASNPPLPSEF 120
DB 77 GRTKYLLTGEAGATVVIDEATGNHVTKSLDREKQYVLLAQVDRASNPPLPSEF 136
QY 121 IIKQDINDNPPFLPGYHATVPEMSNVGTSVIQVTAHDADPSYNSAKLYTVLDGL 180
DB 137 IIKQDINDNPPFLPGYHATVPEMSNVGTSVIQVTAHDADPSYNSAKLYTVLDGL 196
QY 181 PFEVSVDQGTGVRTAIPMDRETEEFLLVVIQAKDMGGMGGLSGSTTVTLISDVNDP 240
DB 197 PFEVSVDQGTGVRTAIPMDRETEEFLLVVIQAKDMGGMGGLSGSTTVTLISDVNDP 256
QY 241 PKFQSLYQFSVETAGPGLVGRRAODPDLGNALMAYSLDGESEAFSISTDLQGR 300
DB 257 PKFQSLYQFSVETAGPGLVGRRAODPDLGNALMAYSLDGESEAFSISTDLQGR 316
QY 301 DGLLTVRKPLDFFESQSYSEFRVEATNTLIDPAYLRGPFKDVASVVAQDAPEPPAFQ 360
DB 317 DGLLTVRKPLDFFESQSYSEFRVEATNTLIDPAYLRGPFKDVASVVAQDAPEPPAFQ 376
QY 361 AAYHLTVPENKAPGTLVGOISAADLDSAPSPIRYSILPHSDPERCSIQPEEGITHTAAP 420
DB 377 AAYHLTVPENKAPGTLVGOISAADLDSAPSPIRYSILPHSDPERCSIQPEEGITHTAAP 436
QY 421 LDREARAHNLTVLATELGSMGPERGWVPLVAEWSAPAAPQSPVSAVGIPODSSA 480
DB 437 LDREARAHNLTVLATELGSMGPERGWVPLVAEWSAPAAPQSPVSAVGIPODSSA 498
QY 481 QASRVQVAIQTLDENNDNAPQLAEPYDTFVCDSPAAPQOLIQVIRALDRDEVGNSSHVFOG 540
DB 499 QASRVQVAIQTLDENNDNAPQLAEPYDTFVCDSPAAPQOLIQVIRALDRDEVGNSSHVFOG 518
QY 541 PLGPDANFTVQDNRD-----LPA-----WPHFLMASASSMH--- 573
DB 519 PLGPDANFTVQDNRDGSASLLPSRPAAPRPAHAPVILVIELMDWQOPALSSATATVYSVCR 578
QY 574 -----WPAERGNQPASOG 587
DB 579 CQPDGVSACWPEALHLSAAGLSTG 602

RESULT 7
US-10-245-107-98
Sequence 98, Application US/10245107
Publication No. US20030068779A1

GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Matembe, Collin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C71
CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-107-98

Query Match 81.4%; Score 2651.5; DB 14; Length 781;
Best Local Similarity 84.5%; Pred. No. 1.3e-187;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 CMGRLAAPARAWAGSREHPGALLTRRSVMWNOFVIEEYAGPEPVILGKLSVDVDRGE 60
DB 17 CMGRLAAPARAWAGSREHPGALLTRRSVMWNOFVIEEYAGPEPVILGKLSVDVDRGE 76
QY 61 GRTKYLLTGEAGATVVIDEATGNHVTKSLDREKQYVLLAQVDRASNPPLPSEF 120
DB 77 GRTKYLLTGEAGATVVIDEATGNHVTKSLDREKQYVLLAQVDRASNPPLPSEF 136
QY 121 IIKQDINDNPPFLPGYHATVPEMSNVGTSVIQVTAHDADPSYNSAKLYTVLDGL 180
DB 137 IIKQDINDNPPFLPGYHATVPEMSNVGTSVIQVTAHDADPSYNSAKLYTVLDGL 196
QY 181 PFEVSVDQGTGVRTAIPMDRETEEFLLVVIQAKDMGGMGGLSGSTTVTLISDVNDP 240
DB 197 PFEVSVDQGTGVRTAIPMDRETEEFLLVVIQAKDMGGMGGLSGSTTVTLISDVNDP 256
QY 241 PKFQSLYQFSVETAGPGLVGRRAODPDLGNALMAYSLDGESEAFSISTDLQGR 300
DB 257 PKFQSLYQFSVETAGPGLVGRRAODPDLGNALMAYSLDGESEAFSISTDLQGR 316
QY 301 DGLLTVRKPLDFFESQSYSEFRVEATNTLIDPAYLRGPFKDVASVVAQDAPEPPAFQ 360
DB 317 DGLLTVRKPLDFFESQSYSEFRVEATNTLIDPAYLRGPFKDVASVVAQDAPEPPAFQ 376
QY 361 AAYHLTVPENKAPGTLVGOISAADLDSAPSPIRYSILPHSDPERCSIQPEEGITHTAAP 420
DB 377 AAYHLTVPENKAPGTLVGOISAADLDSAPSPIRYSILPHSDPERCSIQPEEGITHTAAP 436
QY 421 LDREARAHNLTVLATELGSMGPERGWVPLVAEWSAPAAPQSPVSAVGIPODSSA 480
DB 437 LDREARAHNLTVLATELGSMGPERGWVPLVAEWSAPAAPQSPVSAVGIPODSSA 498
QY 481 QASRVQVAIQTLDENNDNAPQLAEPYDTFVCDSPAAPQOLIQVIRALDRDEVGNSSHVFOG 540
DB 499 QASRVQVAIQTLDENNDNAPQLAEPYDTFVCDSPAAPQOLIQVIRALDRDEVGNSSHVFOG 518
QY 541 PLGPDANFTVQDNRD-----LPA-----WPHFLMASASSMH--- 573
DB 519 PLGPDANFTVQDNRDGSASLLPSRPAAPRPAHAPVILVIELMDWQOPALSSATATVYSVCR 578
QY 574 -----WPAERGNQPASOG 587

Db 579 COPDGSVASCWPEAHLASAAGLSTG 602

RESULT 8

US-10-245-143-98
Sequence 98, Application US/10245143
Publication No. US20030068780A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C90
CURRENT FILING DATE: 2002-09-16
PRIORITY FILING DATE: 2002-09-16
PRIORITY FILING DATE: 2002-07-18
PRIORITY FILING DATE: 2002-07-18
PRIORITY FILING DATE: 1997-09-17
PRIORITY FILING DATE: 1997-10-24
PRIORITY FILING DATE: 1997-11-10
PRIORITY FILING DATE: 1998-03-27
PRIORITY FILING DATE: 1998-05-22
PRIORITY FILING DATE: 1998-06-02
PRIORITY FILING DATE: 1998-06-18
PRIORITY FILING DATE: 1998-06-24
PRIORITY FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
SEQUENCE ID NOS: 116
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-143-98

Query Match 81.4%; Score 2651.5; DB 14; Length 781;
Best Local Similarity 84.5%; Pred. No. 1.3e-187;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 CMGRLAAPARAMAGSREHPGALLRTRRSWVWQFVIEVYAGPEVLIGKLSVDRE 60
Db 17 CMGRLAAPARAMAGSREHPGALLRTRRSWVWQFVIEVYAGPEVLIGKLSVDRE 76
QY 61 GRKTYLLTGAGTAVVIDATNINHTKSLDREKAYVLLAQAVDRASNPLEPPSEF 120
Db 77 GRKTYLLTGAGTAVVIDATNINHTKSLDREKAYVLLAQAVDRASNPLEPPSEF 136
QY 121 IIGODINDNPFIFPGPYATVPEMSNGTSVIOVTADADPSGNSAKIVTVLGL 180
Db 137 IIVQDINDNPFIFPGPYATVPEMSNGTSVIOVTADADPSGNSAKIVTVLGL 196
QY 181 PFSVDPQGTGVVTAIPNDRETQEBFLVVIQAKMGHAGGLSGSTTVTVLSDVNDP 240
Db 197 PFSVDPQGTGVVTAIPNDRETQEBFLVVIQAKMGHAGGLSGSTTVTVLSDVNDP 256

QY 241 EKPQSLVQSVYETAGPGLTVGRRAODPLDGNALMAYSLDGESEAFSISTDLOGR 300
Db 257 EKPQSLVQSVYETAGPGLTVGRRAODPLDGNALMAYSLDGESEAFSISTDLOGR 316

QY 301 DELLTVRKLPDESGRSYFRVEATNTLIDPAYLRGPFKQVASYRVAQDAPEPAFTQ 360
Db 317 DELLTVRKLPDESGRSYFRVEATNTLIDPAYLRGPFKQVASYRVAQDAPEPAFTQ 376

QY 361 AAYHLLTVENKAPGLTVQIISAADLSPASPIRYSILHSDPERCFSLQPEEGITHAP 420
Db 377 AAYHLLTVENKAPGLTVQIISAADLSPASPIRYSILHSDPERCFSLQPEEGITHAP 436

QY 421 LDREARAHNLTIVLATELGWSGPERGWPLVLAWSAPAPQRPVGSVAVGIPDSSA 480
Db 437 LDREARAHNLTIVLATELGWSGPERGWPLVLAWSAPAPQRPVGSVAVGIPDSSA 458

QY 481 QASRYQVAIQITLDEMDNAPOLAEPIOTVCSSAPGQILQVIRALDRDEVNSSHVFSQ 540
Db 459 QASRYQVAIQITLDEMDNAPOLAEPIOTVCSSAPGQILQVIRALDRDEVNSSHVFSQ 518

QY 541 PLGPANFTVQDNRD-----LPA-----WPHPLMASASSMLH--- 573
Db 519 PLGPANFTVQDNRDGSALLPSRPAPFRAPVLPVLELMDQOPALSTAITVSVCR 578

QY 574 -----WPAERGNQPASQ 587
Db 579 COPDGSVASCWPEAHLASAAGLSTG 602

RESULT 9
US-10-245-771-98
Sequence 98, Application US/10245771
Publication No. US20030068781A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C98
CURRENT FILING DATE: 2002-09-16
PRIORITY FILING DATE: 2002-09-16
PRIORITY FILING DATE: 2002-07-18
PRIORITY FILING DATE: 2002-07-18
PRIORITY FILING DATE: 1997-09-17
PRIORITY FILING DATE: 1997-10-24
PRIORITY FILING DATE: 1997-11-10
PRIORITY FILING DATE: 1998-03-27
PRIORITY FILING DATE: 1998-05-22
PRIORITY FILING DATE: 1998-06-02
PRIORITY FILING DATE: 1998-06-18
PRIORITY FILING DATE: 1998-06-24
PRIORITY FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.

QY 241 EKPQSLVQSVYETAGPGLTVGRRAODPLDGNALMAYSLDGESEAFSISTDLOGR 300
Db 257 EKPQSLVQSVYETAGPGLTVGRRAODPLDGNALMAYSLDGESEAFSISTDLOGR 316
QY 301 DELLTVRKLPDESGRSYFRVEATNTLIDPAYLRGPFKQVASYRVAQDAPEPAFTQ 360
Db 317 DELLTVRKLPDESGRSYFRVEATNTLIDPAYLRGPFKQVASYRVAQDAPEPAFTQ 376
QY 361 AAYHLLTVENKAPGLTVQIISAADLSPASPIRYSILHSDPERCFSLQPEEGITHAP 420
Db 377 AAYHLLTVENKAPGLTVQIISAADLSPASPIRYSILHSDPERCFSLQPEEGITHAP 436
QY 421 LDREARAHNLTIVLATELGWSGPERGWPLVLAWSAPAPQRPVGSVAVGIPDSSA 480
Db 437 LDREARAHNLTIVLATELGWSGPERGWPLVLAWSAPAPQRPVGSVAVGIPDSSA 458
QY 481 QASRYQVAIQITLDEMDNAPOLAEPIOTVCSSAPGQILQVIRALDRDEVNSSHVFSQ 540
Db 459 QASRYQVAIQITLDEMDNAPOLAEPIOTVCSSAPGQILQVIRALDRDEVNSSHVFSQ 518
QY 541 PLGPANFTVQDNRD-----LPA-----WPHPLMASASSMLH--- 573
Db 519 PLGPANFTVQDNRDGSALLPSRPAPFRAPVLPVLELMDQOPALSTAITVSVCR 578
QY 574 -----WPAERGNQPASQ 587
Db 579 COPDGSVASCWPEAHLASAAGLSTG 602

NUMBER OF SEQ ID NOS: 116
 SEQ ID NO 98
 LENGTH: 781
 TYPE: PRT
 ORGANISM: Homo sapien
 US-10-245-771-98

Query Match 81.4%; Score 2651.5; DB 14; Length 781;
 Best Local Similarity 84.5%; Pred. No. 1.3e-187;
 Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

```

QY 1 CMGRLAPARAWASREHPGALLRTRRSWVNOFFVIEYAGPEPVLLGKLSVDVDRGE 60
DB 17 CMGRLAPARAWASREHPGALLRTRRSWVNOFFVIEYAGPEPVLLGKLSVDVDRGE 76
QY 61 GRTXYLLTGBGAGTVFVIDEATGNHVTKSLDREKKAQVYLLAQAVDRASNPLEPPSEF 120
DB 77 GRTXYLLTGBGAGTVFVIDEATGNHVTKSLDREKKAQVYLLAQAVDRASNPLEPPSEF 136
QY 121 IIKQDINDNPPIPLGPHYATVPEMSNVGTSVIQTVAHADDPSPYNSAKLVYTVLDGL 180
DB 137 IIKQDINDNPPIPLGPHYATVPEMSNVGTSVIQTVAHADDPSPYNSAKLVYTVLDGL 196
QY 181 PFEFSDPQTGVVTRTAIPMDRETOEFLVVIQAKMGGMGGLSGSTTVTVLSDVNDP 240
DB 197 PFEFSDPQTGVVTRTAIPMDRETOEFLVVIQAKMGGMGGLSGSTTVTVLSDVNDP 256
QY 241 PKFPOSIVQFSVETAGPGTLVGRLEAODPDLDGNALMAYSLIDGSGSAFSLSTDLQGR 300
DB 257 PKFPOSIVQFSVETAGPGTLVGRLEAODPDLDGNALMAYSLIDGSGSAFSLSTDLQGR 316
QY 301 DGLLTVRKPLDPEBSQSYSEFRVEATNTLIDPAYLRGPKVDVASVRAVQADAPPEPAFTQ 360
DB 317 DGLLTVRKPLDPEBSQSYSEFRVEATNTLIDPAYLRGPKVDVASVRAVQADAPPEPAFTQ 376
QY 361 AAYHLTVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCSIQPEEGTITTAAP 420
DB 377 AAYHLTVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCSIQPEEGTITTAAP 436
QY 421 LDREARAHNLTIVLATEL-----DSSA 458
DB 437 LDREARAHNLTIVLATEL-----DSSA 458
QY 481 QASRVOVAIQTLDENNAQOLAEPYDTFVCDSPAAPGQLIQVIRALDDEVGNSHVSFQG 540
DB 459 QASRVOVAIQTLDENNAQOLAEPYDTFVCDSPAAPGQLIQVIRALDDEVGNSHVSFQG 518
QY 541 PLGPDANFTVQDNRD-----LPA-----WHPPLMASASGWLH--- 573
DB 519 PLGPDANFTVQDNRDGASALLPSRPAAPRRAHYPLVPIELMDWQGFALSTATVAVSCR 578
QY 574 -----WPAERGNQPAASQ 587
DB 579 CQPDGCVASCPPEAHLSPAAGLSTG 602

```

```

QY 1 CMGRLAPARAWASREHPGALLRTRRSWVNOFFVIEYAGPEPVLLGKLSVDVDRGE 60
DB 17 CMGRLAPARAWASREHPGALLRTRRSWVNOFFVIEYAGPEPVLLGKLSVDVDRGE 76
QY 61 GRTXYLLTGBGAGTVFVIDEATGNHVTKSLDREKKAQVYLLAQAVDRASNPLEPPSEF 120
DB 77 GRTXYLLTGBGAGTVFVIDEATGNHVTKSLDREKKAQVYLLAQAVDRASNPLEPPSEF 136
QY 121 IIKQDINDNPPIPLGPHYATVPEMSNVGTSVIQTVAHADDPSPYNSAKLVYTVLDGL 180
DB 137 IIKQDINDNPPIPLGPHYATVPEMSNVGTSVIQTVAHADDPSPYNSAKLVYTVLDGL 196
QY 181 PFEFSDPQTGVVTRTAIPMDRETOEFLVVIQAKMGGMGGLSGSTTVTVLSDVNDP 240
DB 197 PFEFSDPQTGVVTRTAIPMDRETOEFLVVIQAKMGGMGGLSGSTTVTVLSDVNDP 256
QY 241 PKFPOSIVQFSVETAGPGTLVGRLEAODPDLDGNALMAYSLIDGSGSAFSLSTDLQGR 300
DB 257 PKFPOSIVQFSVETAGPGTLVGRLEAODPDLDGNALMAYSLIDGSGSAFSLSTDLQGR 316
QY 301 DGLLTVRKPLDPEBSQSYSEFRVEATNTLIDPAYLRGPKVDVASVRAVQADAPPEPAFTQ 360
DB 317 DGLLTVRKPLDPEBSQSYSEFRVEATNTLIDPAYLRGPKVDVASVRAVQADAPPEPAFTQ 376
QY 361 AAYHLTVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCSIQPEEGTITTAAP 420
DB 377 AAYHLTVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCSIQPEEGTITTAAP 436
QY 421 LDREARAHNLTIVLATEL-----DSSA 458
DB 437 LDREARAHNLTIVLATEL-----DSSA 458
QY 481 QASRVOVAIQTLDENNAQOLAEPYDTFVCDSPAAPGQLIQVIRALDDEVGNSHVSFQG 540
DB 459 QASRVOVAIQTLDENNAQOLAEPYDTFVCDSPAAPGQLIQVIRALDDEVGNSHVSFQG 518

```

RESULT 12
 US-10-237-535-98
 Sequence 98, Application US/10237535
 Publication No. US20030073188A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Eaton, Dan
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Smith, Victoria
 APPLICANT: Stephan, Jean-Philippe
 APPLICANT: Wetande, Colin
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 APPLICANT: Fong, Sherman
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRAN POLYPEPTIDES AND NUCLEOTIC
 FILE REFERENCE: P3630R1C3
 CURRENT APPLICATION NUMBER: US/10/237, 535
 CURRENT FILING DATE: 2002-09-06
 PRIOR APPLICATION NUMBER: 10/197942
 PRIOR FILING DATE: 2002-07-18
 PRIOR APPLICATION NUMBER: 60/059114
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/063046
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/065027
 PRIOR FILING DATE: 1997-11-10
 PRIOR APPLICATION NUMBER: 60/079689
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/086478
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18

Wed Dec 8 11:46:33 2004

us-09-788-051-7.rapb

Page 9

```

PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091358
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091976
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/106932
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/115554
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119342
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/123957
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123972
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: 60/127372
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/131271
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/133459
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/135725
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135729
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135750
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/138385
PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: 60/140653
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144732
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144790
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145228
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146843
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/148188
PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/148513
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/149327
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149395
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/150114
PRIOR FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: 60/151700
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/151734
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/170262
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/177118
PRIOR FILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: 60/179851

PRIOR FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 60/180921
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: 60/187202
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/198587
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 60/199614
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 60/206330
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206368
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/209832
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 60/218371
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/222695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/229896
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/230621
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/232887
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/235147
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/261878
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/261910
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/261939
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/262150
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/264395
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/266421
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/267623
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/274399
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/280982
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/282129
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/282199
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/290589
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 60/180997
PRIOR FILING DATE: 1998-11-19
PRIOR APPLICATION NUMBER: 60/267213
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 60/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 60/403297
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 60/423741
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: 60/709238
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/802706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/872035
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/924419
PRIOR FILING DATE: 2001-08-06
```

PRIOR APPLICATION NUMBER: 09/927796
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/929404
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 09/931836
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 09/941992
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 09/946374
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 10/001054
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 10/025866
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 10/081056
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: 10/119480
PRIOR FILING DATE: 2002-04-09

Query Match 81.4%; Score 2651.5; DB 14; Length 781;
Best Local Similarity 84.5%; Pred. No. 1.3e-187;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 CMGRLLAPARAWAGSREHPGALLIRTRSMWNQFVIEEYAGEPVLLIGKLSVDVRCGE 60
DB 17 CMGRLLAPARAWAGSREHPGALLIRTRSMWNQFVIEEYAGEPVLLIGKLSVDVRCGE 76
QY 61 GRTKYLITGEGAGTVFVDEATGNIHYTKSLDREKAOYLLAQVDRASNRPLPPESEF 120
DB 77 GRTKYLITGEGAGTVFVDEATGNIHYTKSLDREKAOYLLAQVDRASNRPLPPESEF 136
QY 121 IIKQDINDNPIPLPGFYHATVPEMSNVGTSVIQVTAHADDDPSYNSAKLYVYLDGL 180
DB 137 IIKQDINDNPIPLPGFYHATVPEMSNVGTSVIQVTAHADDDPSYNSAKLYVYLDGL 196
QY 181 PFEVDQGTGVYRAINMRETOEFLVYIQAQDMGNGHGLSGSTTVYTLSDVNDP 240
DB 197 PFEVDQGTGVYRAINMRETOEFLVYIQAQDMGNGHGLSGSTTVYTLSDVNDP 256
QY 241 PKFQSLYQFSVETAGPGLVGRRAQDDPLGDNALMAVSIIDGESSEAFSISTDQGR 300
DB 257 PKFQSLYQFSVETAGPGLVGRRAQDDPLGDNALMAVSIIDGESSEAFSISTDQGR 316
QY 301 DGLITVKKPLDFESQRSYFRVEATNTLIDPAYIRGPPFVDVASVYAVADAPPAFTQ 360
DB 317 DGLITVKKPLDFESQRSYFRVEATNTLIDPAYIRGPPFVDVASVYAVADAPPAFTQ 376
QY 361 AAYHLTVPENKAPGTLVGOISAADLDSAPSPIRSIIPHSPPRCFSIOPEEGTHTAAP 420
DB 377 AAYHLTVPENKAPGTLVGOISAADLDSAPSPIRSIIPHSPPRCFSIOPEEGTHTAAP 436
QY 421 LDRPARAHNLTIVLATELGMSWGBERGWPVLVAEMSAAPAPQRSFVGSAGVIGPODSSA 480
DB 437 LDRPARAHNLTIVLATELGMSWGBERGWPVLVAEMSAAPAPQRSFVGSAGVIGPODSSA 458
QY 481 QASVVOVAIOTLIDENDNAPOLARPYDTFVCDSSAPQGLIOVTRALDRDVGNSSHVFOG 540
DB 459 QASVVOVAIOTLIDENDNAPOLARPYDTFVCDSSAPQGLIOVTRALDRDVGNSSHVFOG 518
QY 541 PLGDANFTVQDNND-----LPA-----WFHPLMASASWHLH--- 573
DB 519 PLGDANFTVQDNNDGASALLSPRPAPRHAPYVYLIELMDGQALSTNAVTVSVOR 578
QY 574 -----WPPARENGQPSAG 587
DB 579 CQPDGVSACMFEAHLASAAGLSTG 602

RESULT 13
US-10-238-183-98
Sequence 98, Application US/10238183
Publication No. US20030073183A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanabe, Collin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Ford, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3650R1C11
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091358
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/106932
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/115554
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119342
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/123957
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123972
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: 60/127372
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/131271
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/133459
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/135725
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135729
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135750
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/138385
PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: 60/140653
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144732
PRIOR FILING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144790
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145228
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146843
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/148188
PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/148513
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/149327
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149395
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/150114
PRIOR FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: 60/151700
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/151734
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/170262
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/171718
PRIOR FILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: 60/179851
PRIOR FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 60/180921
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: 60/187202
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/198587
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 60/199614
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 60/206330
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206368
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/209832
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 60/218371
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/222695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/229896
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/230621
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/232887
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/235147
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/261878
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/261910
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/261939
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/262150
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/264395
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/266421
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/267623

PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/274399
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/280982
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/282129
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/282199
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/290589
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 09/180997
PRIOR FILING DATE: 1998-11-19
PRIOR APPLICATION NUMBER: 09/267213
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 09/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/403297
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 09/423741
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: 09/709238
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 09/802706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 09/872035
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/924419
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/927796
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/929404
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 09/931836
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 09/941992
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 09/946374
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 10/001054
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 10/081056
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: 10/119480
PRIOR FILING DATE: 2002-04-09

Query Match 81.4%; Score 2651.5; DB 14; Length 781;
Best Local Similarity 84.5%; Pred. No. 1.3e-187;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

1 CMGRLLAPARAWAGSEHGPALILTRRSWVWNOFVIEEYGPPEVLLIGKLSHDVDRGE 60
17 CMGRLLAPARAWAGSEHGPALILTRRSWVWNOFVIEEYGPPEVLLIGKLSHDVDRGE 76
61 GRTKYLITGEGAGTAVVIDEATGNHVTSLDREEAQVYLLAQAADRASNRLPEPSEF 120
77 GRTKYLITGEGAGTAVVIDEATGNHVTSLDREEAQVYLLAQAADRASNRLPEPSEF 136
121 IIRGODINENPPIFFPGPHATVPENSVGTSVIQTVAHDADDPISYGNAKLYTYLDDGI 180
137 IIRGODINENPPIFFPGPHATVPENSVGTSVIQTVAHDADDPISYGNAKLYTYLDDGI 196
181 PFTSVDPQGVVYTAIPNMDRETOEERLVVIAQKDXGSHMGGLSGSTTYVTTLSPDNDP 240
197 PFTSVDPQGVVYTAIPNMDRETOEERLVVIAQKDXGSHMGGLSGSTTYVTTLSPDNDP 256
241 PFTSVDPQGVVYTAIPNMDRETOEERLVVIAQKDXGSHMGGLSGSTTYVTTLSPDNDP 300

```

Db 257 PKFPOSIVQFSVETAGPGLVGRRAQDPDLGNALMAYSILDEGESEAFSISTDIQGR 316
Qy 301 DGLLTVRKPLDFESORSYSFRVEATNTLIDPAYLRGPFKXVAVRVAVODAPPPAFTQ 360
Db 317 DGLLTVRKPLDFESORSYSFRVEATNTLIDPAYLRGPFKXVAVRVAVODAPPPAFTQ 376
Qy 361 AAYHLLTVENKAPGTLVQGISAADLSPASPIRYSILPHSDPERCFSIQPEEGTHTAA 420
Db 377 AAYHLLTVENKAPGTLVQGISAADLSPASPIRYSILPHSDPERCFSIQPEEGTHTAA 436
Qy 421 LDREARAHNLTVALTEIGSMGSPERGVPPLVAMENAPAPPPRSVGSVGTIPQSSA 480
Db 437 LDREARAHNLTVALTEIGSMGSPERGVPPLVAMENAPAPPPRSVGSVGTIPQSSA 458
Qy 481 QASRYOVAIQTLDENDNAPOLAEPYDTFVCDSPAAGQLIYIRALDRDEVGNSSHVSG 540
Db 459 QASRYOVAIQTLDENDNAPOLAEPYDTFVCDSPAAGQLIYIRALDRDEVGNSSHVSG 518
Qy 541 PLGPANTVQDNND-----LPA-----WHPILMASASGWLH--- 573
Db 519 PLGPANTVQDNNDGASLLPLPSRPAPPRHAPYLVPIELMDWGQPALSTATVTVSVCR 578
Qy 574 -----WPPARGNQPPASQG 587
Db 579 CQPDGSVASCWPEAHLSAAGLSTG 602

RESULT 14
US-10-238-283-98
; Sequence 98, Application US/10238283
; Publication No. US20030073190A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C15
; CURRENT APPLICATION NUMBER: US/10/238,283
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98

```

```

; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-238-283-98
Query Match 81.4%; Score 2651.5; DB 14; Length 781;
Best Local Similarity 84.5%; Pred. No. 1,3e-187;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

Qy 1 CMGRILAAPRAAAGREHGPALNTRRSWNNQFVEEYAGPPVYIGLHSDVDRGE 60
Db 17 CMGRILAAPRAAAGREHGPALNTRRSWNNQFVEEYAGPPVYIGLHSDVDRGE 76
Qy 61 GRTKYLITGEGAGTFFVIDEATGNHVTKSIDREKQAYVLLAQAADRASNRPLEPSEF 120
Db 77 GRTKYLITGEGAGTFFVIDEATGNHVTKSIDREKQAYVLLAQAADRASNRPLEPSEF 136
Qy 121 IIKQDINDNPFIFELGTYHATVPMNSVGTSVIQTVAHDADDPSYGNASALVTVVDGL 180
Db 137 IIKQDINDNPFIFELGTYHATVPMNSVGTSVIQTVAHDADDPSYGNASALVTVVDGL 196
Qy 181 PFFSVDPQTGVVTRTAPNMMDRETOEEFLVVIQAQDMGSMGSLGSTTVTVTLSDVNDP 240
Db 197 PFFSVDPQTGVVTRTAPNMMDRETOEEFLVVIQAQDMGSMGSLGSTTVTVTLSDVNDP 256
Qy 241 PKFPOSIVQFSVETAGPGLVGRRAQDPDLGNALMAYSILDEGESEAFSISTDIQGR 300
Db 257 PKFPOSIVQFSVETAGPGLVGRRAQDPDLGNALMAYSILDEGESEAFSISTDIQGR 316
Qy 301 DGLLTVRKPLDFESORSYSFRVEATNTLIDPAYLRGPFKXVAVRVAVODAPPPAFTQ 360
Db 317 DGLLTVRKPLDFESORSYSFRVEATNTLIDPAYLRGPFKXVAVRVAVODAPPPAFTQ 376
Qy 361 AAYHLLTVENKAPGTLVQGISAADLSPASPIRYSILPHSDPERCFSIQPEEGTHTAA 420
Db 377 AAYHLLTVENKAPGTLVQGISAADLSPASPIRYSILPHSDPERCFSIQPEEGTHTAA 436
Qy 421 LDREARAHNLTVALTEIGSMGSPERGVPPLVAMENAPAPPPRSVGSVGTIPQSSA 480
Db 437 LDREARAHNLTVALTEIGSMGSPERGVPPLVAMENAPAPPPRSVGSVGTIPQSSA 458
Qy 481 QASRYOVAIQTLDENDNAPOLAEPYDTFVCDSPAAGQLIYIRALDRDEVGNSSHVSG 540
Db 459 QASRYOVAIQTLDENDNAPOLAEPYDTFVCDSPAAGQLIYIRALDRDEVGNSSHVSG 518
Qy 541 PLGPANTVQDNND-----LPA-----WHPILMASASGWLH--- 573
Db 519 PLGPANTVQDNNDGASLLPLPSRPAPPRHAPYLVPIELMDWGQPALSTATVTVSVCR 578
Qy 574 -----WPPARGNQPPASQG 587
Db 579 CQPDGSVASCWPEAHLSAAGLSTG 602

RESULT 15
US-10-238-370-98
; Sequence 98, Application US/10238370
; Publication No. US20030073191A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C15

```


FILE REFERENCE: P3630R1C10
CURRENT APPLICATION NUMBER: us/10/238,370
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-238-370-98

Query Match 81.4%; Score 2651.5; DB 14; Length 781;
Best Local Similarity 84.5%; Pred. No. 1,3e-187;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 CMGRAPARAWAGREHHPALLTRRSWVWNOFPVIEEYAGPEPVYLGKHSVDVGE 60
DB 17 CMGRAPARAWAGREHHPALLTRRSWVWNOFPVIEEYAGPEPVYLGKHSVDVGE 76
QY 61 GRTXYLLTGEAGTGVIDEATGNHVTKSIDREKQYVLLAQVDRASNRPLEPSEF 120
DB 77 GRTXYLLTGEAGTGVIDEATGNHVTKSIDREKQYVLLAQVDRASNRPLEPSEF 136
QY 121 IIKGODINDNPIIFPLGPHATVPMSVGTSVIOVTHADDDPSYGSATLYTVLDGL 180
DB 137 IIKVODINDNPIIFPLGPHATVPMSVGTSVIOVTHADDDPSYGSATLYTVLDGL 196
QY 181 PFFSVDPOTGVVTRTAIPNMDRETOEFLVIOAKMGHMGSLSGTIVTVLSDVNDP 240
DB 197 PFFSVDPOTGVVTRTAIPNMDRETOEFLVIOAKMGHMGSLSGTIVTVLSDVNDP 256
QY 241 PFFSVDPOTGVVTRTAIPNMDRETOEFLVIOAKMGHMGSLSGTIVTVLSDVNDP 300
DB 257 PFFSVDPOTGVVTRTAIPNMDRETOEFLVIOAKMGHMGSLSGTIVTVLSDVNDP 316
QY 301 DGLTVRKLPDESORSYSFRVEATNTLIDPAYLRGPFKDVASVRAVODAPPEPAFTQ 360
DB 317 DGLTVRKLPDESORSYSFRVEATNTLIDPAYLRGPFKDVASVRAVODAPPEPAFTQ 376
QY 361 AAYHLLVPENKAPGTLVQISADIDSPASPIRYSILPHSDPERCFSTIQPEEGTHTAAP 420
DB 377 AAYHLLVPENKAPGTLVQISADIDSPASPIRYSILPHSDPERCFSTIQPEEGTHTAAP 436
QY 421 LDREARAWNTLVLTGLGMSWGPGRGWPLLVAEWSAPAAPPCRSPVGSAGVIGQDSSA 480
DB 437 LDREARAWNTLVLTGLGMSWGPGRGWPLLVAEWSAPAAPPCRSPVGSAGVIGQDSSA 458
QY 481 QASRVQVAIQTLDENNDAPQLAEPYDTFVCDSPAAPGQLIQVIRALDRDEVANSHVTFQG 540

DB 519 PLGGPDANFTVODNRDGSASLLBPSRPAPPRAPFLVPIELMDKQOPALSSATATVTSVCR 578
QY 574 -----WPPAERGNOPASOG 587
DB 579 CQPDGSVASCWPEAHLASAAGLSTG 602
Search completed: December 8, 2004, 11:34:28
Job time : 635.542 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 73.9315 Seconds
(without alignments)
556.152 Million cell updates/sec

Title: US-09-788-051-7

Perfect score: 3259

Sequence: 1 CMGRLLAPARAWAGSRHPG.....LPSCQLPLGIPALGIIVCAS 620

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents_AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1607	49.3	693	2	US-08-738-349-6
2	1607	49.3	693	2	US-09-919-497-55
3	1607	49.3	796	2	US-08-738-349-4
4	1602	49.2	796	1	US-08-188-228-58
5	1602	49.2	796	1	US-08-332-643-52
6	1602	49.2	796	1	US-08-332-638-58
7	1602	49.2	796	4	US-09-654-328-2
8	1596	49.0	796	2	US-08-738-349-2
9	1530.5	47.0	799	1	US-08-188-228-42
10	1530.5	47.0	799	1	US-08-332-638-42
11	1529.5	46.9	793	1	US-08-188-228-54
12	1529.5	46.9	793	1	US-08-332-643-48
13	1529.5	46.9	793	1	US-08-332-638-54
14	1493	45.8	715	2	US-08-738-349-12
15	1468	45.0	532	1	US-08-188-228-44
16	1468	45.0	532	1	US-08-332-638-44
17	1365.5	41.9	794	1	US-08-188-228-60
18	1365.5	41.9	794	1	US-08-332-643-54
19	1365.5	41.9	794	1	US-08-332-638-60
20	1136.5	34.9	653	1	US-08-188-228-46
21	1136.5	34.9	653	1	US-08-332-638-46
22	933.5	28.6	780	1	US-08-188-228-50
23	933.5	28.6	780	1	US-08-332-643-44
24	933.5	28.6	780	1	US-08-332-638-50
25	596	18.3	506	4	US-09-417-039-11
26	591	18.1	913	2	US-08-474-067-6

28	591	18.1	913	2	US-08-472-481-5	Sequence 5, Appli
29	586	18.0	837	2	US-08-474-067-7	Sequence 7, Appli
30	586	18.0	837	2	US-08-474-068A-7	Sequence 7, Appli
31	586	18.0	837	2	US-08-472-481-6	Sequence 6, Appli
32	580.5	17.8	555	2	US-08-453-702A-98	Sequence 98, Appli
33	576	17.7	556	1	US-07-998-003A-98	Sequence 98, Appli
34	576	17.7	556	1	US-08-453-274B-98	Sequence 98, Appli
35	576	17.7	556	1	US-08-453-695A-98	Sequence 98, Appli
36	576	17.7	556	1	US-08-268-161A-98	Sequence 98, Appli
37	576	17.7	556	3	US-09-099-639-98	Sequence 98, Appli
38	574.5	17.6	712	2	US-08-474-067-2	Sequence 2, Appli
39	574.5	17.6	712	2	US-08-474-067-5	Sequence 5, Appli
40	574.5	17.6	712	2	US-08-474-068A-2	Sequence 2, Appli
41	574.5	17.6	712	2	US-08-474-068A-5	Sequence 5, Appli
42	574.5	17.6	712	2	US-08-472-481-2	Sequence 2, Appli
43	574.5	17.6	717	2	US-08-474-067-4	Sequence 4, Appli
44	574.5	17.6	717	2	US-08-474-068A-4	Sequence 4, Appli
45	574.5	17.6	717	2	US-08-472-481-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-738-349-6
Sequence 6, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shunji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amano, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 693 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-6

Query Match 49.3%; Score 1607; DB 2; Length 693;
Best Local Similarity 50.5%; Pred. No. 2,2e-137;
Matches 324; Conservative 98; Mismatches 133; Indels 86; Gaps 10;

QY 1 CMGRLA-----APAR-----AMAGSRE--HGPALLATRRSWWNQFVILEEYAGPEPV 47
DB 13 CLGMCHSHAFAPERRGHILRPSFHGHKEKGEQVLOQRKGMWNQFVILEEYTGDPV 72
QY 48 LIGKLSHDVDRGEGRKTXLLTGEAGTVFVIDEAGNTHVKSIDREKQAYVLLAQAVD 107
DB 73 LVGRHSDIDSDGNIKXILSGEAGTIFVIDDSGNHAKTIDREERQYTLMAQAVD 132
QY 108 RASNPPLPEPSEFFIKGQDINDNPIPLGPHATVPEMSVGTSVIQTVAHADDDPSYG 167
DB 133 RDTNRPLEPSEFFIKVQDINDNPEPHEHYHANVPERNSVGTSVIQTVAHADDDPSYG 192
QY 168 NSAKLVYTVLDLPFFSVDPQTVGVRATIPNMDETOEPEFVVIQAKDMGSHMGLSGST 227
DB 193 NSAKLVYTVLDLPFFSVDPQTVGVRATIPNMDETOEPEFVVIQAKDMGSHMGLSGST 252
QY 228 TVTVTLSDVNDNPKPFPOSQVQSVETAGPGLVGRIRADDPDLGNALMAYSILDGEG 287
DB 253 KVTITLTVNDNPKPFPOSQVQSVETAGPGLVGRIRADDPDLGNALMAYSILDGEG 312
QY 288 SEAFSISTDLQGRDGLTVRKPLDPEQSORSYFVEATNTLIDPAYLRGPFKDVASRV 347
DB 313 MESEFITTDETOEGVILKKEPVDPEIKRAVSLKVEANVHIDPKFISNGPFKDVTVKI 372
QY 348 AVQDAPEPFAFTQAAYHLTVPENKAPGLTVGQISAADLSPASIRYSILPHSDPERCF 407
DB 373 AVEDADEPMPFLAPSYIHEVQENAAAGTVGRVHAKDPDANSPIRYSIDRHTDLDPFT 432
QY 408 IOPEEGTHTAAPLDREARAHNLTVALTELGMWGPERGVPLLVAMSGAPAPQORSP 467
DB 433 INPEDGFIKTKPLDREBTAMNITVPAELI----- 463
QY 468 VGSAGVIGPOSSAQSRYOVAIOTLDENDNAPQLAPEYDFVCD-----AAPQLQIVR 523
DB 464 -----HNRHQAQVPAIRVLDVNDNAKFAAPYEGFICSDQTKPLSNQPIVTIS 514
QY 524 ALDRDEVGNSSHVFOGP--LGPDAFTVQDNRLPA-----WFHLLM 565
DB 515 ADDKDDTANGRPFFSLPEPIIHNPFTVRDNRNTAGVYARRGFSRQKODLYLPIVI 574
QY 566 ASASSWLMHPPAERGNQPAQKSSLP-CG-RLPGLPSC 604
DB 575 -----SDGIPPMSTNTLTIKVCCDVNGALLSC 604

RESULT 2
US-09-919-497-55
Sequence 55, Application US/09919497
Patent No. 6773863
GENERAL INFORMATION:
APPLICANT: Muller, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patent version 3.0
SEQ ID NO: 55
LENGTH: 693
TYPE: PRT
ORGANISM: Homo sapiens
US-09-919-497-55

Query Match 49.3%; Score 1607; DB 4; Length 693;
Best Local Similarity 50.5%; Pred. No. 2,2e-137;
Matches 324; Conservative 98; Mismatches 133; Indels 86; Gaps 10;

QY 1 CMGRLA-----APAR-----AMAGSRE--HGPALLATRRSWWNQFVILEEYAGPEPV 47
DB 13 CLGMCHSHAFAPERRGHILRPSFHGHKEKGEQVLOQRKGMWNQFVILEEYTGDPV 72
QY 48 LIGKLSHDVDRGEGRKTXLLTGEAGTVFVIDEAGNTHVKSIDREKQAYVLLAQAVD 107
DB 73 LVGRHSDIDSDGNIKXILSGEAGTIFVIDDSGNHAKTIDREERQYTLMAQAVD 132
QY 108 RASNPPLPEPSEFFIKGQDINDNPIPLGPHATVPEMSVGTSVIQTVAHADDDPSYG 167
DB 133 RDTNRPLEPSEFFIKVQDINDNPEPHEHYHANVPERNSVGTSVIQTVAHADDDPSYG 192
QY 168 NSAKLVYTVLDLPFFSVDPQTVGVRATIPNMDETOEPEFVVIQAKDMGSHMGLSGST 227
DB 193 NSAKLVYTVLDLPFFSVDPQTVGVRATIPNMDETOEPEFVVIQAKDMGSHMGLSGST 252
QY 228 TVTVTLSDVNDNPKPFPOSQVQSVETAGPGLVGRIRADDPDLGNALMAYSILDGEG 287
DB 253 KVTITLTVNDNPKPFPOSQVQSVETAGPGLVGRIRADDPDLGNALMAYSILDGEG 312
QY 288 SEAFSISTDLQGRDGLTVRKPLDPEQSORSYFVEATNTLIDPAYLRGPFKDVASRV 347
DB 313 MESEFITTDETOEGVILKKEPVDPEIKRAVSLKVEANVHIDPKFISNGPFKDVTVKI 372
QY 348 AVQDAPEPFAFTQAAYHLTVPENKAPGLTVGQISAADLSPASIRYSILPHSDPERCF 407
DB 373 AVEDADEPMPFLAPSYIHEVQENAAAGTVGRVHAKDPDANSPIRYSIDRHTDLDPFT 432
QY 408 IOPEEGTHTAAPLDREARAHNLTVALTELGMWGPERGVPLLVAMSGAPAPQORSP 467
DB 433 INPEDGFIKTKPLDREBTAMNITVPAELI----- 463
QY 468 VGSAGVIGPOSSAQSRYOVAIOTLDENDNAPQLAPEYDFVCD-----AAPQLQIVR 523
DB 464 -----HNRHQAQVPAIRVLDVNDNAKFAAPYEGFICSDQTKPLSNQPIVTIS 514
QY 524 ALDRDEVGNSSHVFOGP--LGPDAFTVQDNRLPA-----WFHLLM 565
DB 515 ADDKDDTANGRPFFSLPEPIIHNPFTVRDNRNTAGVYARRGFSRQKODLYLPIVI 574
QY 566 ASASSWLMHPPAERGNQPAQKSSLP-CG-RLPGLPSC 604
DB 575 -----SDGIPPMSTNTLTIKVCCDVNGALLSC 604

RESULT 3
US-08-738-349-4
Sequence 4, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sumao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amano, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349

Wed Dec 8 11:46:33 2004

us-09-788-051-7.rai

Page 3

FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-4

Query Match 49.3%; Score 1607; DB 2; Length 796;
Best Local Similarity 50.5%; Pred. No. 2,8e-137;
Matches 324; Conservative 98; Mismatches 133; Indels 86; Gaps 10;

QY 1 CWRGLA-----APAR-----AMAGSR--HGPALLTRRSKVMNQFVIEEYAGPEV 47
DB 13 CLGMLCHSHAFAPERRGHLRPSFHGHEKKGQVLRKSGVMNQFVIEEYAGPEV 72
QY 48 LIGLHSDVDREGGRKYLITGEGAGTVFIDEATGNINHTKSLDREKAQVYLLAQAVD 107
DB 73 LVGRHSDIDSGDNKIKYLSGEGAGTIVIDDKSGNHATKTLDRERKQYTLMAQAVD 132
QY 108 RASNRPLEPPESEFIKQDINDNPPFLPGFYHATVPMSNVGTSVYQVTAHDADPSYG 167
DB 133 RDTNRPLEPPESEFIKQDINDNPPFLPGFYHATVPMSNVGTSVYQVTAHDADPSYG 192
QY 168 NSAKLYVTVLDGLPFSVDPQGVRTAIENMDRETOEELVYVQAKDMGSHMGSLGSGT 227
DB 193 NSAKLYVTVLDGLPFSVDPQGVRTAIENMDRETOEELVYVQAKDMGSHMGSLGSGT 252
QY 228 TVTVTLSDVNDNPPKPFQSLYQFSVETAGPGLVGRRAQDPDLGNALMAYSLDDEG 287
DB 253 KVTITLTDVNDNPPKPFQSLYQFSVETAGPGLVGRRAQDPDLGNALMAYSLDDEG 312
QY 288 SEAFSISTDLQGDGLTVRKPLDPESQRSYFRVEATNTLIDPAYLRGPFQVAVSVY 347
DB 313 MESFEITTYDETQEGVILKRPVDFETRAYSLKVEANVHIDKFTSNGPFQVAVSVY 372
QY 348 AVQDPEPPAFQAAYHVLTPENKAPGTLVQISADLSDSPAPRYSILHSPERCF 407
DB 373 AVEDDEPPEPFLAPYIHEVQENAAAGTVGRVAKDPDANSPIRYSIDHTLDDFT 432
QY 408 IQPEEGTHTAAFLDREARAMNTLVATELGMSWGPGRVPLVAVMSAPAAPQORSP 467
DB 433 INFEDGFIKTKPLDREETAMLNTVFAAEI----- 463
QY 468 VGSAGIIPQDSASQAFVQVAILCTLDENDNAPOLAEPTDFVDS-----AAPGOLIQVIR 523
DB 494 -----HNHQAKVPAALRVLDVNDNAKFPAPYEGFICSDQTKPSNQPITYIS 514
QY 524 ALDRDEGVNSHVSFGP--LGPANFTVQDNRDLPA-----WHPILM 565
DB 545 ADDKODTANGPRFISLPEIITHNPNFTVRDNRDTAGVYARAGGFSRQKODLYLPIVI 574
QY 566 ASASMLHWPAPERGNQAPASQKSSSLP-CG-RLEGALPSC 604
DB 575 -----SDGGLPMSSTNLTITKVCQCDVAGALLSC 604

Sequence 58, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-58

Query Match 49.2%; Score 1602; DB 1; Length 796;
Best Local Similarity 50.4%; Pred. No. 7.9e-137;
Matches 323; Conservative 98; Mismatches 134; Indels 86; Gaps 10;

QY 1 CWRGLA-----APAR-----AMAGSR--HGPALLTRRSKVMNQFVIEEYAGPEV 47
DB 13 CLGMLCHSHAFAPERRGHLRPSFHGHEKKGQVLRKSGVMNQFVIEEYAGPEV 72
QY 48 LIGLHSDVDREGGRKYLITGEGAGTVFIDEATGNINHTKSLDREKAQVYLLAQAVD 107
DB 73 LVGRHSDIDSGDNKIKYLSGEGAGTIVIDDKSGNHATKTLDRERKQYTLMAQAVD 132
QY 108 RASNRPLEPPESEFIKQDINDNPPFLPGFYHATVPMSNVGTSVYQVTAHDADPSYG 167
DB 133 RDTNRPLEPPESEFIKQDINDNPPFLPGFYHATVPMSNVGTSVYQVTAHDADPSYG 192
QY 168 NSAKLYVTVLDGLPFSVDPQGVRTAIENMDRETOEELVYVQAKDMGSHMGSLGSGT 227
DB 193 NSAKLYVTVLDGLPFSVDPQGVRTAIENMDRETOEELVYVQAKDMGSHMGSLGSGT 252
QY 228 TVTVTLSDVNDNPPKPFQSLYQFSVETAGPGLVGRRAQDPDLGNALMAYSLDDEG 287
DB 253 KVTITLTDVNDNPPKPFQSLYQFSVETAGPGLVGRRAQDPDLGNALMAYSLDDEG 312
QY 288 SEAFSISTDLQGDGLTVRKPLDPESQRSYFRVEATNTLIDPAYLRGPFQVAVSVY 347
DB 313 MESFEITTYDETQEGVILKRPVDFETRAYSLKVEANVHIDKFTSNGPFQVAVSVY 372

DQ
Y
I CMGRLLA-----APAR-----AWAGSKR--HGPALIRTRSRSMVWNOFVVIEEYACGEPDV 47

D8
13 CIGMLCHSHAPAERGHLPSPFHGHHKXKGQVLORSKRGVMNOLFVIIETTGDPV 72

COMPUTER READABLE FORM:
 ZL# 65086
 MEDIUM TYPE: IBM floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/332,638
 FILING DATE: 01-NOV-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/872,643
 FILING DATE: 17 APR 1992
 APPLICATION NUMBER: US/08/049,460
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:

NAME: No. 5646250and, Grete E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-58

Query Match 49.2%; Score 1602; DB 1; Length 796;
Best Local Similarity 50.4%; Pred. No. 7,9e-137;
Matches 323; Conservative 98; Mismatches 134; Indels 86; Gaps 10;

```
QY 1 CMGRLA-----APAR-----AMAGSR--HPGPAALTRRSWVWNOFVIEYAGPEPV 47
DB 13 CLGMLCHSHAFAPERRGHLRPSFHGHKEKKGQVLQSKRGWVWNOFVIEYAGPEPV 72
QY 48 LIGKLHSDVDRGEGRTKYLITGEGAGTVFIDEATGNHVTXSLDREBKAYVLLAQA 107
DB 73 LVGRHSDIDSDGDNKXILSGEGAGTIFVIDKSGNHATKILDRERAAQYTLMAQAVD 132
QY 108 RASNRPLEPSEFEIIGKODINDNPIFLPGFYHATVPEMSVGTSVIQTVAHADDP 167
DB 133 RQNRPLEPSEFEIIGKODINDNPIFLPGFYHATVPEMSVGTSVIQTVAHADDP 192
QY 168 NSAKLVYTLVDGLPEFSVDPQTGVNRTAIPNMDRETOEELVVIQAKDMGHWG 227
DB 193 NSAKLVYTLVDGLPEFSVDPQTGVNRTAIPNMDRETOEELVVIQAKDMGHWG 252
QY 228 TVTITLSDVNDNPKPFPQSLYQFSVETAGPTLVGRADPDLDGNALMAYSIL 287
DB 253 KVTITLSDVNDNPKPFPQSLYQFSVETAGPTLVGRADPDLDGNALMAYSIL 312
QY 288 SEAFSISTDLQGRDGLTVRKPLDPEFSQSYSFVEATNTLIDPAVLRGPF 347
DB 313 MESFEITTDYETQEGVILKPKVPDEFETERAYSLKVEAAVHIDPKFISNGP 372
QY 348 AVQDAPEPAPFQAHLTVPENKAPGTLVGQISADLSPASIRISILPHSP 407
DB 373 SVEADPEPMPFAPSIHVEQENAAAGTVGVNAKPDANSPIRYSIDRHT 432
QY 408 IOPEEGTHTAALDREARAHNLTVLATELGWSWGPGRGWPLVAEWSAPAP 467
DB 433 INEDGFITKTKPLDRETAHLNITVFAEI----- 463
QY 468 VGSAGVIPPQSSAQSRVOVAIQTLDENDNAQALAEPIYTVCD 523
DB 464 -----HNRHOEAVPVAIRVLDVNDNAKFAAPYEGFICSDQTKP 514
QY 524 ALDREVGNSHVSFGP--LGPDAFTVQDNRLDPA-----WFHPLM 565
DB 515 ADDKDDTANGPRTIFSLPEIITHNPFYRDNRDNTAGVYARRGFSRQK 574
QY 566 ASASSWLMHPPARGNQAPASQKSSLP-CG-RLPALPSC 604
DB 575 -----SDGSIIPMSSNTLITIKVCGCDVNGALLSC 604
```

RESULT 7
US-09-654-328-2
Sequence 2, Application US/09654328
Patent No. 6787136
GENERAL INFORMATION:
APPLICANT: Brenner, Michael B.
APPLICANT: Valencia, Xavier
TITLE OF INVENTION: Methods and Compositions for Treatment
of Inflammatory Disease Using Cadherin-11 Modulating Agents

FILE REFERENCE: B0801/7187/ERP/MAT
CURRENT APPLICATION NUMBER: US/09/654,328
CURRENT FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/152,456
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: US 60/153,490
PRIOR FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 796
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-654-328-2

Query Match 49.2%; Score 1602; DB 4; Length 796;
Best Local Similarity 50.4%; Pred. No. 7,9e-137;
Matches 323; Conservative 98; Mismatches 134; Indels 86; Gaps 10;

```
QY 1 CMGRLA-----APAR-----AMAGSR--HPGPAALTRRSWVWNOFVIEYAGPEPV 47
DB 13 CLGMLCHSHAFAPERRGHLRPSFHGHKEKKGQVLQSKRGWVWNOFVIEYAGPEPV 72
QY 48 LIGKLHSDVDRGEGRTKYLITGEGAGTVFIDEATGNHVTXSLDREBKAYVLLAQA 107
DB 73 LVGRHSDIDSDGDNKXILSGEGAGTIFVIDKSGNHATKILDRERAAQYTLMAQAVD 132
QY 108 RASNRPLEPSEFEIIGKODINDNPIFLPGFYHATVPEMSVGTSVIQTVAHADDP 167
DB 133 RQNRPLEPSEFEIIGKODINDNPIFLPGFYHATVPEMSVGTSVIQTVAHADDP 192
QY 168 NSAKLVYTLVDGLPEFSVDPQTGVNRTAIPNMDRETOEELVVIQAKDMGHWG 227
DB 193 NSAKLVYTLVDGLPEFSVDPQTGVNRTAIPNMDRETOEELVVIQAKDMGHWG 252
QY 228 TVTITLSDVNDNPKPFPQSLYQFSVETAGPTLVGRADPDLDGNALMAYSIL 287
DB 253 KVTITLSDVNDNPKPFPQSLYQFSVETAGPTLVGRADPDLDGNALMAYSIL 312
QY 288 SEAFSISTDLQGRDGLTVRKPLDPEFSQSYSFVEATNTLIDPAVLRGPF 347
DB 313 MESFEITTDYETQEGVILKPKVPDEFETERAYSLKVEAAVHIDPKFISNGP 372
QY 348 AVQDAPEPAPFQAHLTVPENKAPGTLVGQISADLSPASIRISILPHSP 407
DB 373 SVEADPEPMPFAPSIHVEQENAAAGTVGVNAKPDANSPIRYSIDRHT 432
QY 408 IOPEEGTHTAALDREARAHNLTVLATELGWSWGPGRGWPLVAEWSAPAP 467
DB 433 INEDGFITKTKPLDRETAHLNITVFAEI----- 463
QY 468 VGSAGVIPPQSSAQSRVOVAIQTLDENDNAQALAEPIYTVCD 523
DB 464 -----HNRHOEAVPVAIRVLDVNDNAKFAAPYEGFICSDQTKP 514
QY 524 ALDREVGNSHVSFGP--LGPDAFTVQDNRLDPA-----WFHPLM 565
DB 515 ADDKDDTANGPRTIFSLPEIITHNPFYRDNRDNTAGVYARRGFSRQK 574
QY 566 ASASSWLMHPPARGNQAPASQKSSLP-CG-RLPALPSC 604
DB 575 -----SDGSIIPMSSNTLITIKVCGCDVNGALLSC 604
```

RESULT 8
US-08-738-349-2
Sequence 2, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Aetsushi

```

APPLICANT: Amant, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1223-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-2

Query Match
Best Local Similarity 49.0%; Score 1596; DB 2; Length 796;
Matches 317; Conservative 97; Mismatches 127; Indels 84; Gaps 8;

QY 15 SREHP-----GPAALLRTSRSMVWNOFVIEBYEYAGPEPVLLGKLSHDYDREGRT 63
DB 29 SHLPSFHGHKEKGEQVLRSKRGWVWNOFVIEBYETGPDVVLGR.LHSDIDSGDNI 88
QY 64 KYLLTGGAGTVFVIDATGNIHYTKSLDREKAKQVYLLAQVDRASNRLEPSSFTIK 123
DB 89 KYLLSGGAGTVFVIDKSGNIHATKTLDEERAKQVYLLAQVDRTPNRELPSSFTIK 148
QY 124 GQDINDNPPIEPLGPHYATVPENMNGVTSIQVTAHDADDPSSYGSNAKLVYTVLDGLPFF 183
DB 149 VQDINDNPPELHITIANVPERSNVGTSIQVTAHDADDPPTGNSAKLVYSLTEQPYF 208
QY 184 SVDPQTEGVTALTNMDRETQEEFLVYIAQKMGHNGLSGTTYVTLLSDVNDNPKF 243
DB 209 SVEAQDTGIIKTALPNMDREKKEHYVYIAQKMGHNGLSGTTYVTLLSDVNDNPKF 268
QY 244 POSLYGSEVETGPGTGLVGR.LRAODPDLGDNALMYSIIDGSGSAFSTLDGRDL 303
DB 269 POSLYGSEVETGPGTGLVGR.LRAODPDLGDNALMYSIIDGSGSAFSTLDGRDL 328
QY 304 LTVRKPLDPSQRSYSPREVAATNLLIDPAYLRGPFKDVASVAVQDAPEPPAFTQAY 363
DB 329 VKLKKPVPDFTKRAYSIKIAANVHIDPKFISNGPFEDVTYKISVEDADEPMPFAPSY 388
QY 364 HLTVBEKAPGLVGOISADLDSPASPIRYSLTSPSDPERCSIQPEGTTTAAPLR 423
DB 389 IHEVQENAAAGTVGVGRHAKDPDANSPIRYSIDRHLDLPFTINPEGDFIKTKYPLDR 448

```

```

QY 424 EAPAHNLTVALTEIGMGNGPERGVNPLVAENAPAAPPORSPVGSVAGIIPDSSAQS 483
DB 449 ESTAMINISVPAET-----HNRQET 470
QY 484 RVQVALIQTLDENDNAPQALPEYDFVCDSPAF-----GQLIQRALDRDEGNSHVSFQ 539
DB 471 KVPVARIQVDVNDAPKRAPEYEGICSDHPKLSNPITVAGADQDDTANPPRIFS 530
QY 540 GP-LGPDANFTVQDNRDLPA-----WFHPLMASASSWILHMPAERGN 581
DB 531 LPPEIMHNPNFTVRNDRNTAGVYARRGFSRQKDFYLPILVI-----SDGGI 579
QY 582 OPASQKSSLP-CG-RUGALPSC 604
DB 580 PPMSTNTLITIKVCCGVNGALLSC 604

RESULT 9
US-08-188-228-42
Sequence 42, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-42

Query Match
Best Local Similarity 47.0%; Score 1530.5; DB 1; Length 799;
Matches 300; Conservative 110; Mismatches 135; Indels 81; Gaps 9;

QY 23 LLRTSRSMVWNOFVIEBYEYAGPEPVLLGKLSHDYDREGRTKYLTDGAGTVFVIDEAT 82
DB 56 LNRSKRGWVWNOFVIEBYEYAGPEPVLLGKLSHDYDREGRTKYLTDGAGTVFVIDEAT 115
QY 83 GNIHYTKSLDREKAKQVYLLAQVDRASNRLEPSSFTIKGQDINDNPPIEPLGPHYAT 142

```



```

D75      116 GD|HAIKRLDRREKKAAYTLT|AQAOWMENNKP|LEPSEFI|IKYQDINDPA|EFLNGPYHAT 175
Oy       143 VPEMSVNGSV|OYTHADADPSYGN|SACLVYTV|DGLPFPSVDPQCVVTA|PNNDR 202
Dy       176 VPEMSILGT|SVNTVIT|TDADDPYGN|SACLVYS|ILEGQYPS|IEBTA|ITTA|PNNDR 235
Oy       203 TOEF|LVV|OAKMG|MGAGLS|GSTVY|YTLSDV|NDNPPK|FOS|LYQFSV|EY|AGP|TLV 262
Dy       236 ARKE|LVV|OAKMG|SHSGLS|GTLT|YTLTDV|DNDPPK|FAS|LYHSV|EDV|LGTAI 235
Oy       263 GR|A|ODP|DLGNALMAYS|ILDG|SEAF|S|TDLQ|RDGL|TVRK|PLD|FESQ|RSY|FRV 322
Dy       296 GRV|K|ADQD|IGENAO|SSYD|IDGD|TALFE|ITS|D|AO|ADGV|RLK|PLD|FE|TKS|Y|TLKV 355
Oy       323 E|A|NT|L|D|P|Y|L|R|G|F|K|V|A|S|A|V|V|O|D|A|P|P|A|F|T|O|A|H|L|V|E|N|K|A|G|T|V|G|O|I|S|A 382
Dy       356 E|A|N|H|I|D|P|E|S|G|R|G|P|K|O|T|A|K|V|E|D|A|D|P|P|F|S|E|T|Y|L|E|N|H|A|L|N|S|I|G|O|Y|T|A 415
Oy       383 A|D|D|S|P|A|S|P|R|Y|S|I|L|P|H|S|D|P|E|R|C|F|S|I|O|P|E|G|I|H|T|A|P|L|D|R|E|A|R|A|H|N|L|Y|L|A|T|E|L|G|S|W 442
Dy       416 R|D|D|I|T|S|P|R|F|S|I|D|H|T|L|D|R|E|Q|F|I|N|A|D|D|K|I|T|A|T|P|L|R|E|L|S|V|W|H|N|S|I|I|A|T|E|I 477
Oy       443 G|P|R|G|W|V|L|V|A|W|S|A|P|A|P|P|O|K|S|P|V|G|A|S|V|I|P|O|S|S|A|Q|S|V|O|V|A|I|Q|T|L|D|E|N|N|A|Q|L|A 502
Dy       472 -----R|N|H|S|I|S|R|V|P|A|I|V|L|D|V|N|N|A|E|F|A 497
Oy       503 E|P|Y|D|T|P|V|C|S|A|A|P|G|O|I|O|V|I|A|L|D|R|E|V|G|N|S|H|S|F|O|G|L|P|D|-----A|N|F|V|Q|N|R|D|----- 555
Dy       498 S|E|H|A|P|C|E|N|G|R|G|O|V|I|Q|Y|A|S|A|D|K|D|P|R|O|N|G|H|F|-----F|Y|S|I|L|P|E|N|N|N|E|F|I|K|K|E|D|N|S|L 555
Oy       556 -----L|P|A|F|H|P|L|MA|S|S|W|L|H|P|P|A|R|E|G|N|O|P|A|S|O|Q|K|S|S|L|P|C|G|R|L|P|G|A 600
Dy       556 S|I|A|K|H|G|F|N|R|O|K|O|E|V|L|P|Y|I|-----S|D|S|G|N|P|L|S|T|S|T|I|T|I|V|C|G|S|N|D|G|V 604
Oy       601 L|P|S|C|Q|-----L|P|L|G|I|-----P|A|L|G|V|L|C 618
Dy       605 V|Q|S|C|W|E|A|V|V|L|P|I|G|S|G|A|L|I|A|I|L|A|C 630

RESULT 10
US-08-332-638-42
Sequence 42, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-Nov-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302

```

[illegible]

STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-54

Query Match 46.9%; Score 1529.5; DB 1; Length 793;
Best Local Similarity 47.8%; Pred. No. 3.1e-130;
Matches 299; Conservative 111; Mismatches 135; Indels 81; Gaps 9;
QY 23 LTRRRSMWNQFVIEEYAGPEVILGKHSVDNREGSTKLLTGEAGTYFVDEAT 82
DB 49 LNRKRGWNNQFVLEFSGPEPILVGRHTDLPDSKKIKYILSGDAGTIFQINDVT 108
QY 83 GNHVTSLDREKQAQVYLLAQAADVRASNPLEPPSEFIKGGDINDNPPFLGPYHAT 142
DB 109 GDHAIKRLDREKAEVYLLAQAADVMETSKLEPPSEFIKGGDINDNPEFLNGPYHAT 168
QY 143 VPESNVTGTVIQTADDDPSYNSAKLVYVLDGLPFPSVDPQTGVRTAIPNNDR 202
DB 169 VPESNVTGTVIQTADDDPSYNSAKLVYVLDGLPFPSVDPQTGVRTAIPNNDR 228
QY 203 TOEFLVLIQAKMGHMGSLGSTVTVTLSDVNDNPKFPOSTLQFQSVETAGGTLV 262
DB 229 AKELVYLIQAKMGHMGSLGSTVTVTLSDVNDNPKFPOSTLQFQSVETAGGTLV 288
QY 263 GRLLAQPDLGDNALNAYSLIDBGEFAFISITDLOGRDLTVRKPLDPEFORSYSFRV 322
DB 289 GRVANKQDIDGENAOSYDIIIDDDGTLFEITSDAQAODGIIIRLRKPLFEFTKSYTLMD 348
QY 323 EATYLLDPAVLRGPKDVAAYVAVQDAPPEPAPTAQAYHLTVENKAPGLVQISA 382
DB 349 EAAVNHIDPFRSGPKDVAAYVAVQDAPPEPAPTAQAYHLTVENKAPGLVQISA 408
QY 383 ADDSPASPIRYSLILPHSDPERCFSIQPEEGTITHTAALDREARAWNTLVATELGSMW 442
DB 409 RDPDITSSPIRFSDIRHTDLEOFINADGKITLTPLDRELNVNHTITATEI---- 464
QY 443 GPERGWVLLVAEMSAAPAPQPSVGSANGIPQDSSAQAASRQVAILQLDENDAPOLA 502
DB 465 -----RNHSQISRPVPAIKVLDVNDAPERA 490
QY 503 EPYDITFCDSAPAGQLQVIRALDRDEVGNSHVSFGPLGPD---ANFTVQDNRD--- 555

DB 491 SEYEAFLENGKRGVIOVTSAMDDEPKNGHY--FLYSILPEWNNNPFIXKNEDNSL 548
QY 556 -----LPAFHPILIMASASWMLWPAERGNQASQOKSSL-PCG-RLPGA 600
DB 549 SLLAHGNNRQKQVYLLPIIT-----SDSGNPLSSTITITIVCCGSDGV 597
QY 601 LPSCQ-----LPGLI--PALGIYLC 618
DB 598 VQSCVNEAVVPLIGLSMGALIALIILAC 623

RESULT 12
US-08-332-643-48
Sequence 48, Application US/08332643
Patent No. 5639634
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-643-48

Query Match 46.9%; Score 1529.5; DB 1; Length 793;
Best Local Similarity 47.8%; Pred. No. 3.1e-130;
Matches 299; Conservative 111; Mismatches 135; Indels 81; Gaps 9;
QY 23 LTRRRSMWNQFVIEEYAGPEVILGKHSVDNREGSTKLLTGEAGTYFVDEAT 82
DB 49 LNRKRGWNNQFVLEFSGPEPILVGRHTDLPDSKKIKYILSGDAGTIFQINDVT 108
QY 83 GNHVTSLDREKQAQVYLLAQAADVRASNPLEPPSEFIKGGDINDNPPFLGPYHAT 142
DB 109 GDHAIKRLDREKAEVYLLAQAADVMETSKLEPPSEFIKGGDINDNPEFLNGPYHAT 168
QY 143 VPESNVTGTVIQTADDDPSYNSAKLVYVLDGLPFPSVDPQTGVRTAIPNNDR 202
DB 169 VPESNVTGTVIQTADDDPSYNSAKLVYVLDGLPFPSVDPQTGVRTAIPNNDR 228

STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/739,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-738-349-12

Query Match 45.8%; Score 1493; DB 2; Length 615;
Best Local Similarity 50.9%; Pred. No. 4.4e-127;
Matches 308; Conservative 92; Mismatches 123; Indels 82; Gaps 15;

QY 20 GPALLRRRSWMNQFVIEEYAGPEVLLGKLSHDVDRGEKTKYLITGEGATVVID 79
DB 39 GCVLQKRSKGMWNQFVIEEYAGPEVLLGKLSHDVDRGEKTKYLITGEGATVVID 98
QY 80 EATGNIVHTKSLDREKAAQVYLLAQAVDRASNPLEPSEFIKGGDINDNPFIPLGY 139
DB 99 DKSNIHATKTLDRERAAQYTLMAQAVDRDTPNPLPSEFIKGGDINDNPFIPLGY 157
QY 140 HATVPKSNVGTSVIQTVAHDADDPYSGNSAKLVYTVLDGLPFSVDPQTGVVRAIPM 199
DB 158 HANVPKSNVGTSVIQTVAHDADDPYSGNSAKLVYTVLDGLPFSVDPQTGVVRAIPM 217
QY 200 DRETOEFLVYIAOKMGHMGGLSGSTVTVTLSDVNDNPKPQSLQFVETAGRG 259
DB 218 DREAKEHYVIAOKMGHMGGLSGSTVTVTLSDVNDNPKPQSLQFVETAGRG 276
QY 260 TLVGRLLAODPDLDGNALMAYSILDEGESEAFSISTDLQGRDGLTVRKPLDPESORSYS 319
DB 277 EEWGRVAKXDPDLDGNGLVYNIIVDGDGE--FEITTDYEHOG--VKKKPVDPETKRAVS 332
QY 320 FRYEATNTLLDPAYLARGPKDYASVRVANQDAPPEPAFQAAYHILTVENKAPFTLVGQ 379
DB 333 LK-EAANVHIDPFKISNGPKDYTVYKI-VEDADEPMPFLABPYTHEVEENAAAGTVGR 390
QY 380 ISADJUDSPASPIRYSILPHSDPERCFSLQPEEGITHTAAPLDREARAHMNTLVATELG 439
DB 391 VHAADPDANSP-RYSIDRTDLDREFTINPEDGFKITKPLDRETAHLNI-VFAAEI- 448
QY 440 WMSGPERGWPLVLAEMSAAPAPQASAVGIPQDSSAQASRVQVALIQLDENDNAP 499
DB 449 -----HNRHOEKVPAIRVLVDVNDAP 470
QY 500 QLAPEYDTPVCDAAAGQLIVIRALDRDVGNSHVSFGP-AGPD---ANFTVQDNRL 556
DB 471 KFAAPBEGFICSDKLSNQ-PIVTSADDDDDIANGPFIFSLP--BEIHNPNTVQDNRDN 527
QY 557 PA-----WFFPLIMASASSMLHMPAERGNQASQKSSLP-CG-RLEP 599

DB 528 TAGVYARRCGFSRQKODYLLPIVI-----SDGIDPMSSTNTLTKVCGCDVNG 576
QY 600 ALPSC 604
DB 577 ALLSC 581

RESULT 15
US-08-188-228-44
Sequence 44, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shitaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bortun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-44

Query Match 45.0%; Score 1468; DB 1; Length 532;
Best Local Similarity 54.6%; Pred. No. 6.5e-125;
Matches 271; Conservative 89; Mismatches 98; Indels 38; Gaps 1;

QY 23 LLRTSRWMNQFVIEEYAGPEVLLGKLSHDVDRGEKTKYLITGEGATVVIDEAT 82
DB 56 LNRKRGWMNQFVIEEYAGPEVLLGKLSHDVDRGEKTKYLITGEGATVVIDEAT 115
QY 83 GNIVHTKSLDREKAAQVYLLAQAVDRASNPLEPSEFIKGGDINDNPFIPLGYHAT 142
DB 116 GDIAHAIKRLDREKAAQVYLLAQAVDRASNPLEPSEFIKGGDINDNPFIPLGYHAT 175
QY 143 VPEMSNVGTSVIQTVAHDADDPYSGNSAKLVYTVLDGLPFSVDPQTGVVRAIPM 202
DB 176 VPEMSNVGTSVIQTVAHDADDPYSGNSAKLVYTVLDGLPFSVDPQTGVVRAIPM 235
QY 203 TQEEFLVYIAOKMGHMGGLSGSTVTVTLSDVNDNPKPQSLQFVETAGRGV 262

Wed Dec 8 11:46:33 2004

us-09-788-051-7.rat

Page 11

```
Db 236 AKERYLVVIAQKDMGSHSGGIGTTTLTVLTVNDNPPKFAQSLYHPSVPEDEVIGTAT 295
QY 263 GRLRAODPDLGDNALMAYSLIDGEGSEAFSISTDLQGRDGLTVRKPLDFESQSYSPRV 322
Db 296 GRVXANDODIGENAOSSYDITIDGDTALFEITSDAQADGVIRKRLDDEFETKSYTLKV 355
QY 323 EATNTLIDPAYLRGPFKDVASVRAVODAPPEPPATQAAYHLLVPEKAPGTLVQISA 382
Db 356 EAANIHIDPFPFGRGPFKDTATVKIYVEDADEPVPFSSPTLLEVENAALNSVIGQVTA 415
QY 383 ADLSPAGPIRYSLIFHSDPERCFSTIOPEEGTIHTAAPLDREARAHNLTVLATELGWSW 442
Db 416 RDPDITSSPIRFSIDRHTDLERQENINADDKITLALTPLDRELsvMHNISITATEI---- 471
QY 443 GPERGWVPLVAVWSAPAPAPQSPFVGSVAVGIPODSSAQASRVQVAIQTLDENNDAPOLA 502
Db 472 -----RNHSQISRVPAIKVLDVNDNAPEFA 497
QY 503 ERYDTFVCGDSAPQOL 518
Db 498 SEYBAFLCENGKPGOV 513
```

Search completed: December 8, 2004, 10:01:12
Job time : 76.9315 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model
Run on: December 8, 2004, 09:16:13 / Search time 3.88194 Seconds
(without alignments)
1189.717 Million cell updates/sec

Title: US-09-788-051-8
Perfect score: 259
Sequence: 1 PSEPIKQDINDNPPFPL.....EMSNVGTGVQTADADDP 48
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 segs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	189	73.0	796	2	A38992
2	187	72.2	796	2	I48277
3	187	72.2	796	2	I48556
4	187	72.2	796	2	A53584
5	186	71.8	793	2	D38992
6	177	68.3	790	2	G02678
7	172	66.4	785	2	I50180
8	171	66.0	790	2	I51638
9	166	64.1	790	2	I37016
10	164	63.3	789	2	I52701
11	162	62.5	790	2	I50178
12	162	62.5	794	2	I59372
13	144	55.6	784	1	I4HUC5
14	121	46.7	871	2	S47518
15	111	42.9	713	2	B38992
16	106	40.9	712	1	I4HUC1
17	106	40.9	717	2	I51206
18	106	40.9	877	1	I4HUCN
19	106	40.9	906	1	I4HUCN
20	106	40.9	912	1	I4HUCN
21	106	40.9	1043	1	I4HUC1
22	106	40.9	1049	1	I4HUC1
23	106	40.9	1547	1	I4HUC1
24	104	40.2	4351	1	I4HUC1
25	103	39.8	3097	2	T00021
26	102	39.4	906	1	I4HUCN
27	100	38.6	906	1	I4HUC2
28	99	38.2	896	1	I4HUC2
29	98	37.8	732	1	I4HUCB

30	98	37.8	847	1	I4HUCB	desmocollin 3b pre
31	98	37.8	901	1	I4HUCB	desmocollin 3a pre
32	98	37.8	1117	2	S38673	desmoglein 2 - hum
33	97	37.5	809	1	I4HUCD	desmocollin 2b pre
34	97	37.5	863	1	I4HUCD	desmocollin 2a pre
35	96	37.1	905	1	I4HUC1	N-cadherin 1 precu
36	95	36.7	770	2	B48910	desmocollin 1b pre
37	95	36.7	824	2	A48910	desmocollin 1a pre
38	95	36.7	840	2	I37281	Dscib precursor -
39	95	36.7	894	2	I37282	hypothetical prote
40	94	36.3	26.0	2	T20968	cadherin 1 precurs
41	93	35.9	882	1	I4HUC5	N-cadherin precurs
42	92	35.5	783	2	I50116	desmocollin 1a - b
43	91	35.1	761	1	I4HUCD	desmocollin 1b pre
44	91	35.1	832	2	S53396	desmocollin 1b pre
45	91	35.1	839	1	I4HUCD	desmocollin 1b pre

ALIGNMENTS

RESULT 1
A38992
cadherin 11 precursor - human
N/Alternate names: OB-cadherin, osteoblast
C/Species: Homo sapiens (man)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 03-Jul-2004
C/Accession: A38992
R/Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous
A/Reference number: S24305; MUID:91283540; PMID:2059658
A/Accession: A38992
A/Status: preliminary; translated from GB/EMBL/DDSD
A/Molecule type: mRNA
A/Residues: 1-796 <SUZ>
A/Cross-references: UNIPROT:P55287; GB:U34056; NID:9506403; PIDN:AAA35622.1; PID:950640
C/Genetics:
A/Gene: CDB:CDH11; OB
A/Cross-references: GDB:512891; OMIM:600023
A/Map position: 16q22.1-16q22.1
C/Suprafamily: cadherin; cadherin repeat homology
C/Keywords: calcium binding; cell adhesion; duplication
F/56-159/Domain: cadherin repeat homology <CR1>
F/162-268/Domain: cadherin repeat homology <CR2>
F/271-383/Domain: cadherin repeat homology <CR3>
F/386-488/Domain: cadherin repeat homology <CR4>

Query Match 73.0%; Score 189; DB 2; Length 796;
Best Local Similarity 79.2%; Pred. No. 3.8e-16;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 PSEPIKQDINDNPPFPLGPYHATVPKMSNVGTGVQTADADDP 48
Db 142 PSEPIKQDINDNPPFPLHETHTANVPKMSNVGTGVQTADADDP 189

RESULT 2
I48277
cadherin-11 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I48277
R/Hoffmann, I.; Balling, R.
Dev. Biol. 169, 337-346, 1995
A/Title: Cloning and expression analysis of a novel mesodermally expressed cadherin.
A/Reference number: I48277; MUID:95269866; PMID:7750649
A/Accession: I48277
A/Status: preliminary; translated from GB/EMBL/DDSD
A/Molecule type: mRNA
A/Residues: 1-796 <RBS>
A/Cross-references: UNIPROT:P55288; EMBL:X77557; NID:9642796; PIDN:CAA54674.1; PID:9666
C/Genetics:

A:Gene: cad-11
C:Superfamily: cadherin; cadherin repeat homology
F:156-159/Domain: cadherin repeat homology <CDH>

Query Match
Best Local Similarity 72.2%; Score 187; DB 2; Length 796;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPPFPLGPHATVPEMSNVGTSVQVTAHDADDP 48
DB 142 PSEFIKQDINDNPPFPLGPHATVPEMSNVGTSVQVTAHDADDP 189

RESULT 3
149556
cadherin-11 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: 149556
R:Kimura, Y.; Matsunami, H.; Inoue, T.; Shimamura, K.; Uchida, N.; Ueno, T.; Miyazaki, T.
Dev. Biol. 169, 347-358, 1995
A:Title: Cadherin-11 expressed in association with mesenchymal morphogenesis in the head
A:Reference number: 149556; PMID:95265887; PMID:7750650
A:Accession: 149556
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-796 <RES>

A:Cross-references: UNIPROT:P55288; GB:D12153; NID:G994774; PIDN:BA04797.1; PID:G974191
C:Superfamily: cadherin; cadherin repeat homology
F:156-159/Domain: cadherin repeat homology <CDH>

Query Match
Best Local Similarity 72.2%; Score 187; DB 2; Length 796;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPPFPLGPHATVPEMSNVGTSVQVTAHDADDP 48
DB 142 PSEFIKQDINDNPPFPLGPHATVPEMSNVGTSVQVTAHDADDP 189

RESULT 4

A53584
OB-cadherin precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: A53584
R:Okazaki, M.; Takeshita, S.; Kawai, S.; Kikuno, R.; Tsujimura, A.; Xudo, A.; Amano, E.
J. Biol. Chem. 269, 12092-12098, 1994
A:Title: Molecular cloning and characterization of OB-cadherin, a new member of cadherin
A:Reference number: A53584; PMID:94216322; PMID:8163513
A:Accession: A53584
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-796 <OKA>
A:Cross-references: UNIPROT:P55288; GB:D12153; NID:G994774; PIDN:BA04797.1; PID:G994775
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: transmembrane protein
F:156-159/Domain: cadherin repeat homology <CR1>
F:162-268/Domain: cadherin repeat homology <CR2>
F:162-268/Domain: cadherin repeat homology <CR4>

Query Match
Best Local Similarity 72.2%; Score 187; DB 2; Length 796;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPPFPLGPHATVPEMSNVGTSVQVTAHDADDP 48
DB 142 PSEFIKQDINDNPPFPLGPHATVPEMSNVGTSVQVTAHDADDP 189

RESULT 5
D38992
cadherin 8 - human

C:Species: Homo sapiens (man)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
C:Accession: D38992
R:Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991

A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous
A:Reference number: S24305; PMID:91283540; PMID:2055658
A:Accession: D38992
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-793 <SUZ>
A:Cross-references: GB:L34060; NID:G506411; PIDN:AAA5628.1; PID:G506412
C:Genetics:
A:Gene: GDB:CDH8
A:Cross-references: GDB:5822911
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication
F:163-269/Domain: cadherin repeat homology <CDH>

Query Match
Best Local Similarity 71.8%; Score 186; DB 2; Length 793;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPPFPLGPHATVPEMSNVGTSVQVTAHDADDP 48
DB 143 PSEFIKQDINDNPPFPLGPHATVPEMSNVGTSVQVTAHDADDP 190

RESULT 6

G02678
cadherin-14 - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C:Accession: G02678
R:Shibata, T.; Shimoyama, Y.; Gotoh, M.; Hirohashi, S.
submitted to the EMBL Data Library, May 1996
A:Reference number: H01584
A:Accession: G02678
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-790 <SHI>
A:Cross-references: UNIPROT:Q13634; EMBL:U59325; NID:G1389852; PIDN:AA02933.1; PID:G13
C:Superfamily: cadherin; cadherin repeat homology
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match
Best Local Similarity 68.3%; Score 177; DB 2; Length 790;
Matches 36; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 SEFIKQDINDNPPFPLGPHATVPEMSNVGTSVQVTAHDADDP 48
DB 143 SEFIKQDINDNPPFPLGPHATVPEMSNVGTSVQVTAHDADDP 189

RESULT 7

I50180
cadherin-7 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: I50180
R:Nakagawa, S.; Takeichi, M.
Development 121, 1321-1332, 1995
A:Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spec
A:Reference number: I50178; PMID:95309115; PMID:7540531
A:Accession: I50180
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-785 <NAK>
A:Cross-references: UNIPROT:Q90763; GB:D42150; NID:G868000; PIDN:BA07721.1; PID:G868001
C:Superfamily: cadherin; cadherin repeat homology
F:156-262/Domain: cadherin repeat homology <CDH>

Query Match
Best Local Similarity 66.4%; Score 172; DB 2; Length 785;


```

Best Local Similarity 76.6%; Pred. No. 5.8e-14;
Matches 36; Conservative 2; Mismatches 9; Indels 0; Gaps 0.

```

Qy 2 SEFIKGGDINDNPPETPLGPHYATVPMSNVGSVIQTALHADDP 48
| | | | | : | | | | | : | | | | |
Db 137 SEFVIKIQQDINDNEPKFLDGPTAGVFEMSPVGISVVQVTALDADDP 183

RESULT 8
TEST 639

F:cadherin - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I51638; S55391
R:Espeseth, A.; Johnson, E.; Kintner, C.
Mol. Cell. Neurosci. 6, 199-212, 1995
A>Title: Xenopus F-cadherin, a novel member of the cadherin family of cell adhesion mole
A:Reference number: I51638; MUID:96039533; PMID:7496627
A:Accession: I51638
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-790 <ES>
A:Cross-references: UNIPROT:Q91838; EMBL:X85330; NID:G854634; PIDN:CAAS9679.1; PID:G854634
C:Superfamily: cadherin; cadherin repeat homology
F:161-267//Domain: cadherin repeat homology <CR2>

Query Match	66.0%	Score 171	DB 2	Length 790
Best Local Similarity	74.5%	Pred No	7.9e-14	
Matches 35	Conservative	4	Mismatches 8	Indels 0
				Gaps 0

```

OY      2 SEFIKQGINDPPIFPLGYHATVPEMSNVGTSVIQVTAHADDP 48
      |||:|||||:|||||:|||||
DB      142 SEFIKVIQDINDNEPKFLDGPYASVPEMSVGTSTIIQVSATADDDP 18

```

RESULT

cadherin-6 human
 C|Species: Homo sapiens (man)
 C|Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
 C|Accession: I37016
 R|Shimoyama, Y.; Gotoh, M.; Terasaki, T.; Kitajima, M.; Hirohashi, S.
 C|Cancer Res. 55, 2206-2211, 1995
 A|Title: Isolation and sequence analysis of human cadherin-6 complementary DNA for the E
 A|Reference number: I37016; M01D:95562134; PMID:774525
 A|Accession: I37016
 A|Status: preliminary; translated from GB/EMBL/DBJ
 A|Molecule type: mRNA
 A|Residues: 1-790 <RES>
 A|Cross-references: UNIPROT:P55285; GB:DJ1784; NID:G974184; PIDN:BAA06562.1; PID:G974185
 C|Gene: GDB:CDH6
 A|Gene: GDB:CDH6
 A|Cross-references: GDB:S822908
 C|Superfamily: cadherin; cadherin repeat homology
 F|162-268/Domain: cadherin repeat homology <CDH>

```

Query Match          64.1%;      Score 166; DB 2;      Length 790;
Similarity          74.5%;      Pred. No. 3.5e-13;
Best Local          2; Mismatches 10; Gaps 0;
Matches 35; Conservative

```

```

QY      2 SEFIIRKQDINDNPIPIPLGPHYATVPKMSNVGTSVIGYTAHADDDP 48
      ||||| ||||| ||||| :||| :||| |||||
Db      143 SEFIIRKIHNDINDNEPIFTKEVYATATVPKMSDVGTFVVGQTATDADDP 189

```

RESULT 10

K-cadherin - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I52701
R:Xiang, Y.Y.; Tanaka, M.; Suzuki, M.; Igarashi, H.; Kiyokawa, E.; Naito, Y.; Ohtawara, T. *FEBS Lett* 302:2001 1994

AltTitle: Isolation of complementary DNA encoding K-cadherin, a novel rat cadherin preferring
AltReference number: 152701; MUID:94243827; PMID:8187093
AltAccession: 152701
AltAccession: 152701

A:Stictus: preliminary; translated from GB/ENGB, 1990
A:Molecule type: mRNA
A:Residues: 1-789 <RES>
A:Cross-references: UNIPROT:P55280; GB:D25290; PIDN:BA064975.1; PID:G435461

A/gene: NCAD
C/Superfamily: cadherin; cadherin repeat homology
F;162-268/Domain: cadherin repeat homology <CDH>

Query Match	63.3%	Score 164	DB 2	length 789
Best Local Similarity	72.3%	Pred. No.	6.3e-13	
Matches	34	Conservative	3	Mismatches 10
				Indels 0
				Gaps 0

QY 2 SEFIITKGDINDNPPIFPLPGYHATVPBMSNVGSVIOVTAHADDP 48
 ||||| ||||| :||| :||| |||||
 DB 143 SEFIITKIHNDINNEPIFTKQVYTAVPBMAVDGTFVQVTAATDADDP 188
 ||||| ||||| :||| :||| |||||

RESULT 11

cadherin-6B - chicken
C.Species: Gallus gallus (chicken)
C.Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C.Accession: 150178
R.Nakagawa, S.; Takeichi, M.
Development 121, 1321-1332, 1995
A.Title: Neutral crest cell-cell adhesion controlled by sequential and subpopulation-specific
A.Reference number: 150178; PMID:95309115; PMID:7540531
A.Accession: 150178
A.Status: preliminary; translated from GB/EMBL/DBD
A.Molecule type: mRNA
A.Residues: 1-790 <NA>
C.Cross-references: UNIPROT:Q90762; GB:ID42149; NID:9867998; PIDN:BA007720.1; PID:9867999
C.superfamily: cadherin; cadherin repeat homology
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match	62.5%	Score	162;	DB 2;	Length	790;			
Similarity	68.1%	Pred	No	1..1e-12;					
Best Local									
Matches	32;	Conservative	6;	Mismatches	9;	Indels	0;	Gaps	0

```

Oy      2 SEFIKKODINDNPFIFPLGYPYHATVPEMSNVGTSVIOYTAHADDDP 48
        ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db      143 SEFIKKIHNDNDNEPMFTKDVYNASIPMSDVGTFVWQYATATDADDP 189

```

RESULT 12

cadherin 12 - human
N/Alternate names: Br-cadherin
C/Species: Homo sapiens (man)
C/Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 03-Jul-2004
C/Accession: I59372
R/Sel13, S.; Bruno, S.; Scharf, J.M.; Wang, C.H.; Vitale, E.; Gilliam, T.C.; Kunkel, L.
P/Sci13, Acad. Sci. U.S.A. 92, 3702-3706, 1995
A>Title: Expressed cadherin pseudogenes are localized to the critical region of the sp1
A/Reference number: I59372; MIM:952495.1; PMID:7731868
A/Accession: I59372
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A/Molecule type: mRNA
A/Residues: 1-794 <ES>
A/Cross-references: UNI:PROT:P55289; GB:U33477; NID:G793342; PIDN:AAB40539.1; PID:G79394
C/Genetics: OMIM

A:gene: GDB:ICU412
A:Cross-references: GDB:596324
A:Map position: 5p13-5p.14
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication; transmembrane protein
F:57-160/Domain: cadherin repeat homology <CR1>
F:163-269/Domain: cadherin repeat homology <CR2>
F:272-384/Domain: cadherin repeat homology <CR3>

F:387-489/Domain: cadherin repeat homology <CR4>
F:491-601/Domain: cadherin repeat homology <CR5>
F:610-637/Domain: transmembrane #status predicted <TM>
F:638-794/Domain: intracellular #status predicted <INT>

Query Match 62.5%; Score 162; DB 2; Length 794;
Best Local Similarity 74.5%; Pred. No. 1,1e-12;
Matches 35; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 2 SEFIKQDINDNDPPIPLGPHATVPMSNVGTSTVQVTAHDADD 48
DB 144 SEFIKQDINDNDPPIPLGPHATVPMSNVGTSTVQVTAHDADD 190

RESULT 13

10HUCS

cadherin 5 precursor - human

N/Alternate names: 7B4 antigen; cadherin, endothelial-specific; VE-cadherin

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1993 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C/Accession: S49893; S24305; A43418

R/Reviewer: F.; Cavada, L.; Corada, M.; Martin-Padura, I.; Golay, J.; Introna, M.; Lamg

A/Description: Molecular and functional properties of VE-cadherin (7B4/cadherin-5) a nov

A/Reference number: S49893

A/Accession: S49893

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-784

A/Cross-references: UNIPROT:P3151; EMBL:X79981; NID:G599833; PIDN:CAA56306.1; PID:G5998

R/Suzuki, S.; Sano, K.; Tanhara, H.

Cell Regul. 2, 261-270, 1991

A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t

A/Reference number: S24305; MUID:91283540; PMID:2059658

A/Accession: S24305

A/Molecule type: mRNA

A/Residues: 5-516, 'I', 518-784 <SU2>

A/Cross-references: EMBL:X59796; NID:G639976; PIDN:CA442468.1; PID:G29593

R/Lampunant, M.G.; Resnati, M.; Raiteri, M.; Pigott, R.; Pisacane, A.; Houen, G.; Ruco,

J. Cell Biol. 118, 1511-1522, 1992

A/Title: A novel endothelial-specific membrane protein is a marker of cell-cell contacts

A/Reference number: A43418; MUID:92394977; PMID:1522121

A/Accession: A43418

A/Molecule type: protein

A/Residues: 48-60, 'X', '62', 'X', '64', '108-116', 'X', '118-133', '237-238', 'X', '240', 'X', '242-252', 'X', '254-

A/Experimental source: cultured endothelial cells

A/Note: sequence extracted from NCBI backbone (NCBI:113040, NCBI:113045, NCBI:113047,

C/Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought t

C/Genetics:

A/Genes: GDB:CDHS

A/Cross-references: GDB:134230; OMIM:601120

A/Map position: 16q22.1-16q22.1

C/Superfamily: cadherin; cadherin repeat homology

C/Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane pro

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-47/Domain: propeptide #status predicted <PRO>

F:48-784/Product: cadherin 5 #status predicted <MAT>

F:49-593/Domain: extracellular #status predicted <EXT>

F:50-151/Domain: cadherin repeat homology <CR1>

F:154-258/Domain: cadherin repeat homology <CR2>

F:261-372/Domain: cadherin repeat homology <CR3>

F:375-479/Domain: cadherin repeat homology <CR4>

F:481-587/Domain: cadherin repeat homology <CR5>

F:594-620/Domain: transmembrane #status predicted <TM>

F:621-784/Domain: intracellular #status predicted <INT>

F:736-753/Region: serine-rich

F:61,112,157,362,442,523,535/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 55.6%; Score 144; DB 1; Length 784;

Best Local Similarity 62.5%; Pred. No. 2.4e-10;

Matches 30; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNDPPIPLGPHATVPMSNVGTSTVQVTAHDADD 48

DB 134 PSEFIKQDINDNDPPIPLGPHATVPMSNVGTSTVQVTAHDADD 181

RESULT 14

S47518

cadherin - African clawed frog

C/Species: Xenopus laevis (African clawed frog)

C/Date: 01-Feb-1995 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999

C/Accession: S47518

R/Tool: O.; Fujii, G.; Tashiro, K.; Shikawa, K.

Biochim. Biophys. Acta 1219, 121-128, 1994

A/Title: Molecular cloning of cDNA for XTCAD-1, a novel Xenopus cadherin, and its expe

A/Reference number: S47518; MUID:94368839; PMID:8086449

A/Accession: S47518

A/Molecule type: mRNA

A/Residues: 1-871 <TCO>

C/Superfamily: cadherin; cadherin repeat homology

F:151-256/Domain: cadherin repeat homology <CR1>

Query Match 46.7%; Score 121; DB 2; Length 871;

Best Local Similarity 53.2%; Pred. No. 2.5e-07;

Matches 25; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNDPPIPLGPHATVPMSNVGTSTVQVTAHDADD 47

DB 239 PSEFIKQDINDNDPPIPLGPHATVPMSNVGTSTVQVTAHDADD 265

RESULT 15

B38992

cadherin 13 precursor - human

N/Alternate names: H-cadherin; T-cadherin

C/Species: Homo sapiens (man)

C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C/Accession: B38992; G02676

R/Suzuki, S.; Sano, K.; Tanhara, H.

Cell Regul. 2, 261-270, 1991

A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t

A/Reference number: S24305; MUID:91283540; PMID:2059658

A/Accession: B38992

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-713 <SU2>

A/Cross-references: UNIPROT:P55290; GB:L34058; NID:G506407; PIDN:AAA35624.1; PID:G506408

R/Lue, S.W.

submitted to the EMBL Data Library, May 1996

A/Reference number: H01582

A/Accession: G02676

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-713 <LSE>

A/Cross-references: EMBL:U59288; NID:G1381789; PIDN:AA18911.1; PID:G1381790

C/Genetics:

A/Genes: GDB:CDH13

A/Cross-references: GDB:5822917; OMIM:601364

C/Superfamily: cadherin; cadherin repeat homology

C/Keywords: blocked carboxyl end; calcium binding; cell adhesion; duplication; glycoprot

F:1-32/Domain: signal sequence #status predicted <SIG>

F:723-138/Domain: amino-terminal propeptide #status predicted <PRO>

F:139-693/Product: cadherin 13 #status predicted <MAT>

F:141-245/Domain: cadherin repeat homology <CR1>

F:248-363/Domain: cadherin repeat homology <CR2>

F:366-477/Domain: cadherin repeat homology <CR3>

F:480-585/Domain: cadherin repeat homology <CR4>

F:586-681/Domain: cadherin repeat homology <CR5>

F:684-712/Domain: carboxyl-terminal propeptide #status predicted <CPR>

F:732,500,530,638,671/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:693/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form

Query Match 42.9%; Score 111; DB 2; Length 713;

Best Local Similarity 54.2%; Pred. No. 3.8e-06;

Matches 26; Conservative 5; Mismatches 15; Indels 2; Gaps 1;

QY 1 PSEFIKQDINDNDPPIPLGPHATVPMSNVGTSTVQVTAHDADD 48

Wed Dec 8 11:46:36 2004

us-09-788-051-8.rpr

Page 5

QY 1 PSEFIIRGGDINDNPPIPIPLGPIPHATVPENSNVGTSLVQVTAHDADDP 48
| : | | | | | : : : | | | |
Db 230 PLEVIVIDQ--NDNRPIIFREPGYIGHVMEGSPGTITVMKNTAFDADDP 275

Search completed: December 8, 2004, 10:27:05
Job time : 3.68194 secs

This Page Blank (uspto)

DT	01-OCT-903 (T-EMBLrel_25, Last annotation update)
DE	Hypothetical protein FLJ25193.
OS	Homo sapiens (human).
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxId=9606; [1]
RN	
RP	SEQUENCE FROM N.A.
RC	TISSUE=Thyroid.
RA	Nitomiyu K., Nagasuna M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA	Futuya T., Takahashi M., Kitkawa B., Omura Y., Aze K., Kamihara K.,
RA	Katsuta S., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
RA	Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA	Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA	Nagai K., Isegai T., Sugano S.; Submitted (Oct-2001) to the EMBL/Genbank/DBJ databases.
CC	-1-SIMILARITY: contains 4 cadherin domains.
DR	EMBL; AK057922; BAB71613.1; -
DR	HSSP; F12830; 106S.
DR	GeneW; HGNC:14265; CDH24.
DR	GO; GO:0016020; Cmembrane; IEA.
DR	GO; GO:0005509; P:calcium ion binding; IEA.
DR	GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR	InterPro; IPRO02126; Cadherin.
DR	Pfam; PF00028; Cadherin; 4.
DR	PRINTS; PR0205; CADHERIN.
DR	SMART; SM0112; CA; 4.
DR	PROSITE; PS00232; CADHERIN_1; 2.
DR	PROSITE; PS50268; CADHERIN_2; 4.
DR	Calciun; Calcium-binding.
KW	SEQUENCE 493 AA; 53618 MW; 33F1DFF63AP0FCIE CRC64;
SQ	
Query Match	96.5%; Score 250; DB 2; Length 493;
Best Local Similarity	97.9%; Pred. No. 2e-22;
Matches 47; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Cy	1 PSEFIKGGDINDNDPIPLGLGYATVEMNGTSYICQTADADD 48
Db	133 PSEFIKGVODINDNDPIPLGLGYATVEMNGTSYICQTADADD 180
RESULT 3	
ID	CADO_HUMAN STANDARD; PRT; 819 AA.
AC	O86UF0; O86UPL; Q9NT84;
DT	29-MAR-2004 (Rel. 43, Created)
DT	29-MAR-2004 (Rel. 43, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Cadherin-24 precursor [UNO2834/PRO34009].
GN	Name=CDH24; Synonyms=CDH11L.
OS	Homo sapiens (human).
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxId=9606; [1]
RN	
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND INTERACTIONS WITH
RP	CATENINS.
RX	MEDLINE=22753805; PubMed=12734196; DOI=10.1074/jbc.M304119200;
RA	Katataias B.J., Nieman M.T., Wheelock W.J., Johnson K.R.;
RT	"Characterization of cadherin-24, a novel alternatively spliced type
RT	II cadherin.";
RL	J. Biol. Chem. 278(27):27513-27519(2003).
RN	[2]
RP	SEQUENCE FROM N.A. (ISOFORM 2).
RX	MEDLINE=22867286; PubMed=12975309; DOI=10.1101/gr.1293003;
RA	Clark H.F., Gutney A.L., Adaya E., Baker K., Baldwin D., Brush J.,
RA	Chen J., Chow B., Choi C., Crowley C., Currell B., Deuel B., Dowd P.,
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heidens S.,
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA	Seshgiri S., Simone L., Singh J., Smith V., Stinson J., Vasta A.,
RA	Vandlen R., Watanabe C., Weard D., Woods K., Xie M.-H., Yasuda D.,
RA	Yi S., Yu G., Yuan Y., Zhang W., Zhang Z., Goddard A., Wood W.I.,

RA	Godowak P., Gray A.:
RT	"The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."
RL	Bioinformatics 13:2265-2270(2003).
RN	[3]
RP	SEQUENCE FROM N.A. (ISOFORM 3).
RC	TISSUE=Testis;
RA	Blum H., Banerachs S., Mewes H.-W., Gassenhuber J., Wiemann S.; Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC	-1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins. They preferentially interact with themselves in a homophilic manner in connecting cells; cadherin may thus contribute to the sorting of heterogeneous cell types. Cadherin-24 mediate strong cell-cell adhesion.
CC	-1- SUBUNIT: Associates with alpha-, beta- and delta-catenins.
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC	-1- ALTERNATIVE PRODUCTS:
CC	Name=1; Synonyms=Long form;
CC	Isoid=Q86UP0-1; Sequence=D;Displayed;
CC	Name=2; Synonyms=Short form;
CC	Isoid=Q86UP0-2; Sequence=VSP_008717;
CC	Name=3;
CC	Isoid=Q86UP0-3; Sequence=VSP_008718, VSP_008719;
CC	Note=No experimental confirmation available;
CC	-1- SIMILARITY: Contains 5 cadherin domains.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/isb-sib.ch).
CC	or send an email to license@isb-sib.ch .
CC	-----
DR	EMBL, AY260900, AAP20590.1, -
DR	EMBL, AY260901, AAP20591.1, -
DR	EMBL, AY358199, AAQ85656.1, -
DR	EMBL, AL137477, CAB70758.1, -
DR	PIR, T46418, T46418.
DR	HSSP, P09803, ITTW.
DR	Genev, HGNC:14265; CDH24.
DR	InterPro, IPR002126; Cadherin.
DR	InterPro, IPR000233; Cadherin_C term.
DR	Pfam, PF00028; Cadherin_5.
DR	Pfam, PF01049; Cadherin_C_1.
DR	PRINTS, PRO0203; CADHERIN.
DR	PROSITE, PS00232; CADHERIN.
DR	PROSITE, PS0268; CADHERIN_1; 2.
KM	Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein; Multigene family; Repeat; Signal; Transmembrane.
FT	SIGNAL 1 19
FT	PROPEP 21 44
FT	CHAIN 45 819
FT	DOMAIN 45 641
FT	TRANSMEM 642 662
FT	DOMAIN 663 819
FT	DOMAIN 46 150
FT	DOMAIN 151 259
FT	DOMAIN 250 374
FT	DOMAIN 375 517
FT	DOMAIN 517 630
FT	CARBOHYD 446 446
FT	CARBOHYD 548 548
FT	CARBOHYD 563 563
FT	VARSPLIC 455 492
FT	
FT	VARSPLIC 1 427
FT	
FT	VARSPLIC 428 492
FT	
FT	VARSLIC 428 492
FT	
FT	EGRHTAPEDREARMHLTYLATELGSGMPREGWPLT VAEESAAAPDPSPGVSAVGIDP -> NKIVCTYCSHS ATFESTCTHAVMCFCLMLVASCGIHAIAPMLLVNCVC

FT VWRVCFGLPS (in isoform 3).
 FT /FTID=VSP_008719.
 SO SEQUENCE 819 AA; 87751 MW; 9083034F18BA7E84 CRC64;

Query Match 96.5%; Score 250; DB 1; Length 819;
 Best Local Similarity 97.9%; Pred. No. 3,5e-22;
 Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSEFIIKQDINDNPFPLGPHATVPMSNVGTSVIOVTAHADDP 48
 DB 133 PSEFIIKQDINDNPFPLGPHATVPMSNVGTSVIOVTAHADDP 180

RESULT 4

Q6PFK6 PRELIMINARY; PRT; 781 AA.

AC Q6PFK6;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Cadherin-like 24.
 GN Name=Cdh24;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stajich M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schultz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalski U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 RU Subtitled (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC -1- (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL: BC057373; AAH57373.1; -
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR000233; Cadherin_C-term.
 DR Pfam: PF00028; Cadherin_5.
 DR Pfam: PF01049; Cadherin_C_1.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SM00112; CA; 4.
 DR PROSITE: PS00232; CADHERIN_1; 2.
 DR PROSITE: PS00268; CADHERIN_2; 5.
 KW Calcium-binding; Cell adhesion; Transmembrane.
 SO SEQUENCE 781 AA; 84104 MW; 15996DE6C9835AA CRC64;

Query Match 96.1%; Score 249; DB 2; Length 781;
 Best Local Similarity 95.8%; Pred. No. 4.4e-22;

Matches 46; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSEFIIKQDINDNPFPLGPHATVPMSNVGTSVIOVTAHADDP 48
 DB 133 PSEFIIKQDINDNPFPLGPHATVPMSNVGTSVIOVTAHADDP 180

RESULT 5

AAH57373 PRELIMINARY; PRT; 781 AA.

AC AAH57373;
 DT 02-MAR-2004 (TRENBLrel. 27, Created)
 DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)
 DE Cadherin-like 24.
 GN Cdh24.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stajich M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schultz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalski U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC057373; AAH57373.1; -
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR000233; Cadherin_C-term.
 DR Pfam: PF00028; Cadherin_5.
 DR Pfam: PF01049; Cadherin_C_1.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SM00112; CA; 4.
 DR PROSITE: PS00232; CADHERIN_1; 2.
 DR PROSITE: PS00268; CADHERIN_2; 5.
 KW Calcium-binding; Cell adhesion; Transmembrane.
 SO SEQUENCE 781 AA; 84104 MW; 15996DE6C9835AA CRC64;

QY 1 PSEFIIKQDINDNPFPLGPHATVPMSNVGTSVIOVTAHADDP 48
 DB 133 PSEFIIKQDINDNPFPLGPHATVPMSNVGTSVIOVTAHADDP 180

RESULT 6

093264 PRELIMINARY; PRT; 794 AA.

AC 093264;
 DT 01-NOV-1998 (TRENBLrel. 08, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Cadherin precursor.
 GN Name=Cad-11;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

```

OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=zygote;
RA MEDLINE=9820517; PubMed=9533956;
RA Hagedall B., Borchers A., Medlich D.;
RT "Xenopus cadherin-11 (Xcadherin-11) expression requires the wg/mnt
RT signal";
RL Mech. Dev. 72:101-113(1998).
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 5 cadherin domains.
DR EMBL: AF002983; AAC8073.1; -
DR HSSP: P09803; 117W.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C-term.
DR Pfam: PF00028; Cadherin; 5.
DR Pfam: PF01049; Cadherin; C. 1.
DR PRINTS: PR00205; CADHERIN.
DR SMART: SM00112; CA; 5.
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS00268; CADHERIN_2; 5.
KW Calcium; Calcium-binding; Cell adhesion; Signal; Transmembrane.
FT SIGNAL 1 53 Potential.
FT CHAIN 54 794 cadherin.
SQ SEQUENCE 794 AA; 88302 MW; 7221AD4CEA719DB CRC64;

Query Match 74.9%; Score 194; DB 2; Length 794;
Best Local Similarity 81.2%; Pred.No. 3,1e-15;
Matches 39; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Cy 1 PSEFICQDINDNPFPLGPAATVPEMSNVGTSTVCTAHADDP 48
Db 142 PSEFIVKQDINDNPFPLHNVHANVPEMSNVGTSTVCTAHADDP 189

RESULT 7
CADA_HUMAN STANDARD; PRT; 796 AA.
AC P55287; Q15065; Q15066; Q9U093; Q9U094;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSF-4).
GN Name=CDH11;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RX [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RA MEDLINE=9507306; PubMed=7982033;
RA Tanihara H., Sato K., Heilmark R.W., St John T., Suzuki S.;
RT "Cloning of five human cadherins clarifies characteristic features of
RT cadherin extracellular domain and provides further evidence for two
RT structurally different types of cadherin.";
RL Cell Adhes. Commun. 2:15-26(1994).
CC [2]
CC SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Osteosarcoma;
RX MEDLINE=9421632; PubMed=916513;
RA Okazaki M., Takeshita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,
RA Amann E.;
RT "Molecular cloning and characterization of OB-cadherin, a new member
RT of cadherin family expressed in osteoblasts.";
RL J. Biol. Chem. 269:12092-12098(1994).
RX [3]

RP SEQUENCE OF 269-796 FROM N.A. (ISOFORM 1).
RC TISSUE=Fetal Brain;
RX MEDLINE=91283540; PubMed=20596658;
RA Suzuki S., Sano K., Tanihara H.;
RT "Diversity of the cadherin family: evidence for eight new cadherins in
RT nervous tissue.";
RL Cell Regul. 2:261-270(1991).
RN [4]
RP SEQUENCE OF 600-668 FROM N.A. (ISOFORMS 1 AND 2).
RA Kools P.F., Hogendoorn P.C.W., Boeve J.V.M.G., Van Roy F.;
RT "Alternative cadherin-11 transcripts encoding truncated adhesion
RT molecules are detectable in both human cancer and normal cells.";
RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P55287-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P55287-2; Sequence=VSP_000640, VSP_000641;
CC -1- TISSUE SPECIFICITY: Expressed mainly in brain but also found in
CC other tissues. Expressed in neuroblasts.
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL: U34056; AAA35622.1; -
DR EMBL: D21254; BAA04798.1; -
DR EMBL: D21255; BAA04799.1; -
DR EMBL: AF060370; AAD27755.1; -
DR EMBL: AF060369; AAD27755.1; JOINED.
DR EMBL: AF060370; AAD27756.1; -
DR EMBL: AF060369; AAD27756.1; JOINED.
DR PIR: A38992; A38992.
DR HSSP: P09803; 117W.
DR GeneW: HGNC:1750; CDH11.
DR MIM: 600023; -
DR GO: GO:0016021; C:integral to membrane; NAS.
DR GO: GO:0007156; P:homophilic cell adhesion; NAS.
DR GO: GO:0001503; P:ossification; NAS.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C-term.
DR Pfam: PF00028; Cadherin; 5.
DR Pfam: PF01049; Cadherin; C. 1.
DR PRINTS: PR00205; CADHERIN.
DR SMART: SM00112; CA; 5.
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS00268; CADHERIN_2; 5.
KW Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 22 Potential.
FT PROPEP 23 53 Potential.
FT CHAIN 54 796 Cadherin-11.
FT DOMAIN 54 617 Extracellular (Potential).
FT TRANSMEM 618 640 Potential.
FT DOMAIN 641 796 Cytoplasmic (Potential).
FT DOMAIN 54 159 Cadherin 1.
FT DOMAIN 160 268 Cadherin 2.
FT DOMAIN 269 383 Cadherin 3.
FT DOMAIN 384 486 Cadherin 4.
FT DOMAIN 487 612 Cadherin 5.
FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 540 540 N-linked (GlcNAc...) (Potential).

```


FT VARSPIC 632 693 VIVLFTVLRQKKEPLIVEEDVENITITDDEGGED
 FT TEADITLONPDINGFIR -> GCPSPMEPSREDWR
 FT LLYVQQLMCFYKVRFRCLGVFKLPFLVYVATESPT
 FT TITSL (in isoform 2).
 FT /FTID=VSP_000640.
 FT Missing (in isoform 2).
 FT VARSPIC 694 796 /FTID=VSP_000641.
 FT CONFLICT 271 272 RL -> SV (in Ref. 2).
 FT CONFLICT 275 275 M -> I (in Ref. 2).
 FT CONFLICT 340 340 E -> K (in Ref. 2).
 FT CONFLICT 373 373 S -> A (in Ref. 2).
 FT CONFLICT 471 471 Q -> K (in Ref. 2).
 SQ SEQUENCE 796 AA; 88049 MW; 2C67044C7BAUBB2E CRC64;

Query Match 73.0%; Score 189; DB 1; Length 796;
 Best Local Similarity 79.2%; Pred. No. 1.3e-14;
 Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Oy 1 PSEFTIKGQDINDNPPIFLGPHATVPENSVGTSVIQTADADDP 48
 Db 142 PSEFTIVKQDINDNPPEFLHETHTANVPERSNVGTSVIQTADADDP 189

RESULT 8
 ID Q96CZ9 PRELIMINARY; PRT; 796 AA.
 AC Q96CZ9;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Cadherin 11, type 2, isoform 1 preproprotein.
 GN Name=CDH11;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Ditschenko L., Marzetta K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshyuki S., Carninci P., Prange C.,
 RA Bask S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosnak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalski U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC EMBL: BC013609; AAH13609.1; -.
 CC HSSP: P09803; 117W.
 CC GO: GO:0016020; C:membrane; IEA.
 CC GO: GO:0005509; F:calcium ion binding; IEA.

DR GO: GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR000233; Cadherin_C_term.
 DR InterPro: IPR001901; SECE.
 DR Pfam: PF00028; Cadherin_5.
 DR Pfam: PF01049; Cadherin_C_1.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SM00112; CA; 5.
 DR PROSITE: PS00232; CADHERIN_1; 3.
 DR PROSITE: PS00268; CADHERIN_2; 5.
 DR PROSITE: PS01067; SECE_SECEIG; UNKNOWN_1.
 DR Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 796 AA; 87979 MW; 8497F9B834F7547C CRC64;

Query Match 73.0%; Score 189; DB 2; Length 796;
 Best Local Similarity 79.2%; Pred. No. 1.3e-14;
 Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Oy 1 PSEFTIKGQDINDNPPIFLGPHATVPENSVGTSVIQTADADDP 48
 Db 142 PSEFTIVKQDINDNPPEFLHETHTANVPERSNVGTSVIQTADADDP 189

RESULT 9
 ID CADB_CHICK STANDARD; PRT; 792 AA.
 AC Q93319;
 DT 16-OCT-2001 (rel. 40, Created)
 DT 16-OCT-2001 (rel. 40, Last sequence update)
 DT 05-JUL-2004 (rel. 44, Last annotation update)
 DE Cadherin-11 precursor.
 GN Name=CDH11;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
 CC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White Leghorn;
 RA Wei U., Dong X.R., Topczus S., Zimmer W.E., Broders F., Thierry J.P.,
 RA Kotliarsky V., Majesky M.W.;
 RT "Molecular cloning of chick cadherin 11 and its expression during
 RT smooth muscle differentiation and formation of the tunica media.";
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC EMBL: AF055342; AAC33675.1; -.
 DR HSSP: P09803; 117W.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR000233; Cadherin_C_term.
 DR Pfam: PF00028; Cadherin_5.
 DR Pfam: PF01049; Cadherin_C_1.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SM00112; CA; 5.
 DR PROSITE: PS00232; CADHERIN_1; 3.
 DR PROSITE: PS00268; CADHERIN_2; 5.
 DR Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 22 Potential.

FT PROPEP 23 53 Potential.
 FT CHAIN 54 792 Cadherin-11.
 FT DOMAIN 54 613 Extracellular (Potential).
 FT TRAMEM 614 634 Potential.
 FT DOMAIN 635 792 Cytoplasmic (Potential).
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.
 FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 608 Cadherin 5.
 FT CAROXYD 455 455 N-linked (GlcNAc...) (Potential).
 FT CAROXYD 536 536 N-linked (GlcNAc...) (Potential).
 FT CAROXYD 594 594 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 792 AA: 87572 MW: 353486C6868731AB CRC64;

Query Match 72.6%; Score 188; DB 1; Length 792;
 Best Local Similarity 79.2%; Pred. No. 1.7e-14;
 Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Cy 1 PSEFIRKQDINDNPNPLPGPYATYPEKSNVTSYIQTADHPD 48
 142 PSEFIRKQDINDNPNPLPGPYATYPEKSNVTSYIQTADHPD 189

Db 142 PSEFIRKQDINDNPNPLPGPYATYPEKSNVTSYIQTADHPD 189

RESULT 10
 CADD_MOUSE STANDARD; PRT; 796 AA.
 ID P55288.
 AC 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSF-4).
 GN Name=Cad11; Synonyms=Cad-11;
 OS Mus musculus (Mouse).
 OC Buthyotia Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95269886; PubMed=7750649;
 RA Hofmann I.H., Balling R.,
 RT "Cloning and expression analysis of a novel mesodermally expressed
 RT cadherin.",
 RL Dev. Biol. 169:337-346(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95269887; PubMed=7750650;
 RA Kimura Y., Matsunami H., Inoue T., Shimamura K., Uchida N., Ueno T.,
 RA Miyazaki T., Takeichi M.,
 RT "Cadherin-11 expressed in association with mesenchymal morphogenesis
 RT in the head, somite, and limb bud of early mouse embryos.",
 RL Dev. Biol. 169:347-358(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6; TISSUE=Calvaria;
 RX MEDLINE=94216322; PubMed=616511;
 RA Okazaki M., Takeshita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,
 RA Amano E.,
 RT "Molecular cloning and characterization of OB-cadherin, a new member
 RT of cadherin family expressed in osteoblasts.",
 RL J. Biol. Chem. 269:12092-12098(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Olfactory epithelium;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schler G.D.,
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Slaton K., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Tohilyuki S., Carninci P., Prange C.,
 RA Raha S.S., Liguori N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
 RA Vallat D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP DEVELOPMENTAL STAGE.
 RC STRAIN=C57BL/6; TISSUE=Testis;
 RX MEDLINE=97033837; PubMed=8879495;
 RA Munro S.B., Blaschuk O.W.,
 RT "A comprehensive survey of the cadherins expressed in the testes of
 RT fetal, immature, and adult mice utilizing the polymerase chain
 RT reaction.",
 RL Biol. Reprod. 55:822-827(1996).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Selectively expressed in osteoblastic cell
 CC lines, precursor cell lines of osteoblasts, and primary
 CC osteoblastic cells from calvaria, as well as in lung, testis, and
 CC brain tissues at low levels.
 CC -1- DEVELOPMENTAL STAGE: In the testis, expression is highest in fetal
 CC gonad and decreases 8-fold in newborn.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL, X77557; CAA54674.1; -;
 DR EMBL, D31963; BA06730.1; -;
 DR EMBL, D21253; BA004797.1; -;
 DR EMBL, BC046314; AA046314.1; -;
 DR PIR, A53584; A53584.
 DR PIR, I48277; I48277.
 DR PIR, I49556; I49556.
 DR HSSP, P09803; I17W.
 DR MGD, MGI:99217; Cdh11.
 DR GO, GO:0005737; Cytoplasm; IDA.
 DR GO, GO:0005886; Cytoplasm membrane; IDA.
 DR InterPro, IPR002126; Cadherin.
 DR InterPro, IPR000233; Cadherin_C-term.
 DR Pfam, PF00028; Cadherin_5.
 DR Pfam, PF01049; Cadherin_C_1.
 DR PRINTS, PR00205; CADHERIN.
 DR PROSITE, PS00232; CADHERIN_1; 3.
 DR PROSITE, PS0268; CADHERIN_2; 5.
 DR KX
 KW Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Transmembrane.
 KM
 FT SIGNAL 1 24
 FT PROPEP 25 53 Potential.
 FT CHAIN 54 796 Extracellular (Potential).
 FT DOMAIN 54 617 Potential.
 FT TRAMEM 618 640 Potential.
 FT DOMAIN 641 796 Cytoplasmic (Potential).
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.
 FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 612 Cadherin 5.

```

FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 540 540 N-linked (GlcNAc...) (Potential).
FT CONFLICT 462 462 E -> D (in Ref. 1).
FT CONFLICT 589 589 T -> L (in Ref. 2).
FT CONFLICT 655 655 D -> N (in Ref. 2).
FT CONFLICT 751 751 V -> M (in Ref. 1).
FT CONFLICT 777 777 P -> Q (in Ref. 2).
FT CONFLICT 782 782 L -> P (in Ref. 2).
SQ SEQUENCE 796 AA; 88112 MW; 0D584D24641D529 CRC64;

Query Match 72.2%; Score 187; DB 1; Length 796;
Best Local Similarity 79.2%; Pred. No. 2.3e-14;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Cy 1 PSEFIIKGDINDNPPIFLGPYHATVPEMSNGSVIVQVTAHDADDP 48
Db 142 PSEFIVKQDINDNPPEFLHEIYHANVPERSNVGSIVQVTAHDADDP 189

RESULT 11
08C706 PRELIMINARY; PRT; 796 AA.
AC 08C706:
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length
DE enriched library, clone:C530015F15 product:cadherin 11, full insert
DE sequence.
GN Name=Cdh11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN 12
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN 13
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RT The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN 14
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=20493974; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN 15
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama T., Ashi K., Katsunari T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Harada A.,
RA Nishino T., Yoshitake T.,

```

```

RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system:384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:11757-11771 (2000).
RN 16
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA Adachi U., Aizawa K., Akimura T., Hara A., Hashizume W.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai U., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tanaka T.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBS databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 5 cadherin domains.
DR EMBL: AK049652; BAC33860.1; -.
DR HSSP: P09803; ITW.
DR MGD: MGI:99217; Cdh11.
DR GO: GO:0005737; Cytoplasm; IDA.
DR GO: GO:0005886; Cytoplasmic membrane; IDA.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C-term.
DR Pfam: PF00028; Cadherin_5.
DR Pfam: PF01049; Cadherin_C_1.
DR PRINTS: PR00205; CADHERIN.
DR SMART: SM00112; CA; 5.
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS0268; CADHERIN_2; 5.
DR Calcium; Calcium-binding; Cell adhesion; Transmembrane.
SQ SEQUENCE 796 AA; 88126 MW; 71963374B2E1B29 CRC64;

Query Match 72.2%; Score 187; DB 2; Length 796;
Best Local Similarity 79.2%; Pred. No. 2.3e-14;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Cy 1 PSEFIIKGDINDNPPIFLGPYHATVPEMSNGSVIVQVTAHDADDP 48
Db 142 PSEFIVKQDINDNPPEFLHEIYHANVPERSNVGSIVQVTAHDADDP 189

RESULT 12
06PAN4 PRELIMINARY; PRT; 508 AA.
AC 06PAN4:
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Cdh8 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=22386257; PubMed=12477932;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Stenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bietow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.L., Wang J., Hsieh F.,
RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant P., Schaefer T.E.,
RA Brownstein M.J., Udén T.B., Yoshizaki S., Carninci P., Prange C.,

```

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wexley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.",
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: Contains 4 cadherin domains.
 DR EMBL: BC062000; AAH60200.1; -
 DR InterPro: IPR002126; Cadherin.
 DR Pfam: PF00028; Cadherin; 4.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SMO0112; CA; 4.
 DR PROSITE: PS00232; CADHERIN_1; 2.
 DR PROSITE: PS0268; CADHERIN_2; 4.
 KM Calcium-binding.
 SQ SEQUENCE 508 AA; 5638 MW; 9053F774BCF52255 CRC64;

Query Match 71.8%; Score 186; DB 2; Length 508;
 Best Local Similarity 79.2%; Pred. No. 1.9e-14;
 Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 1 PSEFIIKQDINDNPPILPGYATVPEMSNVGTSTVQTADADDP 48
 DB 150 PSEFIIKQDINDNAPFLNGPHTVPEMSILGTSTVNTATADADP 197

RESULT 13
 AAH60200 PRELIMINARY; PRT; 508 AA.

ID AAH60200
 AC AAH60200
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DB Cdh8 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen K.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L.,
 RA Stepien M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wexley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.",

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC062000; AAH60200.1; -
 SQ SEQUENCE 508 AA; 5638 MW; 9053F774BCF52255 CRC64;

Query Match 71.8%; Score 186; DB 2; Length 508;
 Best Local Similarity 79.2%; Pred. No. 1.9e-14;
 Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 1 PSEFIIKQDINDNPPILPGYATVPEMSNVGTSTVQTADADDP 48
 DB 150 PSEFIIKQDINDNAPFLNGPHTVPEMSILGTSTVNTATADADP 197

RESULT 14
 OAC375 PRELIMINARY; PRT; 716 AA.

ID OAC375
 AC OAC375
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched
 DE library, clone: D93046N17 product: cadherin 8, full insert
 DE sequence.
 GN Name=Cdh8;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RC MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.",
 RL Meth. Enzymol. 303:19-44(1999).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RC MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RC The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.",
 RL Nature 420:563-573(2002).
 RN (4)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RC MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.",
 RL Genome Res. 10:1617-1630(2000).
 RN (5)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RC MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama U., Nishi K., Kitanai T., Tashiro H., Itoh M.,
 RA Saito N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayata N., Hiramoto K., Hirooka T., Hirozane T.,
RA Horii F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai C., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
(By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 5 cadherin domains.
DR EMBL; AK086711; BAC39724.1; -.
DR HSP; P15116; INCU.
DR MGP; MGI:107434; Cdh8.
DR GO; GO:0016020; C:calcium ion binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:007156; F:homophilic cell adhesion; IEA.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR000233; Cadherin_C-term.
DR Pfam; PF00028; Cadherin; 5.
DR Pfam; PF01049; Cadherin; 1.
DR PRINTS; P300205; CADHERIN.
DR SMART; SM00112; CA; 5.
DR PROSITE; PS00232; CADHERIN_1; 3.
DR PROSITE; PS00268; CADHERIN_2; 5.
DR KEGG; KEGG:04300; CADHERIN; 2; 5.
KW Calcium-binding; Cell adhesion; Transmembrane.
SQ SEQUENCE 716 AA; 79149 MW; 58BD598F638624A CRC64;
Query Match 71.8%; Score 186; DB 2; Length 716;
Best Local Similarity 79.2%; Pred. No. 2,88-14;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
QY 1 PSEFIIKQDINDNPPIFLPGPYATVPEMSNVGTSTQVTAHDDP 48
DB 150 PSEFIIKQDINDNPPIFLPGPYATVPEMSNVGTSTQVTAHDDP 197
RESULT 15
Q8C449 PRELIMINARY; PRT; 716 AA.
AC Q8C449;
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DT 01-OCT-2004 (TREMblrel. 28, Last annotation update)
DE Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched
DE library, clone:G53002D14 Product:cadherin 8, full insert sequence
DE (cdh8 protein).
GN Name=Cdh8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning";
RL Mech. Enzymol. 303:19-44(1999).
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
[5]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Katsunai T., Taahiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wachihi M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heist F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stappleton M., Soares M.B., Bonaldo M.F., Cassavani T.L., Scheetz T.E.,
RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalka U., Smalls D.E., Scherch A., Schein J.E.,
RA Torres S.I., Marra M.A.

RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC -!- (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR EMBL: AK083092; BAC38758.1; -.
DR EMBL: BC057581; AAH57581.1; -.
DR HSSP: P15116; INCT
DR MGD: MGI:107434; Cdh8.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C-term.
DR Pfam: PF00028; Cadherin_5.
DR Pfam: PF01049; Cadherin_C; 1.
DR PRINTS: PR00205; CADHERIN.
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS50268; CADHERIN_2; 5.
KW Calcium; Calcium-binding; Cell adhesion; Transmembrane.
SQ SEQUENCE 716 AA; 79145 MW; 976FF5D845F938BD CRC64;

Query Match 71.8%; Score 186; DB 2; Length 716;
Best local Similarity 79.2%; Pred. No. 2.8e-14;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
Qy 1 PSEFIKQDINDNPPIFLGPHATVPKSNVGTSTVIOYTAHDADDP 48
Db 150 PSEFIKQDINDNPPIFLGPHATVPKSNVGTSTVIOYTAHDADDP 197

Search completed: December 8, 2004, 10:24:38
Job time : 20.2397 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 19.863 seconds
(without alignments)
866.886 Million cell updates/sec

Title: US-09-788-051-8

Perfect score: 259
Sequence: 1 PSEFIIKGDINDNPPIFL.....EMSNVGTSVIQTADADDP 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_238904:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	259	100.0	48	7	ADD29449 Human cad
2	259	100.0	620	7	ADD29448 Human cad
3	259	100.0	636	7	ADD29445 Human cad
4	250	96.5	493	5	AD116946 Human NOV
5	250	96.5	607	5	ABB53295 Human pol
6	250	96.5	781	5	ABB53296 Human pol
7	250	96.5	781	5	AAW48736 Human cad
8	250	96.5	781	5	ABG34078 Human NOV
9	250	96.5	781	5	AD116604 Human NOV
10	250	96.5	781	5	AD116606 Human cel
11	250	96.5	781	6	ABR40114 Human cel
12	250	96.5	781	6	ADA01366 Human PRO
13	250	96.5	781	6	ADA43795 Human sec
14	250	96.5	781	6	ADA43563 Human sec
15	250	96.5	781	6	ADA01238 Human PRO
16	250	96.5	781	7	ADA01122 Human sec
17	250	96.5	781	7	ADA43679 Human sec
18	250	96.5	781	7	ADA06941 Human PRO
19	250	96.5	781	7	ADA08429 Novel hum
20	250	96.5	781	7	ADBS9722 Human PRO
21	250	96.5	781	7	ADBS7005 Human PRO
22	250	96.5	781	7	ADBS6160 Human sec
23	250	96.5	781	7	ADBS9838 Human PRO
24	250	96.5	781	7	ADBS9493 Novel hum
25	250	96.5	781	7	ADBS6044 Human sec

26	250	96.5	781	7	ADC23442 Human tra
27	250	96.5	781	7	ADC26135 Human PRO
28	250	96.5	781	7	ADB04962 Human PRO
29	250	96.5	781	7	ADB11268 Human PRO
30	250	96.5	781	7	ADB88199 Human PRO
31	250	96.5	781	7	ADB95494 Human sec
32	250	96.5	781	7	ADB06424 Human PRO
33	250	96.5	781	7	ADB38199 Human PRO
34	250	96.5	781	7	ADB88315 Human PRO
35	250	96.5	781	7	ADD90896 Human sec
36	250	96.5	781	7	ADP99451 Human sec
37	250	96.5	781	7	ADG06544 Human PRO
38	250	96.5	781	7	ADG05495 Human PRO
39	250	96.5	781	7	ADG82496 Human PRO
40	250	96.5	781	8	ADE51749 Human sec
41	250	96.5	781	8	ADE51865 Human sec
42	250	96.5	781	8	ADE37723 Human sec
43	250	96.5	781	8	ADE37607 Human sec
44	250	96.5	781	8	ADP95378 Human PRO
45	250	96.5	781	8	ADE38078 Human PRO

ALIGNMENTS

RESULT 1
ADD29449
ID ADD29449 standard; protein; 48 AA.
XX
AC ADD29449;
XX
DT 15-JUN-2004 (first entry)
XX
DE Human cadherin-like protein peptide fragment Seq ID8.
XX
KW cadherin-like protein; transmembrane protein; cadherin domain;
KW homotypic cell-cell adhesion; cytostatic; osteopetrotic; cancer;
KW osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
KW metastatic tumour; human.
XX
OS Homo sapiens.
XX
PN US200314491-A1.
XX
PD 31-JUL-2003.
XX
PF 16-FEB-2001; 2001US-00788051.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PA (GODB/) GODBOLE S D.
PA (KUOC/) KUO C.
PA (ARTE/) ARTERBURN M C.
PA (YEUN/) YEUNG G.
PA (PALE/) PALENCIA S.
PA (TANG/) TANG Y T.
PA (LITC/) LIT C.
PA (DRMA/) DRMANAC R T.
XX
PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;
Liu C, Drmanac RT;
XX
DR WPI; 2003-829799/77.
XX
PT Novel isolated human secreted cadherin-like polypeptide useful for
PT treating diseases such as cancers, osteoporosis, Paget's disease,
PT osteomalacia, hyperostosis, osteopetrosis.
XX
PS Claim 11; SEQ ID NO 8; 63bp; English.
XX
CC This invention relates to a novel isolated human secreted cadherin-like
protein and the DNA sequence which encodes it. Cadherins are a family of

transmembrane proteins which share a common cadherin domain in their extracellular region. The extracellular portion mediates homotypic cell-cell adhesion that is calcium dependent. Modulators of the protein of the invention may have cytostatic or osteopathic activity. The invention may allow development of therapeutics useful for the treatment of diseases such as cancers, osteoporosis, Paget's disease, osteomalacia, osteopetrosis and osteopetrosis. The protein and DNA sequence of the invention may also be useful as markers for prognosis of metastatic tumours. The present sequence is that of a peptide fragment of the human secreted cadherin-like protein which was used during the exemplification of the invention.

Sequence 48 AA;

Query Match 100.0%; Score 259; DB 7; Length 48;
Best Local Similarity 100.0%; Pred. No. 1,6e-28;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPFIFPLGPHATVPEMNVGTSVIQVTAHADDP 48
DB 1 PSEFIKQDINDNPFIFPLGPHATVPEMNVGTSVIQVTAHADDP 48

RESULT 2
ADD29448
ID ADD29448 standard; protein; 620 AA.

AC ADD29448;
XX 15-JAN-2004 (first entry)

DE Human cadherin-like mature protein.

XX cadherin-like protein; transmembrane protein; cadherin domain;
XX homotypic cell-cell adhesion; cytostatic; osteopathic; cancer;
XX osteopetrosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
XX metastatic tumour; human.

OS Homo sapiens.

PN US2003144491-A1.

XX 31-JUL-2003.

XX 16-FEB-2001; 2001US-00788051.

XX 03-FEB-2000; 2000US-00496914.

XX 27-APR-2000; 2000US-00560875.

XX (GDB/) GODBOLE S D.

XX (KIOC/) KUO C.

XX (ARTE/) ARTERBURN M C.

XX (YEUN/) YEUNG G.

XX (PALE/) PALENCIA S.

XX (TANG/) TANG Y T.

XX (LIUC/) LIU C.

XX (DRMA/) DRMANAC R T.

XX Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;

XX Liu C, Drmanac RT;

XX WPI; 2003-829799/77.

XX Novel isolated human secreted cadherin-like polypeptide useful for

XX treating diseases such as cancers, osteoporosis, Paget's disease,

XX osteomalacia, hyperostosis, osteopetrosis.

XX Claim 11; SEQ ID NO 7; 63bp; English.

cell adhesion that is calcium dependent. Modulators of the protein of the invention may have cytostatic or osteopathic activity. The invention may allow development of therapeutics useful for the treatment of diseases such as cancers, osteoporosis, Paget's disease, osteomalacia, osteopetrosis and osteopetrosis. The protein and DNA sequence of the invention may also be useful as markers for prognosis of metastatic tumours. The present sequence is that of the mature human secreted cadherin-like protein which was used during the exemplification of the invention.

Sequence 620 AA;

Query Match 100.0%; Score 259; DB 7; Length 620;
Best Local Similarity 100.0%; Pred. No. 4e-27;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPFIFPLGPHATVPEMNVGTSVIQVTAHADDP 48
DB 117 PSEFIKQDINDNPFIFPLGPHATVPEMNVGTSVIQVTAHADDP 164

RESULT 3
ADD29445
ID ADD29445 standard; protein; 636 AA.

AC ADD29445;
XX 15-JAN-2004 (first entry)

DE Human cadherin-like protein amino acid sequence.

XX cadherin-like protein; transmembrane protein; cadherin domain;
XX homotypic cell-cell adhesion; cytostatic; osteopathic; cancer;
XX osteopetrosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
XX metastatic tumour; human.

OS Homo sapiens.

PN US2003144491-A1.

XX 31-JUL-2003.

XX 16-FEB-2001; 2001US-00788051.

XX 03-FEB-2000; 2000US-00496914.

XX 27-APR-2000; 2000US-00560875.

XX (GDB/) GODBOLE S D.

XX (KIOC/) KUO C.

XX (ARTE/) ARTERBURN M C.

XX (YEUN/) YEUNG G.

XX (PALE/) PALENCIA S.

XX (TANG/) TANG Y T.

XX (LIUC/) LIU C.

XX (DRMA/) DRMANAC R T.

XX Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;

XX Liu C, Drmanac RT;

XX WPI; 2003-829799/77.

XX N-Psdb; ADD29446.

XX Novel isolated human secreted cadherin-like polypeptide useful for

XX treating diseases such as cancers, osteoporosis, Paget's disease,

XX osteomalacia, hyperostosis, osteopetrosis.

XX Claim 11; SEQ ID NO 4; 63bp; English.

XX This invention relates to a novel isolated human secreted cadherin-like
CC protein and the DNA sequence which encodes it. Cadherins are a family of
CC transmembrane proteins which share a common cadherin domain in their
CC extracellular region. The extracellular portion mediates homotypic cell-
CC cell adhesion that is calcium dependent. Modulators of the protein of the
CC invention may have cytosolic or osteopathic activity. The invention may
CC allow development of therapeutics useful for the treatment of diseases
CC such as cancers, osteoporosis, Paget's disease, osteomalacia,
CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
CC invention may also be useful as markers for prognosis of metastatic
CC tumours. The present sequence is that of the human secreted cadherin-like
CC protein of the invention.
XX
SQ Sequence 636 AA:
Query Match 100.0%; Score 259; DB 7; Length 636;
Best Local Similarity 100.0%; Pred. No. 4, 2e-27;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PSEFIKQDINDNPFIFPGPHATVPENSNVGTSVIQVTADDDP 48
133 PSEFIKQDINDNPFIFPGPHATVPENSNVGTSVIQVTADDDP 180
Db
RESULT 4
AD116946
ID AD116946 standard; protein, 493 AA.
AC AD116946;
XX
XX 15-APR-2004 (first entry)
DT
XX Human NOVX protein homologue Segid 482.
DE
XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
KW inflammation; autoimmune disorder; allergy; blood disorder;
KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
KW Alzheimer's disease; infection; str.
XX
XX Homo sapiens.
OS
XX
XX WO200268649-A2.
PN
XX 06-SEP-2002.
PD
XX 31-JAN-2002; 2002WO-US0002785.
PF
XX 31-JAN-2001; 2001US-0265395P.
PR 31-JAN-2001; 2001US-0265412P.
PR 31-JAN-2001; 2001US-0265514P.
PR 31-JAN-2001; 2001US-0265517P.
PR 02-FEB-2001; 2001US-0265406P.
PR 05-FEB-2001; 2001US-0266767P.
PR 07-FEB-2001; 2001US-0266975P.
PR 07-FEB-2001; 2001US-0267057P.
PR 08-FEB-2001; 2001US-0267459P.
PR 09-FEB-2001; 2001US-0267823P.
PR 15-FEB-2001; 2001US-0268974P.
PR 26-FEB-2001; 2001US-0271664P.
PR 27-FEB-2001; 2001US-0271839P.
PR 02-MAR-2001; 2001US-0271855P.
PR 02-MAR-2001; 2001US-0272788P.
PR 14-MAR-2001; 2001US-0275925P.
PR 14-MAR-2001; 2001US-0275947P.
PR 14-MAR-2001; 2001US-0275950P.
PR 14-MAR-2001; 2001US-0275989P.
PR 15-MAR-2001; 2001US-0276448P.
PR 15-MAR-2001; 2001US-0276450P.
PR 16-MAR-2001; 2001US-0276397P.
PR 16-MAR-2001; 2001US-0276768P.

PR 20-MAR-2001; 2001US-0278652P.
PR 26-MAR-2001; 2001US-0278775P.
PR 26-MAR-2001; 2001US-0278778P.
PR 29-MAR-2001; 2001US-0279882P.
PR 29-MAR-2001; 2001US-0279884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0280992P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285135P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0286327P.
PR 03-MAY-2001; 2001US-0286504P.
PR 29-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312889P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313390P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0316415P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 18-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Tchernyev VT, Spyrek KA, Zerhusen BP, Patrujan M, Shinkets RA;
PI Li L, Gangolli EA, Padigam M, Anderson DM, Rastelli L, Miller CE;
PI Gerlach VL, Taupier RJ, Gusev VI, Colman SD, Wolenc AR, Pena CE;
PI Furtak K, Grosse WM, Alsdbrook JP, Lepley DM, Rieger DK, Burgess CE;
XX
XX WPI; 2002-706998/76.
PT New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Disclosure; SEQ ID NO 482; 1498bp; English.
XX
XX This invention relates to a novel nucleic acids, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOVX polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC cytosolic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
CC hemostatic, anti-HIV, antidiabetic, antiatherosclerotic, anorectic,
CC antistimulant, nephrotoxic, antibacterial, virucide, antiparasitic,
CC neuroprotective, nootropic, anticholinergic, anticholinergic, anticholinergic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
CC of the invention.

CC Alzheimer's, parapneumonic palsy, Huntington's disease, myoclonic
CC dystrophy, anorexia and depression, cardiovascular diseases including
CC congestive heart failure, Hodgkin's disease and myocardial infarction,
CC respiratory diseases including asthma, chronic obstructive pulmonary
CC disease, cystic fibrosis and adult respiratory distress syndrome, liver
CC diseases including hypercholesterolaemia, cirrhosis, viral and nonviral
CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
CC renal diseases including renal failure, acute tubular necrosis and
CC glomerulonephritis; skeletal muscle diseases including Eulenburg's
CC disease, hypoglycaemia and obesity; gastrointestinal diseases including
CC myotonia congenita and intestinal obstruction; lymph diseases including
CC lymphedematias; diseases of placenta including choriocarcinoma; disease
CC of testes including testicular cancer, male reproductive diseases
CC including low testosterone and male infertility, and disease of pancreas
CC including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The
CC present sequence is a polypeptide of the invention
CQ
CX Sequence 781AA;
XQ

Query Match	96.5%	Score 250;	DB 5;	Length 781;
Best Local Similarity	97.9%	Pred. No. 9.9e-26;		
Matches	477;	Conservative	1;	Indels 0; Gaps 0;
Qy	1	PSEFIKGGDINDNDPIPLPLGAYHATVPEMSNVGTSVQVTAHDDDP	48	
Db	133	PSEFIKGGDINDNDPIPLPLGAYHATVPEMSNVGTSVQVTAHDDDP	180	

Qy 1 PSEFIKQDINDNPPIFPLGPHATVPEMSNVGSTVIQVTAHDAADD 48
 |||||
Db 133 PSEFIKQDINDNPPIFPLGPHATVPEMSNVGSTVIQVTAHDAADD 180

RESULT 7
AAM48736
ID AAM48736 standard; protein; 781 AA

AC	AAAM48736;
XX	
DT	28-MAR-2002 (first entry)

DE Human cadherin family member 57805 protein SEQ ID NO 2.
XX
KW Human; cadherin 57805; osteopachis; hepatotropic; antibacterial;
KW antidiabetic; neuroprotective; antiatheric; antirheumatic;
KW dermatological; immunosuppressive; antinflammatory;
KW antisthenic; antiallergic; antileptotic; haemostatic; antipruritic;
KW antihypertoid; hypotenodulatory; antiretriosclerotic; candid; antiarthritic;
KW anorectic; immunomodulatory; vasotropic; virucide; cytostatic; liver;
KW thrombolytic; analgesic; anabolic; immune disorder; cardiovascular;
KW viral; pain; metabolism; osteoporosis; diabetes mellitus; arthritis;
KW osteoarthritis; multiple sclerosis; Crohn's disease; asthma; allergy;
KW thrombus; inflammation; infection; ischaemia; irritable bowel syndrome
KW gene therapy.

OS	Homo sapiens.
XX	
PN	MO200190145-A2.
XX	
PD	29-NOV-2001.

PF 18-MAY-2001; 2001WO-US016013
XX
PR 19-MAY-2000; 2000US-0205674P
XX
PA (MILL-) MILLENNIUM PHARM INC

PI Curtis RAJ;

DR WPI; 2002-083082/11.
DR N-PSDB; ABA96406, ABA96407.

PT New human cadherin family protein and polynucleotides, useful for diagnosing and treating disorders e.g. obstructive jaundice, multiple sclerosis, encephalomyelitis and atherosclerosis and to identify modulators of therapeutic use.

XX The invention relates to human cadherin family polypeptide designated
CC 57805 with osteopontin, hepatotropin, antibacterial, antidiabetic,
CC neuroprotective, antiarthritic, antirheumatic, dermatological,
CC immunosuppressive, antinflammatory, antiproliferative, antitumoral,
CC antiallergic, antileptotic, haemostatic, antipruritic, antihydrotic,
CC antipneumatic, antidiabetic, cardiact, antiarthritic, anorectic,
CC immunomodulatory, vasotropin, vincide, cytostatic, thrombolytic,
CC analgesic and anabolic activity. The 57805 molecules are useful for
CC diagnosing and treating disorders which include disorders associated with
CC bone metabolism, immune disorders, cardiovascular disorders, liver
CC disorders, viral diseases, pain or metabolic disorders. Especially bone
CC metabolism including osteoporosis, rickets, osteosclerosis, cirrhosis;
CC immune disorders including autoimmune disease including diabetes mellitus
CC arthritis, including rheumatoid arthritis and osteoarthritis, multiple
CC sclerosis, systemic lupus, dermatitis, psoriasis, Crohn's disease,
CC asthma, thrombocytopenia, Graves' disease, graft-versus-host disease,
CC allergy, cardiovascular disorders, thrombus, hypertension,
CC atherosclerosis, arrhythmias and cardiomyopathy, liver disorders,
CC glycogen storage disease, vascular disorders, chronic heart failure,
CC portal vein thrombosis; viral diseases; metabolic or pain disorders
CC include obesity, anorexia nervosa and diabetes, inflammation, infection
CC and ischaemia, irritable bowel syndrome. The polynucleotides are also
CC useful in gene therapy

```

Query Match      96.5%   Score 250; DB 5; Length 781;
Best Local Similarity 97.9%   Pred. No. 9,9e-2e;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0
Oy 1 PSEFFIKGODINDNDPEFLPGFHYATYKENSNSVTSYIQVTADADD 48
    bb
    133 PSEFFIKGODINDNDPEFLPGFHYATYKENSNSVTSYIQVTADADD 180

```

```

QY      1 PSEFIKQDINDNPRIFFPLGEYHATVPKSNVGTSVIQTAHADDDP 48
        |||||
DB      133 PSEFIKQDINDNPRIFFPLGEYHATVPKSNVGTSVIQTAHADDDP 180

```

RESULT 8
ABG34078
ID ABG34078 standard; protein; 781 AA

AC	ABG34078;
XX	
DT	15-JUL-2002 (first entry)

XX Human; PRO; secreted protein; transmembrane protein; genetic disorder
KW tumour; cancer.

OS	Homo sapiens.
XX	
PN	WO200224888-A2.
XX	
PD	28-MAR-2002.

PF 29-AUG-2001; 2001WO-US027099.

PR 01-SEP-2000; 200UTS-0229896F.
PR 05-SEP-2000; 200UTS-0230621P.
PR 22-SEP-2000; 200UTS-0235147P.
PR 10-NOV-2000; 200OWO-US030873.
PR 12-JAN-2001; 2001IUS-0261878P.
PR 16-JAN-2001; 2001IUS-0261910P.
PR 16-JAN-2001; 2001IUS-0261939P.
PR 16-JAN-2001; 2001IUS-0262150P.
PR 25-JAN-2001; 2001IUS-0264395P.
PR 02-FEB-2001; 2001IUS-0266421P.
PR 09-FEB-2001; 2001IUS-0267623P.
PR 28-FEB-2001; 2001WO-US006520.
PR 09-MAR-2001; 2001IUS-0274399P.
PR 03-APR-2001; 2001IUS-0280982P.
PR 04-APR-2001; 2001IUS-0282129P.
PR 04-APR-2001; 2001IUS-0282199P.

XX	chromosome mapping; tissue typing; pharmacogenetic; SNP;
XX	single nucleotide polymorphism.
XX	
OS	Homo sapiens.
XX	
XX	WO200268649-A2.
XX	
XX	06-SEP-2002.
PD	
XX	
EP	31-JAN-2002; 2002WO-US002785.
XX	
XX	
PR	31-JAN-2001; 2001US-0265395P.
PR	31-JAN-2001; 2001US-0265412P.
PR	31-JAN-2001; 2001US-0265514P.
PR	31-JAN-2001; 2001US-0265517P.
PR	02-FEB-2001; 2001US-0266405P.
PR	05-FEB-2001; 2001US-0266767P.
PR	07-FEB-2001; 2001US-0266975P.
PR	08-FEB-2001; 2001US-0267459P.
PR	09-FEB-2001; 2001US-0267823P.
PR	15-FEB-2001; 2001US-0268974P.
PR	26-FEB-2001; 2001US-0271664P.
PR	27-FEB-2001; 2001US-0271839P.
PR	27-FEB-2001; 2001US-0271855P.
PR	02-MAR-2001; 2001US-0272788P.
PR	02-MAR-2001; 2001US-0273046P.
PR	14-MAR-2001; 2001US-0275525P.
PR	14-MAR-2001; 2001US-0275847P.
PR	14-MAR-2001; 2001US-0275850P.
PR	14-MAR-2001; 2001US-0275859P.
PR	15-MAR-2001; 2001US-0276448P.
PR	15-MAR-2001; 2001US-0276450P.
PR	16-MAR-2001; 2001US-0276397P.
PR	16-MAR-2001; 2001US-0276768P.
PR	20-MAR-2001; 2001US-0278652P.
PR	26-MAR-2001; 2001US-0278775P.
PR	26-MAR-2001; 2001US-0278778P.
PR	29-MAR-2001; 2001US-0279682P.
PR	30-MAR-2001; 2001US-0280147P.
PR	11-APR-2001; 2001US-0282992P.
PR	11-APR-2001; 2001US-0283083P.
PR	20-APR-2001; 2001US-0285133P.
PR	23-APR-2001; 2001US-0285149P.
PR	03-MAY-2001; 2001US-0288327P.
PR	03-MAY-2001; 2001US-0288504P.
PR	29-MAY-2001; 2001US-0294473P.
PR	30-MAY-2001; 2001US-0294473P.
PR	08-JUN-2001; 2001US-0296664P.
PR	18-JUN-2001; 2001US-0298559P.
PR	19-JUN-2001; 2001US-0299324P.
PR	13-AUG-2001; 2001US-0312020P.
PR	16-AUG-2001; 2001US-0312889P.
PR	16-AUG-2001; 2001US-0313908P.
PR	21-AUG-2001; 2001US-0313390P.
PR	28-AUG-2001; 2001US-0315470P.
PR	31-AUG-2001; 2001US-0316447P.
PR	07-SEP-2001; 2001US-0318115P.
PR	07-SEP-2001; 2001US-0318118P.
PR	12-SEP-2001; 2001US-0318740P.
PR	13-SEP-2001; 2001US-0323379P.
PR	18-OCT-2001; 2001US-0330245P.
PR	18-OCT-2001; 2001US-0330308P.
PR	14-NOV-2001; 2001US-0332701P.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
PI	Therney VT, Spyrek KA, Zernhusen BD, Paturajan M, Shinkels RA;
PI	Li L, Ganggilli EA, Padigan M, Anderson DM, Rastelli L, Miller CE;
PI	Gersch VL, Taupier RJ, Gusev VI, Colman SD, Wolenc AR, Pena CEA;
XX	Furtak K, Grosse WM, Aisbrook JP, Lepley DM, Rieger DK, Burgess CE

DR WPI; 2002-706998/76.
DR N-PSDB; AD11603.
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.

XX Claim 1; SEQ ID NO 140; 1498bp; English.

XX This invention relates to a novel nucleic acid, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOVX polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC haemostatic, cardiac, anti-inflammatory, immunosuppressive, antiallergic,
CC anasthmatic, nephrotropic, antidiabetic, antihypertensive, anorectic,
CC neuroprotective, nocutropic, antibacterial, vitricide, antiparasitic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a human NOVX protein of the
CC invention.

XX Sequence 781 AA;

Query Match 96.5%; Score 250; DB 5; Length 781;
Best Local Similarity 97.9%; Pred. No. 9.9e-26;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPPFLPGYATVEMSNVGTSTVIQVTAHDDDP 48
Db 133 PSEFIKQDINDNPPFLPGYATVEMSNVGTSTVIQVTAHDDDP 180

RESULT 10
AD11606
ID AD11606 standard; protein; 781 AA.

AC AD11606;

DT 15-APR-2004 (first entry)

DE Human NOVX protein to treat human pathological conditions SeqId142.

XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
KW inflammation; autoimmune disorder; allergy; blood disorder;
KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
KW Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
KW cytoskeletal; cardiac; anti-inflammatory; immunosuppressive; antiallergic;
KW haemostatic; anti-HIV; antidiabetic; antiatherosclerotic; anorectic;
KW antiasthmatic; nephrotropic; antidiabetic; antiallergic; hepatotropic;
KW neuroprotective; nocutropic; antibacterial; vitricide; antiparasitic;
KW relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
KW chromosome mapping; tissue typing; pharmacogenomic.

OS Homo sapiens.

XX WO200268649-A2.
PN

XX 06-SEP-2002.
XX 31-JAN-2002; 2002WO-US002785.
XX 31-JAN-2001; 2001US-0265395P.
XX 31-JAN-2001; 2001US-0265412P.
XX 31-JAN-2001; 2001US-0265514P.
XX 31-JAN-2001; 2001US-0265517P.
XX 02-FEB-2001; 2001US-0266406P.
XX 05-FEB-2001; 2001US-0266767P.
XX 07-FEB-2001; 2001US-0266975P.
XX 08-FEB-2001; 2001US-0267057P.
XX 09-FEB-2001; 2001US-0267459P.
XX 15-FEB-2001; 2001US-0268974P.
XX 26-FEB-2001; 2001US-0271664P.
XX 27-FEB-2001; 2001US-0271839P.
XX 27-FEB-2001; 2001US-0271855P.
XX 02-MAR-2001; 2001US-0272788P.
XX 02-MAR-2001; 2001US-0273046P.
XX 14-MAR-2001; 2001US-0275925P.
XX 14-MAR-2001; 2001US-0275947P.
XX 14-MAR-2001; 2001US-0275950P.
XX 14-MAR-2001; 2001US-0275989P.
XX 15-MAR-2001; 2001US-0276448P.
XX 15-MAR-2001; 2001US-0276450P.
XX 16-MAR-2001; 2001US-0276397P.
XX 16-MAR-2001; 2001US-0276768P.
XX 20-MAR-2001; 2001US-0276852P.
XX 26-MAR-2001; 2001US-0278775P.
XX 26-MAR-2001; 2001US-0278778P.
XX 29-MAR-2001; 2001US-0279882P.
XX 29-MAR-2001; 2001US-0279884P.
XX 30-MAR-2001; 2001US-0280147P.
XX 11-APR-2001; 2001US-0282892P.
XX 11-APR-2001; 2001US-0283083P.
XX 20-APR-2001; 2001US-0285133P.
XX 23-APR-2001; 2001US-0285749P.
XX 03-MAY-2001; 2001US-0288327P.
XX 03-MAY-2001; 2001US-0288504P.
XX 29-MAY-2001; 2001US-0294047P.
XX 30-MAY-2001; 2001US-0294473P.
XX 08-JUN-2001; 2001US-0296364P.
XX 18-JUN-2001; 2001US-0298959P.
XX 19-JUN-2001; 2001US-0299324P.
XX 13-AUG-2001; 2001US-0312020P.
XX 16-AUG-2001; 2001US-0312889P.
XX 16-AUG-2001; 2001US-0312908P.
XX 21-AUG-2001; 2001US-0313390P.
XX 28-AUG-2001; 2001US-0315470P.
XX 31-AUG-2001; 2001US-0316447P.
XX 07-SEP-2001; 2001US-0318115P.
XX 07-SEP-2001; 2001US-0318118P.
XX 12-SEP-2001; 2001US-0318740P.
XX 19-SEP-2001; 2001US-0323379P.
XX 18-OCT-2001; 2001US-0330245P.
XX 18-OCT-2001; 2001US-0330308P.
XX 14-NOV-2001; 2001US-0332701P.

XX (CURA-) CURAGEN CORP.

XX Tchernev VT, Spyrek KA, Zernhusen BD, Patnirajan M, Shinkets RA;
PI Li L, Ganggalli E, Padigaru M, Anderson DW, Rastelli L, Miller CE;
PI Gerlach VL, Taupier RV, Gusev VI, Colman SD, Wolenc AR, Pena CA, Rieger DK, Burgess CE;
PI Furrak K, Grosse WM, Alsdorck JP, Lepley DM, Rieger DK, Burgess CE;
XX WPI; 2002-706998/76.
DR N-PSDB; AD11605.

XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or

PT pharmacogenomics.

XX Claim 1; SEQ ID NO 142; 1498bp; English.

XX

XX This invention relates to a novel nucleic acid, and encoded polypeptides thereof, which have properties related to the stimulation of biochemical or physiological responses in a cell, tissue, organ or organism.

XX Specifically, it refers to the use of biologically active fragments for diagnostic and prognostic assays and furthermore in the treatment of diverse pathological conditions. The present invention describes novel human and murine NOVX proteins, as well as methods to modulate their expression using antisense oligos, ribozymes and peptide nucleic acids.

XX The NOVX polypeptides, polynucleotides and antibodies are useful in treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, cancer and diabetes. Furthermore, they may be used in treating or preventing diseases such as inflammation, autoimmune disorders, allergies, blood disorders, acquired immunodeficiency syndrome (AIDS), obesity, asthma, immunoglobulin (Ig) A nephropathy, cirrhosis, arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy and epilepsy. Accordingly, these molecules have many activities including cyostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic, haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic, antiasthmatic, nephroprotective, hepatotropic, neurotrophic, neuroprotective, neurotropic, antibacterial, virucide, antiparasitic, relaxant and anticonvulsant. In addition, they are useful in screening assays to identify small molecules that modulate or inhibit, for example, neurogenesis, wound healing and angiogenesis. The nucleic acids are also used as in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. This polypeptide is a human NOVX protein of the invention.

XX

XX Sequence 781 AA;

SQ

Query Match 96.5%; Score 250; DB 5; Length 781;
Best Local Similarity 97.9%; Pred. No. 9.9e-26;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PSEFTIKGQDINDNPPIPLGPHATVPEMSNVTSTVQTADADDP 48
Db 133 PSEFTIKVQDINDNPPIPLGPHATVPEMSNVTSTVQTADADDP 180

RESULT 11

ABR40114

ID ABR40114 standard; protein; 781 AA.

XX

AC ABR40114;

XX

XX 04-JUL-2003 (first entry)

XX

DE Human cell adhesion and extracellular matrix protein, CADECM-11.

XX

XX Human; anti-HIV; antiallergic; cerebroprotective; antiparkinsonian; anticonvulsant; neurotrophic; neuroprotective; immunosuppressive; dermatological; anti-inflammatory; cyostatic; antiarteriosclerotic; immune therapy; cell adhesion; extracellular matrix; CADCM;

XX

XX Immune system disorder; AIDS; allergy; neurological disorder; stroke; Parkinson's disease; epilepsy; developmental disorder; Down's syndrome; cerebral palsy; connective tissue disorder; systemic lupus erythematosus; genetic disorder; Alport's syndrome; cell proliferative disorder; cancer; atherosclerosis.

XX

XX Homo sapiens.

OS

XX

PN WO2003027230-A2.

XX

PD 03-APR-2003.

XX

XX 02-AUG-2002; 2002MO-US024649.

PF

XX 03-AUG-2001; 2001US-0309664P.

PR 03-AUG-2001; 2001US-0310119P.

PR 17-AUG-2001; 2001US-0313031P.

PR 31-AUG-2001; 2001US-0316771P.

PR 07-SEP-2001; 2001US-0317896P.

PR 21-SEP-2001; 2001US-0324781P.

PR 05-OCT-2001; 2001US-0327606P.

PR 12-OCT-2001; 2001US-0328960P.

PR 09-NOV-2001; 2001US-0344471P.

PR 17-MAY-2002; 2002US-0381291P.

XX

XX (INCYTE GENOMICS INC.

XX

XX Burford N, Warren BA, Duggan BM, Mason PM, Richardson TW, Yue H, Foraythe JU, Elliott VS, Griffin JA, Gorvad AE, Azimzai Y, Kallick DA, Xu Y, Honchell CD, Baughn KE, Gietzen KJ, Lee S, Walle NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Rammunar J, WPI, 2003-354645/33.

DR N-PSDB; ACC00402.

XX

XX New human cell adhesion and extracellular matrix proteins (CADECM), useful for diagnosing, treating or preventing disorders associated with aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies or stroke.

PT

PS Claim 1; Page 192-194; 234pp; English.

XX

XX The present invention relates to novel human cell adhesion and extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding sequences (ACC00392-ACC00413 and ABR40104-ABR40125). The coding sequences and proteins are useful in diagnosing, treating and preventing disorders associated with aberrant expression of CADECM, such as immune system disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke, Parkinson's disease or epilepsy), developmental disorders (e.g. Down's syndrome or cerebral palsy), connective tissue disorders (e.g. systemic lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell proliferative disorders (e.g. cancer or atherosclerosis).

XX

SQ

Sequence 781 AA;

Query Match 96.5%; Score 250; DB 6; Length 781;
Best Local Similarity 97.9%; Pred. No. 9.9e-26;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PSEFTIKGQDINDNPPIPLGPHATVPEMSNVTSTVQTADADDP 48
Db 133 PSEFTIKVQDINDNPPIPLGPHATVPEMSNVTSTVQTADADDP 180

RESULT 12

ADA01366

ID ADA01366 standard; protein; 781 AA.

XX

XX ADA01366;

XX

XX 06-NOV-2003 (first entry)

XX

DE Human PRO polypeptide #49.

XX

XX Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour; adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer; microvascular endothelial cell; endothelial cell tube formation; sports-related joint problem; articular cartilage defect; osteoarthritis; rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.

XX

XX Homo sapiens.

OS

XX

PN US2003068779-A1.

XX

PD 10-APR-2003.

XX

XX 16-SEP-2002; 2002US-00245107.

PF

XX 09-MAY-2001; 2001US-0290589P.

PR 29-AUG-2001; 2001MO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX (GENENTECH INC.)
 XX
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S;
 XX WPI; 2003-625484/59.
 DR N-PDB; ADA01365.
 XX
 PT Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
 PT stimulating proliferation of human microvascular endothelial cells, and
 PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
 PT cells.
 XX
 XX Claim 11; Fig 98; 307pp; English.
 PS
 XX The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
 CC colon, breast, prostate, rectal, cervical and liver tumours). The
 CC polynucleotides are useful in molecular biology, including uses as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA, and in gene therapy. The polynucleotides may also
 CC be used in preparing PRO polypeptides by recombinant techniques and in
 CC generating either transgenic animals or knock-out animals which are
 CC useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides or antibodies are used in preparing a
 CC medicament for treating a condition responsive to the polypeptides or
 CC antibodies, such as tumours, for stimulating and inhibiting proliferation
 CC of human microvascular endothelial cells, for inducing endothelial cell
 CC tube formation and for treating sports-related joint problems, articular
 CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
 CC represents a human PRO polypeptide of the invention.
 CC
 XX Sequence 781 AA;
 SQ
 Query Match 96.5%; Score 250; DB 6; Length 781;
 Best Local Similarity 97.9%; Pred. No. 9.9e-26;
 Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PSEFIKQDINDNPFIFLGPYHATVPEMSNVGTSVIQVTAHDADDP 48
 DB 133 PSEFIKQDINDNPFIFLGPYHATVPEMSNVGTSVIQVTAHDADDP 180
 RESULT 13
 ADA43795
 ID ADA43795 standard; protein; 781 AA.
 XX
 AC ADA43795;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted/transmembrane polypeptide PRO34009.
 XX
 XX Human; PRO; secreted protein; transmembrane protein;
 KW endothelial cell tube formation; chondrocyte cell differentiation;
 KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
 XX liver tumour; cytosolic; vaccine.
 XX
 OS Homo sapiens.
 XX
 XX US2003064474-A1.
 XX
 XX PN 03-APR-2003.

XX
 XX 16-SEP-2002; 2002US-00245859.
 XX
 XX 29-AUG-2001; 2001MO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX (GENENTECH INC.)
 XX
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S;
 XX WPI; 2003-605867/57.
 DR N-PDB; ADA43794.
 XX
 PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
 PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
 PT generating antisense RNA and DNA, and in gene therapy.
 XX
 XX Claim 11; Fig 98; 308pp; English.
 PS
 XX The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acids deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide. Also included are vectors,
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
 CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
 CC and PRO21383 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumour in a mammal, including tumours of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence represents a PRO protein.
 CC
 XX Sequence 781 AA;
 SQ
 Query Match 96.5%; Score 250; DB 6; Length 781;
 Best Local Similarity 97.9%; Pred. No. 9.9e-26;
 Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PSEFIKQDINDNPFIFLGPYHATVPEMSNVGTSVIQVTAHDADDP 48
 DB 133 PSEFIKQDINDNPFIFLGPYHATVPEMSNVGTSVIQVTAHDADDP 180
 RESULT 14
 ADA43563
 ID ADA43563 standard; protein; 781 AA.
 XX
 AC ADA43563;
 XX
 DT 20-NOV-2003 (first entry)
 XX

DE Human secreted/transmembrane polypeptide PRO34009.
 XX
 XX Human; PRO; secreted protein; transmembrane protein;
 KW endothelial cell tube formation; chondrocyte cell differentiation;
 KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KW liver tumour; cytostatic; vaccine.
 XX
 OS Homo sapiens.
 XX
 XX US2003073196-A1.
 XX
 XX 17-APR-2003.
 XX
 XX 18-SEP-2002; 2002US-00246210.
 XX
 XX 04-APR-2001; 2001US-0282199P.
 XX 29-AUG-2001; 2001WO-US027099.
 XX 18-JUL-2002; 2002US-00197942.
 XX
 XX (GENENTECH INC.
 XX
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S;
 XX
 DR MPI; 2003-743914/70.
 DR N-PSDB; ADA43562.
 XX
 PT New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
 PT PRO21383 useful for stimulating the proliferation or differentiation of
 PT chondrocyte cells and detecting the presence of a tumor in a mammal.
 XX
 PS Claim 11; Fig 98; 307pp; English.
 XX
 CC The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acids deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide. Also included are vectors,
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO189, PRO499, PRO6008, PRO6000,
 CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO1317, PRO20080
 CC and PRO21383 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumour in a mammal, including tumours of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO499, PRO6008, PRO10275, PRO21207, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence represents a PRO protein.
 XX
 SQ Sequence 781 AA;
 Query Match 96.5%; Score 250; DB 6; Length 781;
 Best Local Similarity 97.9%; Pred. No. 9.9e-26;
 Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPPIPLGPHATVPENSGTSTVQTVAHADDP 48
 |||||
 DB 133 PSEFIKQDINDNPPIPLGPHATVPENSGTSTVQTVAHADDP 180
 |||||
 RESULT 15
 ADA01238
 ID ADA01238 standard; protein; 781 AA.
 XX
 XX ADA01238;
 XX
 XX 06-NOV-2003 (first entry)
 XX
 XX Human PRO polypeptide #49.
 DE
 XX Human; PRO; secreted polypeptide; transmembrane polypeptide;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
 KW cancer; lung; colon; breast; prostate; rectum; kidney; liver;
 KW microvascular endothelial cell; endothelial cell tube formation.
 XX
 OS Homo sapiens.
 XX
 XX US2003068782-A1.
 XX
 XX 10-APR-2003.
 XX
 XX 16-SEP-2002; 2002US-00245851.
 XX
 XX 27-APR-1999; 99US-0131271P.
 XX 29-OCT-1999; 99US-0162506P.
 XX 02-DEC-1999; 99WO-US028551.
 XX 29-AUG-2001; 2001WO-US027099.
 XX 18-JUL-2002; 2002US-00197942.
 XX
 XX (GENENTECH INC.
 XX
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S;
 XX
 DR MPI; 2003-625487/59.
 DR N-PSDB; ADA01237.
 XX
 PT Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
 PT preparation of a medicament for treating a condition responsive to PRO
 PT polypeptide, and as therapeutic agents e.g. vaccines.
 XX
 PS Claim 11; Fig 98; 308pp; English.
 XX
 CC The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
 CC prostate, rectal, kidney and liver tumours). The polynucleotides are
 CC useful in molecular biology, including uses as hybridisation probes, in
 CC chromosome and gene mapping, in generating antisense RNA and DNA, and in
 CC gene therapy. The polynucleotides may also be used in preparing PRO
 CC polypeptides by recombinant techniques and in generating either
 CC transgenic animals or knock-out animals which are useful in the
 CC development and screening of therapeutically useful reagents. The PRO
 CC polypeptides or antibodies are used in preparing a medicament for
 CC treating a condition responsive to the polypeptides or antibodies, such
 CC as tumours, for stimulating and inhibiting proliferation of human
 CC microvascular endothelial cells and for inducing endothelial cell tube
 CC formation. This sequence represents a human PRO polypeptide of the
 CC invention.
 XX
 SQ Sequence 781 AA;

Query Match 96.5%; Score 250; DB 6; Length 781;
Best Local Similarity 97.9%; Pred. No. 9.9e-26;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PSEFIKQDINDNPFIFPGPYHATVPKMSNVGTSVIQVTAHDADDP 48
Db 133 PSEFIKQDINDNPFIFPGPYHATVPKMSNVGTSVIQVTAHDADDP 180

Search completed: December 8, 2004, 10:13:05
Job time : 20.863 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 10:13:18 : Search time 49.0484 Seconds
(without alignments)
349.544 Million cell updates/sec

Title: US-09-788-051-8

Perfect score: 259

Sequence: 1 PSEFIIKGDINDNPPIFLP.....EMSNVGTSTVIVTAHADDP 48

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	259	100.0	48	10	US-09-788-051-8
2	259	100.0	620	10	US-09-788-051-7
3	259	100.0	636	10	US-09-788-051-4
4	250	96.5	493	15	US-10-072-012-482
5	250	96.5	607	15	US-10-258-951-74
6	250	96.5	781	9	US-09-860-868-2
7	250	96.5	781	14	US-10-245-752-98
8	250	96.5	781	14	US-10-245-859-98
9	250	96.5	781	14	US-10-245-103-98
10	250	96.5	781	14	US-10-245-107-98
11	250	96.5	781	14	US-10-245-143-98
12	250	96.5	781	14	US-10-245-771-98
13	250	96.5	781	14	US-10-245-851-98

14	250	96.5	781	14	US-10-245-883-98	Sequence 98, Appl
15	250	96.5	781	14	US-10-237-535-98	Sequence 98, Appl
16	250	96.5	781	14	US-10-238-183-98	Sequence 98, Appl
17	250	96.5	781	14	US-10-238-283-98	Sequence 98, Appl
18	250	96.5	781	14	US-10-238-370-98	Sequence 98, Appl
19	250	96.5	781	14	US-10-245-055-98	Sequence 98, Appl
20	250	96.5	781	14	US-10-245-147-98	Sequence 98, Appl
21	250	96.5	781	14	US-10-245-730-98	Sequence 98, Appl
22	250	96.5	781	14	US-10-246-210-98	Sequence 98, Appl
23	250	96.5	781	14	US-10-239-156-98	Sequence 98, Appl
24	250	96.5	781	14	US-10-243-024-98	Sequence 98, Appl
25	250	96.5	781	14	US-10-243-409-98	Sequence 98, Appl
26	250	96.5	781	14	US-10-245-621-98	Sequence 98, Appl
27	250	96.5	781	14	US-10-245-880-98	Sequence 98, Appl
28	250	96.5	781	14	US-10-245-033-98	Sequence 98, Appl
29	250	96.5	781	14	US-10-245-035-98	Sequence 98, Appl
30	250	96.5	781	14	US-10-245-185-98	Sequence 98, Appl
31	250	96.5	781	14	US-10-245-427-98	Sequence 98, Appl
32	250	96.5	781	14	US-10-245-473-98	Sequence 98, Appl
33	250	96.5	781	14	US-10-245-770-98	Sequence 98, Appl
34	250	96.5	781	14	US-10-245-877-98	Sequence 98, Appl
35	250	96.5	781	14	US-10-246-976-98	Sequence 98, Appl
36	250	96.5	781	14	US-10-245-340-98	Sequence 98, Appl
37	250	96.5	781	14	US-10-162-435-13	Sequence 13, Appl
38	250	96.5	781	14	US-10-242-743-98	Sequence 98, Appl
39	250	96.5	781	14	US-10-242-845-98	Sequence 98, Appl
40	250	96.5	781	14	US-10-237-636-98	Sequence 98, Appl
41	250	96.5	781	14	US-10-238-325-98	Sequence 98, Appl
42	250	96.5	781	14	US-10-238-346-98	Sequence 98, Appl
43	250	96.5	781	14	US-10-238-411-98	Sequence 98, Appl
44	250	96.5	781	14	US-10-245-124-98	Sequence 98, Appl
45	250	96.5	781	14		

ALIGNMENTS

RESULT 1
US-09-788-051-8
; Sequence 8, Application US/09788051
; Publication No. US20030144491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Atterburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dmanac, Radocic T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES A
; FILE REFERENCE: HYS-39
; CURRENT FILING DATE: 2001-02-16
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; ORGANISM: Homo sapiens
; TYPE: PRT
; LENGTH: 48
; US-09-788-051-8
Query Match 100.0%; Score 259; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 6.4e-27;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 PSEFIIKGDINDNPPIFLPGLPHTVPEMSNVGTSTVIVTAHADDP 48
|||||

Db 1 PSEFIKGQDINDNPPIFPLGPHYATVPKMSNVGTSTVQTADADDP 48

RESULT 2

US-09-788-051-7

Sequence 7, Application US/09788051

Publication No. US20030144491A1

GENERAL INFORMATION:

APPLICANT: Godbole, Shubhada D

APPLICANT: Kuo, Chiaoyun

APPLICANT: Arterburn, Matthew C

APPLICANT: Yeung, George

APPLICANT: Palencia, Servando

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Drmanac, Radoje T

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN

FILE REFERENCE: POLYNUCLEOTIDES

FILE REFERENCE: HYS-39

CURRENT APPLICATION NUMBER: US/09/788, 051

PRIOR FILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: US 09/560, 875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 09/496, 914

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3.0

SEQ ID NO: 7

LENGTH: 620

TYPE: PRT

ORGANISM: Homo sapiens

US-09-788-051-7

Query Match 100.0%; Score 259; DB 10; Length 620;

Best Local Similarity 100.0%; Pred. No. 1.4e-25;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSEFIKGQDINDNPPIFPLGPHYATVPKMSNVGTSTVQTADADDP 48

Db 117 PSEFIKGQDINDNPPIFPLGPHYATVPKMSNVGTSTVQTADADDP 164

RESULT 3

US-09-788-051-4

Sequence 4, Application US/09788051

Publication No. US20030144491A1

GENERAL INFORMATION:

APPLICANT: Godbole, Shubhada D

APPLICANT: Kuo, Chiaoyun

APPLICANT: Arterburn, Matthew C

APPLICANT: Yeung, George

APPLICANT: Palencia, Servando

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Drmanac, Radoje T

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN

FILE REFERENCE: POLYNUCLEOTIDES

FILE REFERENCE: HYS-39

CURRENT APPLICATION NUMBER: US/09/788, 051

PRIOR FILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: US 09/560, 875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 09/496, 914

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3.0

SEQ ID NO: 4

LENGTH: 636

TYPE: PRT

ORGANISM: Homo sapiens

US-09-788-051-4

Query Match 100.0%; Score 259; DB 10; Length 636;

Best Local Similarity 100.0%; Pred. No. 1.4e-25;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSEFIKGQDINDNPPIFPLGPHYATVPKMSNVGTSTVQTADADDP 48

Db 133 PSEFIKGQDINDNPPIFPLGPHYATVPKMSNVGTSTVQTADADDP 180

RESULT 4

US-10-072-012-482

Sequence 482, Application US/10072012

Publication No. US20040033493A1

GENERAL INFORMATION:

APPLICANT: Tchernev, Velizar

APPLICANT: Spyrek, Kimberly

APPLICANT: Zernusen, Bryan

APPLICANT: Patutajan, Meera

APPLICANT: Shinkets, Richard

APPLICANT: Li, Li

APPLICANT: Gangolli, Esha

APPLICANT: Padigaru, Muralidhara

APPLICANT: Anderson, David W.

APPLICANT: Rastelli, Luca

APPLICANT: Miller, Charles E.

APPLICANT: Gerlach, Valerie

APPLICANT: Taupier Jr, Raymond J.

APPLICANT: Gusev, Vladimir Y.

APPLICANT: Colman, Steven D.

APPLICANT: Molenc, Adam R.

APPLICANT: Pena, Carol E. A

APPLICANT: Furtak, Katarzyna

APPLICANT: Groesse, William M.

APPLICANT: Alsobrook II, John P.

APPLICANT: Lepley, Denise M.

APPLICANT: Rieger, Daniel K.

APPLICANT: Burgess, Catherine E.

TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-258

CURRENT APPLICATION NUMBER: US/10/072, 012

PRIOR FILING DATE: 2002-01-31

PRIOR APPLICATION NUMBER: 60/265, 102

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: 60/265, 514

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265, 517

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265, 412

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265, 395

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/266, 406

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 60/266, 767

PRIOR FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: 60/267, 057

PRIOR FILING DATE: 2001-02-07

PRIOR APPLICATION NUMBER: 60/266, 975

PRIOR FILING DATE: 2001-02-07

PRIOR APPLICATION NUMBER: 60/267, 459

PRIOR FILING DATE: 2001-02-08

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 1391

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO: 482

LENGTH: 493

TYPE: PRT

ORGANISM: Homo sapiens

US-10-072-012-482

Query Match 96.5%; Score 250; DB 15; Length 493;

Best Local Similarity 97.9%; Pred. No. 1.7e-24;

Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


```

APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watande, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C78
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-859-98

Query Match
Best Local Similarity 96.5%; Score 250; DB 14; Length 781;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSEFIKGQDINDNPPIFPLGPHATVPKMSNVGTSTVQVTAHADDDP 48
133 PSEFIKGQDINDNPPIFPLGPHATVPKMSNVGTSTVQVTAHADDDP 180

RESULT 9
US-10-245-103-98
Sequence 98, Application US/10245103
Publication No. US20030068778A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watande, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C12
CURRENT FILING DATE: 2002-09-17
CURRENT APPLICATION NUMBER: US/10/245, 103

```

```

PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-103-98

Query Match
Best Local Similarity 96.5%; Score 250; DB 14; Length 781;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSEFIKGQDINDNPPIFPLGPHATVPKMSNVGTSTVQVTAHADDDP 48
133 PSEFIKGQDINDNPPIFPLGPHATVPKMSNVGTSTVQVTAHADDDP 180

RESULT 10
US-10-245-107-98
Sequence 98, Application US/10245107
Publication No. US20030068779A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watande, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C71
CURRENT FILING DATE: 2002-09-16
CURRENT APPLICATION NUMBER: US/10/245, 107
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02

```

PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-107-98

Query Match 96.5%; Score 250; DB 14; Length 781;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 PSEFIKQDINDNPFIFLGPYHATVPEMSVGTSVIQVTAHDADDP 48
Db 133 PSEFIKQDINDNPFIFLGPYHATVPEMSVGTSVIQVTAHDADDP 180

RESULT 11

US-10-245-143-98

Sequence 98, Application US/10245143
Publication No. US20030068780A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Bacon, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Goddard, Audrey
APPLICANT: Guiney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watande, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C98
CURRENT APPLICATION NUMBER: US/10/245, 143
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-143-98

Query Match 96.5%; Score 250; DB 14; Length 781;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 PSEFIKQDINDNPFIFLGPYHATVPEMSVGTSVIQVTAHDADDP 48
Db 133 PSEFIKQDINDNPFIFLGPYHATVPEMSVGTSVIQVTAHDADDP 180

RESULT 12

US-10-245-771-98

Sequence 98, Application US/10245771
Publication No. US20030068781A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Bacon, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Goddard, Audrey
APPLICANT: Guiney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watande, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C98
CURRENT APPLICATION NUMBER: US/10/245, 771
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-771-98

Query Match 96.5%; Score 250; DB 14; Length 781;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 PSEFIKQDINDNPFIFLGPYHATVPEMSVGTSVIQVTAHDADDP 48
Db 133 PSEFIKQDINDNPFIFLGPYHATVPEMSVGTSVIQVTAHDADDP 180

RESULT 13

US-10-245-851-98

Sequence 98, Application US/10245851
Publication No. US20030068782A1

GENERAL INFORMATION:

```

/ APPLICANT: Baker, Kevin
/ APPLICANT: Eaton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Matambe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3630R1C70
/ CURRENT APPLICATION NUMBER: US/10/245,851
/ CURRENT FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See file Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
/ US-10-245-851-98

Query Match      96.5%; Score 250; DB 14; Length 781;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY      1 PSEFIKQDINDNPIPLGPHATVPENSVGTSVIQTADADDP 48
Db      133 PSEFIKQDINDNPIPLGPHATVPENSVGTSVIQTADADDP 180

RESULT 14
US-10-245-883-98
/ Sequence 98, Application US/10245883
/ Publication No. US20030068783A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Eaton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Matambe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
```

```

/ FILE REFERENCE: P3630R1C70
/ CURRENT APPLICATION NUMBER: US/10/245,883
/ CURRENT FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See file Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
/ US-10-245-883-98

Query Match      96.5%; Score 250; DB 14; Length 781;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY      1 PSEFIKQDINDNPIPLGPHATVPENSVGTSVIQTADADDP 48
Db      133 PSEFIKQDINDNPIPLGPHATVPENSVGTSVIQTADADDP 180

RESULT 15
US-10-237-535-98
/ Sequence 98, Application US/10237535
/ Publication No. US20030073188A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Eaton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Matambe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3630R1C3
/ CURRENT APPLICATION NUMBER: US/10/237,535
/ CURRENT FILING DATE: 2002-09-06
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
```


Wed Dec 8 11:46:35 2004

us-09-788-051-8.rapb

Page 7

```

? PRIOR FILING DATE: 1998-05-22
? PRIOR APPLICATION NUMBER: 60/087607
? PRIOR FILING DATE: 1998-06-02
? PRIOR APPLICATION NUMBER: 60/089801
? PRIOR FILING DATE: 1998-06-18
? PRIOR APPLICATION NUMBER: 60/090557
? PRIOR FILING DATE: 1998-06-24
? PRIOR APPLICATION NUMBER: 60/090689
? PRIOR FILING DATE: 1998-06-25
? PRIOR APPLICATION NUMBER: 60/091358
? PRIOR FILING DATE: 1998-07-01
? PRIOR APPLICATION NUMBER: 60/091978
? PRIOR FILING DATE: 1998-07-07
? PRIOR APPLICATION NUMBER: 60/099803
? PRIOR FILING DATE: 1998-09-10
? PRIOR APPLICATION NUMBER: 60/106932
? PRIOR FILING DATE: 1998-11-03
? PRIOR APPLICATION NUMBER: 60/115554
? PRIOR FILING DATE: 1999-01-12
? PRIOR APPLICATION NUMBER: 60/119342
? PRIOR FILING DATE: 1999-02-09
? PRIOR APPLICATION NUMBER: 60/123957
? PRIOR FILING DATE: 1999-03-12
? PRIOR APPLICATION NUMBER: 60/123972
? PRIOR FILING DATE: 1999-03-11
? PRIOR APPLICATION NUMBER: 60/127372
? PRIOR FILING DATE: 1999-04-01
? PRIOR APPLICATION NUMBER: 60/131271
? PRIOR FILING DATE: 1999-04-27
? PRIOR APPLICATION NUMBER: 60/134459
? PRIOR FILING DATE: 1999-05-11
? PRIOR APPLICATION NUMBER: 60/135725
? PRIOR FILING DATE: 1999-05-25
? PRIOR APPLICATION NUMBER: 60/135729
? PRIOR FILING DATE: 1999-05-25
? PRIOR APPLICATION NUMBER: 60/135750
? PRIOR FILING DATE: 1999-05-25
? PRIOR APPLICATION NUMBER: 60/138385
? PRIOR FILING DATE: 1999-06-09
? PRIOR APPLICATION NUMBER: 60/140653
? PRIOR FILING DATE: 1999-06-22
? PRIOR APPLICATION NUMBER: 60/141037
? PRIOR FILING DATE: 1999-06-23
? PRIOR APPLICATION NUMBER: 60/144732
? PRIOR FILING DATE: 1999-07-20
? PRIOR APPLICATION NUMBER: 60/144758
? PRIOR FILING DATE: 1999-07-20
? PRIOR APPLICATION NUMBER: 60/144790
? PRIOR FILING DATE: 1999-07-20
? PRIOR APPLICATION NUMBER: 60/145228
? PRIOR FILING DATE: 1999-07-20
? PRIOR APPLICATION NUMBER: 60/145698
? PRIOR FILING DATE: 1999-07-26
? PRIOR APPLICATION NUMBER: 60/146222
? PRIOR FILING DATE: 1999-07-28
? PRIOR APPLICATION NUMBER: 60/146843
? PRIOR FILING DATE: 1999-08-03
? PRIOR APPLICATION NUMBER: 60/148188
? PRIOR FILING DATE: 1999-08-10
? PRIOR APPLICATION NUMBER: 60/148513
? PRIOR FILING DATE: 1999-08-12
? PRIOR APPLICATION NUMBER: 60/149327
? PRIOR FILING DATE: 1999-08-17
? PRIOR APPLICATION NUMBER: 60/149395
? PRIOR FILING DATE: 1999-08-17
? PRIOR APPLICATION NUMBER: 60/150114
? PRIOR FILING DATE: 1999-08-20
? PRIOR APPLICATION NUMBER: 60/151700
? PRIOR FILING DATE: 1999-08-31
? PRIOR APPLICATION NUMBER: 60/151734
? PRIOR FILING DATE: 1999-08-31
? PRIOR APPLICATION NUMBER: 60/162506
? PRIOR FILING DATE: 1999-10-29
? PRIOR APPLICATION NUMBER: 60/170262
? PRIOR FILING DATE: 1999-12-09
? PRIOR APPLICATION NUMBER: 60/177118
? PRIOR FILING DATE: 2000-01-20
? PRIOR APPLICATION NUMBER: 60/179851
? PRIOR FILING DATE: 2000-02-02
? PRIOR APPLICATION NUMBER: 60/180921
? PRIOR FILING DATE: 2000-02-08
? PRIOR APPLICATION NUMBER: 60/187202
? PRIOR FILING DATE: 2000-03-03
? PRIOR APPLICATION NUMBER: 60/198587
? PRIOR FILING DATE: 2000-04-18
? PRIOR APPLICATION NUMBER: 60/199614
? PRIOR FILING DATE: 2000-04-25
? PRIOR APPLICATION NUMBER: 60/206330
? PRIOR FILING DATE: 2000-05-23
? PRIOR APPLICATION NUMBER: 60/206368
? PRIOR FILING DATE: 2000-05-23
? PRIOR APPLICATION NUMBER: 60/209832
? PRIOR FILING DATE: 2000-06-05
? PRIOR APPLICATION NUMBER: 60/218371
? PRIOR FILING DATE: 2000-07-13
? PRIOR APPLICATION NUMBER: 60/222695
? PRIOR FILING DATE: 2000-08-02
? PRIOR APPLICATION NUMBER: 60/229896
? PRIOR FILING DATE: 2000-09-01
? PRIOR APPLICATION NUMBER: 60/230621
? PRIOR FILING DATE: 2000-09-05
? PRIOR APPLICATION NUMBER: 60/232887
? PRIOR FILING DATE: 2000-09-15
? PRIOR APPLICATION NUMBER: 60/235147
? PRIOR FILING DATE: 2000-09-22
? PRIOR APPLICATION NUMBER: 60/261878
? PRIOR FILING DATE: 2001-01-12
? PRIOR APPLICATION NUMBER: 60/261910
? PRIOR FILING DATE: 2001-01-16
? PRIOR APPLICATION NUMBER: 60/261939
? PRIOR FILING DATE: 2001-01-16
? PRIOR APPLICATION NUMBER: 60/262150
? PRIOR FILING DATE: 2001-01-16
? PRIOR APPLICATION NUMBER: 60/264395
? PRIOR FILING DATE: 2001-01-25
? PRIOR APPLICATION NUMBER: 60/266421
? PRIOR FILING DATE: 2001-02-02
? PRIOR APPLICATION NUMBER: 60/267623
? PRIOR FILING DATE: 2001-02-09
? PRIOR APPLICATION NUMBER: 60/274399
? PRIOR FILING DATE: 2001-03-09
? PRIOR APPLICATION NUMBER: 60/280982
? PRIOR FILING DATE: 2001-04-03
? PRIOR APPLICATION NUMBER: 60/282129
? PRIOR FILING DATE: 2001-04-04
? PRIOR APPLICATION NUMBER: 60/282199
? PRIOR FILING DATE: 2001-04-04
? PRIOR APPLICATION NUMBER: 60/290589
? PRIOR FILING DATE: 2001-05-09
? PRIOR APPLICATION NUMBER: 09/180997
? PRIOR FILING DATE: 1998-11-19
? PRIOR APPLICATION NUMBER: 09/267213
? PRIOR FILING DATE: 1999-03-12
? PRIOR APPLICATION NUMBER: 09/380137
? PRIOR FILING DATE: 1999-08-25
? PRIOR APPLICATION NUMBER: 09/380138
? PRIOR FILING DATE: 1999-08-25
? PRIOR APPLICATION NUMBER: 09/403297
? PRIOR FILING DATE: 1999-10-18
? PRIOR APPLICATION NUMBER: 09/423741
? PRIOR FILING DATE: 1999-11-10
? PRIOR APPLICATION NUMBER: 09/709238
? PRIOR FILING DATE: 2000-11-08
? PRIOR APPLICATION NUMBER: 09/802706
? PRIOR FILING DATE: 2001-03-09
? PRIOR APPLICATION NUMBER: 09/872035
```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 5.72373 Seconds
(without alignments)
556.152 Million cell updates/sec

Title: US-09-788-051-8
Perfect score: 259
Sequence: 1 PSEFIIKQDINDNPPIFL.....EMSNVGSYVQTADHDDP 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.dep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.dep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.dep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.dep.*
5: /cgn2_6/ptodata/1/1aa/PCUS.COMB.dep.*
6: /cgn2_6/ptodata/1/1aa/backfilest.dep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	189	73.0	693	2	US-08-738-349-6 Sequence 6, Appl
2	189	73.0	693	4	US-09-919-497-55 Sequence 55, Appl
3	189	73.0	796	1	US-08-188-228-58 Sequence 58, Appl
4	189	73.0	796	1	US-08-332-643-52 Sequence 52, Appl
5	189	73.0	796	1	US-08-332-638-58 Sequence 58, Appl
6	189	73.0	796	2	US-08-738-349-4 Sequence 4, Appl
7	189	73.0	796	4	US-09-654-348-2 Sequence 2, Appl
8	188.5	72.2	615	2	US-08-738-349-12 Sequence 12, Appl
9	187	72.2	796	2	US-08-188-228-44 Sequence 44, Appl
10	186	71.8	532	1	US-08-332-638-44 Sequence 44, Appl
11	186	71.8	532	1	US-08-332-638-54 Sequence 54, Appl
12	186	71.8	793	1	US-08-332-643-48 Sequence 48, Appl
13	186	71.8	793	1	US-08-332-643-54 Sequence 54, Appl
14	186	71.8	793	1	US-08-332-638-54 Sequence 54, Appl
15	186	71.8	799	1	US-08-188-228-42 Sequence 42, Appl
16	186	71.8	799	1	US-08-332-638-42 Sequence 42, Appl
17	186	71.8	799	1	US-08-188-228-46 Sequence 46, Appl
18	186	71.8	799	1	US-08-332-638-46 Sequence 46, Appl
19	186	71.8	799	1	US-08-188-228-46 Sequence 46, Appl
20	186	71.8	799	1	US-08-332-643-54 Sequence 54, Appl
21	186	71.8	799	1	US-08-332-638-60 Sequence 60, Appl
22	186	71.8	799	1	US-08-188-228-50 Sequence 50, Appl
23	186	71.8	799	1	US-08-332-643-44 Sequence 44, Appl
24	186	71.8	799	1	US-08-332-638-50 Sequence 50, Appl
25	186	71.8	799	1	US-09-187-859-5 Sequence 5, Appl
26	186	71.8	799	1	US-09-839-542B-5 Sequence 5, Appl
27	186	71.8	799	1	US-09-535-855-5 Sequence 5, Appl

28	115	44.4	109	3	US-09-187-859-17 Sequence 17, Appl
29	115	44.4	109	4	US-09-839-542B-17 Sequence 17, Appl
30	115	44.4	109	3	US-09-535-852-17 Sequence 17, Appl
31	114	44.0	109	3	US-09-187-859-11 Sequence 11, Appl
32	114	44.0	109	4	US-09-839-542B-11 Sequence 11, Appl
33	114	44.0	109	4	US-09-535-852-11 Sequence 11, Appl
34	111	42.9	713	1	US-08-188-228-62 Sequence 62, Appl
35	111	42.9	713	1	US-08-332-643-56 Sequence 56, Appl
36	111	42.9	713	1	US-08-332-638-62 Sequence 62, Appl
37	106	40.9	712	2	US-08-474-067-2 Sequence 2, Appl
38	106	40.9	712	2	US-08-474-067-5 Sequence 5, Appl
39	106	40.9	712	2	US-08-474-068A-2 Sequence 2, Appl
40	106	40.9	712	2	US-08-474-068A-5 Sequence 5, Appl
41	106	40.9	712	2	US-08-474-481-2 Sequence 2, Appl
42	106	40.9	717	2	US-08-474-068A-4 Sequence 4, Appl
43	106	40.9	717	2	US-08-474-068A-4 Sequence 4, Appl
44	106	40.9	717	2	US-08-472-481-4 Sequence 4, Appl
45	106	40.9	906	4	US-09-417-029-11 Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-738-349-6
Sequence 6, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shunji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amano, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: Finnegan, Henderson, Farabow, Garrett &
ADDRESSER: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 693 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-6

Query Match 73.0%; Score 189; DB 2; Length 693;
Best Local Similarity 79.2%; Pred. No. 2.5e-18;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 PSEFIKGQDINDNPPIPLGPHATVPENSVGTSTVYQVTAHADDP 48
Db 142 PSEFIKXQDINDNPPEFLHETHTANVPERSNVGTSTVYQVTAHADDP 189

RESULT 2
US-09-919-497-55
Sequence 55, Application US/09919497
Patent No. 6773883
GENERAL INFORMATION:
APPLICANT: Muller, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patent version 3.0
SEQ ID NO 55
LENGTH: 693
TYPE: PRT
ORGANISM: Homo sapiens
US-09-919-497-55

Query Match 73.0%; Score 189; DB 4; Length 693;
Best Local Similarity 79.2%; Pred. No. 2.5e-18;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 PSEFIKGQDINDNPPIPLGPHATVPENSVGTSTVYQVTAHADDP 48
Db 142 PSEFIKXQDINDNPPEFLHETHTANVPERSNVGTSTVYQVTAHADDP 189

RESULT 3
US-08-188-228-58
Sequence 58, Application US/08188228
Patent No. 559725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 559725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340

TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-58

Query Match 73.0%; Score 189; DB 1; Length 796;
Best Local Similarity 79.2%; Pred. No. 3e-18;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 PSEFIKGQDINDNPPIPLGPHATVPENSVGTSTVYQVTAHADDP 48
Db 142 PSEFIKXQDINDNPPEFLHETHTANVPERSNVGTSTVYQVTAHADDP 189

RESULT 4
US-08-332-643-52
Sequence 52, Application US/08332643
Patent No. 5639634
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-643-52

Query Match 73.0%; Score 189; DB 1; Length 796;
Best Local Similarity 79.2%; Pred. No. 3e-18;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 PSEFIKGQDINDNPPIPLGPHATVPENSVGTSTVYQVTAHADDP 48
Db 142 PSEFIKXQDINDNPPEFLHETHTANVPERSNVGTSTVYQVTAHADDP 189

RESULT 5

US-08-332-638-58

Sequence 58, Application US/08332638

Patent No. 5646250

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSEE: Borun

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/332,638

FILING DATE: 01-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/872,643

FILING DATE: 17 APR 1992

APPLICATION NUMBER: US/08/049,460

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: No. 5646250and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31340

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:

LENGTH: 796 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-332-638-58

Query Match 73.0%; Score 189; DB 1; Length 796;

Best Local Similarity 79.2%; Pred. No. 3e-18;

Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPPIPLGPHATVPEMSNVGTSVIQVTAHDADDP 48

Db 142 PSEFIKQDINDNPPIPLGPHATVPEMSNVGTSVIQVTAHDADDP 189

RESULT 6

US-08-738-349-4

Sequence 4, Application US/08738349

Patent No. 5689638

GENERAL INFORMATION:

APPLICANT: Takeshita, Sunao

APPLICANT: Okazaki, Makoto

APPLICANT: Kawai, Shintji

APPLICANT: Tsujimura, Atsushi

APPLICANT: Amano, Egon

TITLE OF INVENTION: Bone-Related Cadherin-like Protein and

PROCESS FOR ITS PRODUCTION

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finegan, Henderson, Farabow, Garrett &

ADDRESSEE: Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/738,349

FILING DATE: 25-OCT-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/364,439

FILING DATE:

APPLICATION NUMBER: US 08/112,061

FILING DATE: 26-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Barker, M. P.

REGISTRATION NUMBER: 32,013

REFERENCE/DOCKET NUMBER: 02481.1323-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4400

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 796 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-738-349-4

Query Match 73.0%; Score 189; DB 2; Length 796;

Best Local Similarity 79.2%; Pred. No. 3e-18;

Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPPIPLGPHATVPEMSNVGTSVIQVTAHDADDP 48

Db 142 PSEFIKQDINDNPPIPLGPHATVPEMSNVGTSVIQVTAHDADDP 189

RESULT 7

US-09-654-328-2

Sequence 2, Application US/09654328

Patent No. 6787136

GENERAL INFORMATION:

APPLICANT: Brenner, Michael B.

APPLICANT: Valencia, Xavier

TITLE OF INVENTION: Methods and Compositions for Treatment

OF INFLAMMATORY DISEASE USING CADHERIN-11 MODULATING AGENTS

FILE REFERENCE: B0801/7187/ERP/MAT

CURRENT APPLICATION NUMBER: US/09/654,328

CURRENT FILING DATE: 2000-09-01

PRIOR APPLICATION NUMBER: US 60/152,456

PRIOR FILING DATE: 1999-09-03

PRIOR APPLICATION NUMBER: US 60/153,490

PRIOR FILING DATE: 1999-09-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 796

TYPE: PRT

ORGANISM: Homo Sapiens

US-09-654-328-2

Query Match 73.0%; Score 189; DB 4; Length 796;

Best Local Similarity 79.2%; Pred. No. 3e-18;

Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPPIPLGPHATVPEMSNVGTSVIQVTAHDADDP 48

Db 142 PSEFIVKQDINDNPPEFLHETVHANVPERSNVGTSVIQVTASDADDP 189

RESULT 8

US-08-738-349-12

Sequence 12, Application US/08738349

Patent No. 5869638

GENERAL INFORMATION:

APPLICANT: Takeshita, Sunao

APPLICANT: Okazaki, Makoto

APPLICANT: Kawai, Shinji

APPLICANT: Tsujimura, Atsushi

APPLICANT: Aman, Egon

TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and

TITLE OF INVENTION: Process for Its Production

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

ADDRESSEE: Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/738,349

FILING DATE: 25-OCT-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/364,439

FILING DATE: 26-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Barker, M. P.

REGISTRATION NUMBER: 32,013

REFERENCE/DOCKET NUMBER: 02481.1323-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 615 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-738-349-12

Query Match 72.8%; Score 188.5; DB 2; Length 615;

Best Local Similarity 81.2%; Pred. No. 2.6e-18;

Matches 39; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

Db 136 PSEFIVKQDINDNPPEFLHETVHANVPERSNVGTSVIQVTASDADDP 182

RESULT 9

US-08-738-349-2

Sequence 2, Application US/08738349

Patent No. 5869638

GENERAL INFORMATION:

APPLICANT: Takeshita, Sunao

APPLICANT: Okazaki, Makoto

APPLICANT: Kawai, Shinji

APPLICANT: Tsujimura, Atsushi

APPLICANT: Aman, Egon

TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and

TITLE OF INVENTION: Process for Its Production

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

ADDRESSEE: Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/738,349

FILING DATE: 25-OCT-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/364,439

FILING DATE: 26-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Barker, M. P.

REGISTRATION NUMBER: 32,013

REFERENCE/DOCKET NUMBER: 02481.1323-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 796 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-738-349-2

Query Match 72.2%; Score 187; DB 2; Length 796;

Best Local Similarity 79.2%; Pred. No. 5.9e-18;

Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Db 142 PSEFIVKQDINDNPPEFLHETVHANVPERSNVGTSVIQVTASDADDP 189

RESULT 10

US-08-188-228-44

Sequence 44, Application US/08188228

Patent No. 5597725

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSEE: Borun

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/188,228

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 559725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
MOLECULE TYPE: protein
US-08-188-228-44

Query Match 71.8%; Score 186; DB 1; Length 532;
Best Local Similarity 79.2%; Pred. No. 4,8e-18;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 PSEFIKQDINDNPPFPLGPHYATVPEMSNVTGSIQVTAHDADDP 48
Db 150 PSEFIKQDINDNAPFLNGPYHATVPEMSILGTSVNTATADDP 197

RESULT 11
US-08-332-638-44
Sequence 44, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray &
ADDRESSER: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 564625and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
MOLECULE TYPE: protein

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-44

Query Match 71.8%; Score 186; DB 1; Length 532;
Best Local Similarity 79.2%; Pred. No. 4,8e-18;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 PSEFIKQDINDNPPFPLGPHYATVPEMSNVTGSIQVTAHDADDP 48
Db 150 PSEFIKQDINDNAPFLNGPYHATVPEMSILGTSVNTATADDP 197

RESULT 12
US-08-188-228-54
Sequence 54, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray &
ADDRESSER: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
MOLECULE TYPE: linear

Query Match 71.8%; Score 186; DB 1; Length 793;
Best Local Similarity 79.2%; Pred. No. 8,1e-18;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 PSEFIKQDINDNPPFPLGPHYATVPEMSNVTGSIQVTAHDADDP 48
Db 143 PSEFIKQDINDNAPFLNGPYHATVPEMSILGTSVNTATADDP 190

RESULT 13
US-08-332-643-48
Sequence 48, Application US/08332643
Patent No. 5639634

GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSER: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-643-48

Query Match 71.8%; Score 186; DB 1; Length 793;
Best Local Similarity 79.2%; Pred. No. 8.1e-18;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPFLPGPYHATVEMSNVGTSTVQTAAHADDP 48
DB 143 PSEFIKQDINDNAPFLNGPYHATVEMSIIGTSTVNTATADDDP 190

RESULT 14
US-08-332-638-54
Sequence 54, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSER: Borum
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638

FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-54

Query Match 71.8%; Score 186; DB 1; Length 793;
Best Local Similarity 79.2%; Pred. No. 8.1e-18;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPFLPGPYHATVEMSNVGTSTVQTAAHADDP 48
DB 143 PSEFIKQDINDNAPFLNGPYHATVEMSIIGTSTVNTATADDDP 190

RESULT 15
US-08-188-228-42
Sequence 42, Application US/08188228
Patent No. 5587725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSER: Borum
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:

Wed Dec 8 11:46:35 2004

us-09-788-051-8.ra1

Page 7

LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-42

Query Match 71.8%; Score 186; DB 1; Length 799;
Best Local Similarity 79.2%; Pred. No. 8.2e-18;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
QY 1 PSEFIKQDINDNPPIFPLGYPYHATVPEMSNVGTSYIQVTAHDADDP 48
Db 150 PSEFIKQDINDNPPIFPLGYPYHATVPEMSNVGTSYIQVTAHDADDP 197

Search completed: December 8, 2004, 10:01:12
Job time : 5.72373 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 : Search time 3.86194 seconds
(without alignments)
1189.717 Million cell updates/sec

Title: US-09-788-051-9
Perfect score: 247
Sequence: 1 STVTVTLSVDVNDNPKFPQ.....ETAGPTLVGRLRAQDDPLG 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR_79:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	180	72.9	796	2	cadherin-11 - mouse
2	180	72.9	796	2	cadherin-11 - mouse
3	180	72.9	796	2	cadherin-11 - mouse
4	180	72.9	796	2	cadherin-11 - mouse
5	169	68.4	789	2	cadherin-11 precursor
6	169	68.4	789	2	cadherin-11 precursor
7	163	66.0	793	2	cadherin-6 - human
8	150	60.7	790	2	cadherin-8 - human
9	150	60.7	790	2	cadherin-8 - human
10	147	59.5	794	2	cadherin-14 - human
11	140	56.7	790	2	cadherin-12 - human
12	139	56.3	785	2	cadherin-7 - chick
13	120	48.6	709	2	hypothetical prote
14	120	48.6	709	2	hypothetical prote
15	114	45.2	5147	1	cadherin-11 precursor
16	111.5	45.1	3343	1	cadherin-11 precursor
17	110	44.5	784	1	cadherin-11 precursor
18	110	44.5	784	1	cadherin-11 precursor
19	110	44.5	784	1	cadherin-11 precursor
20	110	44.5	784	1	cadherin-11 precursor
21	106.5	43.1	2809	2	cadherin-11 precursor
22	105	42.5	2610	2	cadherin-11 precursor
23	104	42.1	1200	2	cadherin-11 precursor
24	103	41.7	3034	2	cadherin-11 precursor
25	100	40.5	732	1	cadherin-11 precursor
26	100	40.5	732	1	cadherin-11 precursor
27	96	38.9	882	1	cadherin-11 precursor
28	96	38.9	882	1	cadherin-11 precursor
29	96	38.9	882	1	cadherin-11 precursor

30	96	38.9	896	2	A55363	desmocollin, type
31	95	38.5	373	2	T34563	hypothetical prote
32	95	38.5	505	2	S43064	cadherin - African
33	95	38.5	1544	2	T29482	hypothetical prote
34	94.5	38.3	1311	2	T33757	hypothetical prote
35	94	38.1	701	2	T17243	hypothetical prote
36	92	37.2	141	2	PC4298	cadherin FIB2 - hu
37	92	37.2	809	1	TUBODD	desmocollin 2b pre
38	92	37.2	822	1	TUBSCP	P-cadherin precursor
39	92	37.2	863	1	TUBODC	desmocollin 2a pre
40	92	37.2	884	2	S34438	uvomorulin - mouse
41	92	37.2	4307	2	T20721	hypothetical prote
42	91	36.8	3097	2	T00021	DN-cadherin - fru1
43	90.5	36.6	137	2	PC4297	cadherin FIB1 - hu
44	90.5	36.6	829	2	T45336	Ksp-cadherin - rab
45	90	36.4	895	1	IUXLCP	EP-cadherin precursor

ALIGNMENTS

RESULT 1
148277
cadherin-11 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 148277
R/Hoffmann, I.; Balling, R.
Dev. Biol. 169, 337-346, 1995
A/Title: Cloning and expression analysis of a novel mesodermally expressed cadherin.
A/Reference number: 148277; PMID:95269866; PMID:7750649
A/Accession: 148277
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-796 <RES>
A/Cross-references: UNIPROT:P55288; EMBL:X77557; NID:g642736; PDB:CA54674.1; PID:g666
C/Genetics:
A/Gene: cad-11
C/Superfamily: cadherin; cadherin repeat homology
F/56-159/Domain: cadherin repeat homology <CDH>

Query Match 72.9% Score 180; DB 2; Length 796;
Best Local Similarity 68.8%; Pred. No. 2.7e-15;

Matches 33; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 STVTVTLSVDVNDNPKFPQSLYQSVETAGPTLVGRLRAQDDPLG 48
DB 251 TTKVTTITLVDVNDNPKFPQSVYQMSVBAVGEVGVKAKDDPLG 298

RESULT 2

149556
cadherin-11 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 149556
R/Kimura, Y.; Matsunami, H.; Inoue, T.; Shimamura, K.; Uchida, N.; Ueno, T.; Miyazaki, Dev. Biol. 169, 347-358, 1995
A/Title: Cadherin-11 expressed in association with mesenchymal morphogenesis in the hea
A/Reference number: 149556; PMID:95269867; PMID:7750650
A/Accession: 149556
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-796 <RES>
A/Cross-references: UNIPROT:P55288; GB:D31963; NID:g974190; PDB:BA06730.1; PID:g97419
C/Superfamily: cadherin; cadherin repeat homology
F/56-159/Domain: cadherin repeat homology <CDH>

Query Match 72.9% Score 180; DB 2; Length 796;
Best Local Similarity 68.8%; Pred. No. 2.7e-15;
Matches 33; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 STVTVTLSVDVNDNPKFPQSLYQSVETAGPTLVGRLRAQDDPLG 48

A:Residues: 1-785 <NA>
A:Cross-references: UNIPROT:Q90763; GB:D42150; NID:9868000; PIDN:BA07721.1; PID:9868001
C:Superfamily: cadherin; cadherin repeat homology
F:156-262/Domain: cadherin repeat homology <CDH>

Query Match 56.3%; Score 139; DB 2; Length 785;
Best Local Similarity 52.1%; Pred. No. 6.2e-10;
Matches 25; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

Qy 1 TTVTLSVDVNDNPPKFPQSLVQFVSVEYTAGPGLVGRRLAODPDIG 48
Db 245 TTSTVTLTDVNDNPPKFRFRSYQVNPESLPLASVARIKADADVG 292

RESULT 13

hypothetical protein DKFPZ434B0923.1 - human (fragment)
T6413

C:Species: Homo sapiens (man)

C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C:Accession: T6413

R:Blum, H.; Baurebach, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

Submitted to the Protein Sequence Database, January 2000

A:Reference number: Z23034

A:Accession: T6413

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-709 <AA>

A:Cross-references: UNIPROT:Q9NT87; EMBL:AL137471

A:Experimental source: adult testis; clone DKFPZ434B0923

C:Genetics:

A:Note: DKFPZ434B0923.1

Query Match 48.6%; Score 120; DB 2; Length 709;
Best Local Similarity 47.7%; Pred. No. 1.7e-07;
Matches 21; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

Qy 5 TTTLSDVNDNPPKFPQSLVQFVSVEYTAGPGLVGRRLAODPDIG 48
Db 26 TVQINDINDNPPHFRSRYEVEISENNSPGAYITVTATPDIG 69

RESULT 14

MEGF1 protein - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004

C:Accession: T00252

R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.

Genomics 51; 27-34, 1998

A>Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs

A:Reference number: Z14126; MUID:98360089; PMID:9693030

A:Accession: T00252

A:Status: preliminary; translated from GB/EMBL/DD34

A:Molecule type: mRNA

A:Residues: 1-4351 <NA>

A:Cross-references: UNIPROT:O86277; EMBL:AB011527; NID:93445285; PIDN:BA032458.1; PID:93

A:Experimental source: Brain

C:Genetics:

A:Gene: MEGF1

C:Superfamily: rat MEGF1 protein; cadherin repeat homology; EGF homology; laminin G repe

F:3798-3949/Domain: laminin G repeat homology <LGR>

F:3953-3985/Domain: EGF homology <EGF>

F:3992-4023/Domain: EGF homology <EGF>

Query Match 48.6%; Score 120; DB 2; Length 4351;
Best Local Similarity 51.1%; Pred. No. 1.4e-06;
Matches 24; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

Qy 2 TTVTLSVDVNDNPPKFPQSLVQFVSVEYTAGPGLVGRRLAODPDIG 48
Db 2363 TLVVANVSDINDNPPKFRFPYBANVSELTGCHLVTKQALDPDIG 2409

RESULT 15
IUFFTM
cadherin-related tumor suppressor precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997
C:Accession: A41087; E41087
R:Mahoney, P.A.; Weber, U.; Onofrechuk, P.; Biesemann, H.; Bryant, P.J.; Goodman, C.S.
Cell 67, 853-868, 1991
A>Title: The fat tumor suppressor gene in Drosophila encodes a novel member of the cadh
A:Reference number: A41087; MUID:92069752; PMID:1959133

A:Accession: A41087

A:Molecule type: mRNA

A:Residues: 143-485;1279-5147 <NA>

A:Cross-references: GB:M80537

A:Accession: B41087

A:Molecule type: DNA

A:Residues: 1-142;487-1278 <MA>

A:Cross-references: GB:M80537

A:Note: 1229-Gly and 1233-Ser were also found

C:Genetics:

A:Gene: fat

A:Cross-references: FlyBase:FBgn0001075

C:Superfamily: cadherin-related tumor suppressor; cadherin repeat homology; EGF homology

C:Keywords: calcium binding; cell adhesion; duplication; transmembrane protein

F:1-35/Domain: signal sequence #status predicted <SIG>

F:36-5147/Product: cadherin-related tumor suppressor #status predicted <MAT>

F:36-5147/Domain: extracellular #status predicted <EXT>

F:36-5147/Domain: extracellular #status predicted <EXT>

F:51-156/Domain: cadherin repeat homology <CR1>

F:159-270/Domain: cadherin repeat homology <CR2>

F:271-382/Domain: cadherin repeat homology <CR3>

F:390-494/Domain: cadherin repeat homology <CR4>

F:497-599/Domain: cadherin repeat homology <CR5>

F:602-708/Domain: cadherin repeat homology <CR6>

F:718-822/Domain: cadherin repeat homology <CR7>

F:831-942/Domain: cadherin repeat homology <CR8>

F:948-1049/Domain: cadherin repeat homology <CR9>

F:1052-1153/Domain: cadherin repeat homology <CR10>

F:1156-1278/Domain: cadherin repeat homology <CR11>

F:1281-1384/Domain: cadherin repeat homology <CR12>

F:1387-1489/Domain: cadherin repeat homology <CR13>

F:1492-1601/Domain: cadherin repeat homology <CR14>

F:1607-1713/Domain: cadherin repeat homology <CR15>

F:1717-1823/Domain: cadherin repeat homology <CR16>

F:1826-1922/Domain: cadherin repeat homology <CR17>

F:1925-2027/Domain: cadherin repeat homology <CR18>

F:2028-2167/Domain: cadherin repeat homology <CR19>

F:2169-2278/Domain: cadherin repeat homology <CR20>

F:2281-2384/Domain: cadherin repeat homology <CR21>

F:2387-2491/Domain: cadherin repeat homology <CR22>

F:2494-2596/Domain: cadherin repeat homology <CR23>

F:2599-2703/Domain: cadherin repeat homology <CR24>

F:2707-2810/Domain: cadherin repeat homology <CR25>

F:2813-2813/Domain: cadherin repeat homology <CR26>

F:2915-3013/Domain: cadherin repeat homology <CR27>

F:3014-3124/Domain: cadherin repeat homology <CR28>

F:3127-3229/Domain: cadherin repeat homology <CR29>

F:3233-3334/Domain: cadherin repeat homology <CR30>

F:3337-3439/Domain: cadherin repeat homology <CR31>

F:3442-3545/Domain: cadherin repeat homology <CR32>

F:3548-3651/Domain: cadherin repeat homology <CR33>

F:3654-3756/Domain: cadherin repeat homology <CR34>

F:3954-4010/Domain: EGF homology <EG1>

F:4017-4048/Domain: EGF homology <EG2>

F:4056-4089/Domain: EGF homology <EG3>

F:4096-4127/Domain: EGF homology <EG4>

F:4584-4609/Domain: transmembrane #status predicted <TM>

F:4610-5147/Domain: intracellular #status predicted <INT>

Query Match 46.2%; Score 114; DB 1; Length 5147;
Best Local Similarity 57.8%; Pred. No. 1e-05;
Matches 26; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

Qy 4 VTTLSDVNDNPPKFPQSLVQFVSVEYTAGPGLVGRRLAODPDIG 48

Wed Dec 8 11:46:38 2004

us-09-788-051-9.rpr

Page 5

Db 256 VNVTLIDVNDNPPFI FDHSDYVNSLNETALPGTPVVTVMASDNDLG 300

Search completed: December 8, 2004, 10:27:06
Job time : 4.88194 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 19.2397 Seconds (without alignments)

Title: US-09-788-051-9
Perfect score: 247
Sequence: 1 STTVTVTLSDVNDNPEKFPQ.....ETAGPTLVGRRLRAQPDFLG 48

Scoring table:	BLOSUM62	Caracas	0	5
	Caracas	10	0	5
	Caracas	10	0	5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Post-processing:	Minimum Match	0%
------------------	---------------	----

```
1: uniprot_sprot:*
2: uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	247	100.0	370	2	086T00	086T00 homo sapien
2	247	100.0	493	2	086I07	086Iq7 homo sapien
3	247	100.0	819	1	CAD0_HUMAN	086Uq0 homo sapien
4	244	98.8	781	2	06PFX6	06PFX6 mus musculu
5	244	98.8	781	2	AAH57373	AAH57373 mus musculu
6	180	72.9	792	1	CAD6_CHICK	093319 gallus galli
7	180	72.9	796	1	CAD8_MOUSE	P55288 mus musculu
8	180	72.9	796	2	08C706	08C706 mus musculu
9	178	72.1	796	1	CAD8_HUMAN	P55287 homo sapien
10	174	70.4	795	1	096C59	096C59 homo sapien
11	173	70.0	794	2	093264	093264 xenopus lae
12	172	69.6	813	1	CAD6_MOUSE	09wC5 mus musculu
13	172	69.6	813	1	CAD6_RAT	063315 rattus norv
14	172	69.6	828	1	CAD6_HUMAN	09u359 homo sapien
15	169	68.4	789	1	CAD6_RAT	P55280 rattus norv
16	169	68.4	790	1	CAD6_HUMAN	P55285 homo sapien
17	169	68.4	790	1	CAD6_MOUSE	P97336 mus musculu
18	163	66.0	508	2	06P8N4	06P8N4 mus musculu
19	163	66.0	508	2	AAH60200	AAH60200 mus musculu
20	163	66.0	716	2	08C375	08C375 mus musculu
21	163	66.0	716	2	08C449	08C449 mus musculu
22	163	66.0	716	2	AAH57581	AAH57581 mus musculu
23	163	66.0	754	2	08BRX4	08BRX4 mus musculu
24	163	66.0	799	1	CAD8_HUMAN	P55284 homo sapien
25	163	66.0	799	1	CAD8_MOUSE	P97291 mus musculu
26	163	66.0	799	1	CAD8_RAT	O54800 rattus norv
27	158	64.0	789	1	CAD9_HUMAN	09uL4 homo sapien
28	150	60.7	377	2	08B155	08B155 mus musculu
29	150	60.7	790	1	CAD6_CHICK	090762 gallus galli
30	150	60.7	790	1	CAD1_HUMAN	Q13664 homo sapien
31	147	59.5	794	1	CAD0_C_HUMAN	P53269 homo sapien

ALIGNMENTS

32	147	59.5	794	2	Q86UD2	086ud2	homo sapien
33	147	59.5	798	2	Q7ZYV7	087d22	gallus gall
34	147	59.5	798	2	Q8QG33	08eqn3	gallus gall
35	146	59.1	801	1	Q8QK3	09hb6	homo sapien
36	146	59.1	801	2	Q9ZOM3	092om3	homo muscicu
37	142	57.5	790	2	Q8R5Z2	08ns22	homo sapien
38	141	57.1	340	2	Q8BLT4	08bl4	mus muscicu
39	141	57.1	630	2	Q81Y78	081y78	homo sapien
40	141	57.1	785	1	CAD7_HUMAN	Q9ulb5	homo sapien
41	141	57.1	785	2	Q8BM92	Q8bm2	mus muscicu
42	140	56.7	790	2	Q91838	091838	xenopus lae
43	139	56.3	551	2	Q9AKW2	08awk2	gallus gall
44	139	56.3	785	1	CAD7_CHICK	Q90763	gallus gall
45	138	55.9	963	1	CHC1_HUMAN	Q9hi58	homo sapien

RESULT	1
ID	Q96T00
AC	Q96T00; PRELIMINARY; PRT; 370 AA.
DT	01-JUN-2003 (TREMBLrel_24, Created)
DR	01-JUN-2003 (TREMBLrel_24, Last sequence update)
DE	Full-length cDNA clone CSDDK003Y017 of Hela cells of Homo sapiens (human) (Fragment).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NCBI	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN	[1]
RA	Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RC	LI W.B., Gruber C., Jesssee J., Polayes D.;
CC	-I SIMILARITY: Contains 4 cadherin domains.
EMBL	BX248303; CAD62630.1; -
GO	GO:00216020; Cmembrane; IEA.
GO	GO:0005509; Fcalcium ion binding; IEA.
GO	GO:0007156; Phomophilic cell adhesion; IEA.
Pfam	Pfam00028; Cadherin; 3.
PRINTS	PR00205; CADHERIN.
SMART	SM00112; CA; 2.
PROSITE	PS00232; CADHERIN_1; 1.
PROSITE	PS50268; CADHERIN_2; 4.
Cadherin	Calcium-binding.
FT	NON TER 1
FT	NON TER 1
SQ	SEQUENCE 370 AA; 39479 MW; 3996D4AF6A4500E0 CRC64;
Query Match	100.0%; Score 247; DB 2; Length 370;
Best Local Similarity	100.0%; Pred. NO. 7.7e-23;
Matches	48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 STTVVTLSDVDNDNPKEPKOSLYOFVSVEETAGPGLTVGRLEADPDIG 48
Db	3 STTVIVLSDVDNDNPKEPKOSLYOFVSVEETAGPGLTVGRLEADPDIG 50
RESULT	2
ID	Q96LO7
AC	Q96LO7; PRELIMINARY; PRT; 493 AA.
DT	01-DEC-2001 (TREMBLrel_19, Created)
DR	01-DEC-2001 (TREMBLrel_19, Last sequence update)

	RA	Gowdask P., Gray A.;	"We secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."
	RT	Bioinformatic assessment."	Rt Genome Res. 13:2265-2270(2003).
	RL	[3]	
	RN	SEQUENCE FROM N.A.	(ISOFORM 3).
	RP	TISSUE:	
	RC	Blum H., Baerisachs S., Mewes H.-W., Gassenhuber U., Wiemann S.;	Submitted (JMAN-2000) to the EMBL/GeneBank/DBS databases.
	RA	- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.	
	CC	They preferentially interact with themselves in a homophilic manner in connecting cells; cadherin may thus contribute to the sorting of heterogeneous cell types. Cadherin-24 mediate strong cell-cell adhesion.	
	CC	- SUBUNIT: Associates with alpha-, beta- and delta-catensins.	
	CC	- SUBCELLULAR LOCATION: Type I membrane protein (Potential).	
	CC	- ALTERNATIVE PRODUCTS:	
	CC	Event=Alternative splicing; Named isoforms=3;	
	CC	Name=1; Synonyms=Long form;	
	CC	IsoId=Q86UPD-1; Sequence=Dfsplayed;	
	CC	Name=2; Synonyms=Short form;	
	CC	IsoId=Q86UPD-2; Sequence=VSP_008717;	
	CC	Name=3;	
	CC	IsoId=Q86UPD-3; Sequence=VSP_008718, VSD_008719;	
	CC	Note=No experimental confirmation available;	
	CC	- SIMILARITY: Contains 5 cadherin domains.	
	CC	-----	
	CC	This SWIS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.ch/announce/ or send an email to license@isb-sib.ch).	
	CC	-----	
	DR	EMBL; AY260900; AAP20590.1; --	
	DR	EMBL; AY260901; AAP20591.1; --	
	DR	EMBL; AY358199; CAG8566.1; --	
	DR	EMBL; AI137477; CAB70758.1; --	
	DR	PIR; T46418; T46418.	
	DR	HSSP; P09803; I17K.	
	DR	Genev; HGNC:14265; CDS24.	
	DR	InferPro; IPRO02126; Cadherin.	
	DR	InferPro; IPRO02233; Cadherin_C.term.	
	DR	Pfam; PF00028; Cadherin; 5.	
	DR	Pfam; Pf01049; Cadherin_C; 1.	
	DR	PRINTS; PR00205; CADHERIN.	
	DR	PROSITE; PS00223; CADHERIN_1; 2.	
	DR	PROSITE; PSS0268; CADHERIN_2; 5.	
	KM	Altternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;	
	KW	Multigene family; Repeat; Signal; Transmembrane.	
	FT SIGNAL	1 .. 19	Potential.
	FT PROPEP	21 .. 44	Potential.
	FT CHAIN	45 .. 819	Cadherin-24.
	FT DOMAIN	45 .. 641	Extracellular (Potential).
	FT TRANSERM	642 .. 662	Potential.
	FT DOMAIN	663 .. 819	Cytoplasmic (Potential).
	FT DOMAIN	46 .. 150	Cadherin 1.
	FT DOMAIN	151 .. 259	Cadherin 2.
	FT DOMAIN	260 .. 374	Cadherin 3.
	FT DOMAIN	375 .. 517	Cadherin 4.
	FT CARBOHYD	517 .. 630	Cadherin 5.
	FT CARBOHYD	446 .. 446	N-linked (GlcNAc...) (Potential).
	FT CARBOHYD	548 .. 548	N-linked (GlcNAc...) (Potential).
	FT CARBOHYD	563 .. 563	N-linked (GlcNAc...) (Potential).
	FT VARSLPIC	455 .. 492	/Frid=VSP_008717.
	FT FT	VARSLPIC	Missing (In Isoform 2).
	FT FT	VARSLPIC	/Frid=VSP_008717.
	FT FT	VARSLPIC	Missing (In Isoform 3).
	FT FT	VARSLPIC	/Frid=VSP_008718.
	FT FT	VARSLPIC	EGLTIRAPALDEPARAMENUTLATELGWMSGERSGWPVL
	FT FT	VARSLPIC	VARSWAAPQRSVPVGSAVGIHQ -> MNIVTWCSHS
	FT FT	VARSLPIC	AFLFSCTIHAAYFMFCIMLVASCGIHAPHMLRVNCVCV

FT VMAPCGVLPs (4n isoform 3).
FT /FTId=VSP_008719.
SQ SEQUENCE 819 AA; 87751 MW; 9083034f18b47e84 CRC64;

Query Match 100.0%; Score 247; DB 1; Length 819;
Best Local Similarity 100.0%; Pred. No. 1.9e-22;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STVTVTLSDVNDNPKPKFPOSILYQFSVETAGPGLVGRLRADPDIG 48
DB 242 STVTVTLSDVNDNPKPKFPOSILYQFSVETAGPGLVGRLRADPDIG 289

RESULT 4

ID Q6PFX6 PRELIMINARY; PRT; 781 AA.
AC Q6PFX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cadherin-like 24.
GN Name=ch24;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
RU Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC EMBL: BC057373; AAH57373.1; -
CC InterPro: IPR002126; Cadherin.
CC InterPro: IPR000233; Cadherin_C-term.
CC Pfam: PF00028; Cadherin_S.
CC Pfam: PF01049; Cadherin_C; 1.
CC PRINTS: PR00205; CADHERIN.
CC SMART: SM00112; CA; 4.
CC PROSITE: PS00332; CADHERIN_1; 2.
CC PROSITE: PS00368; CADHERIN_2; 5.
KM Calcium-binding; Cell adhesion; Transmembrane.
SQ SEQUENCE 781 AA; 84104 MW; 15996D6E6C9835AA CRC64;

Query Match 98.8%; Score 244; DB 2; Length 781;
Best Local Similarity 97.9%; Pred. No. 4.2e-22;

Matches 47; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STVTVTLSDVNDNPKPKFPOSILYQFSVETAGPGLVGRLRADPDIG 48
DB 242 STVTVTLSDVNDNPKPKFPOSILYQFSVETAGPGLVGRLRADPDIG 289

RESULT 5

ID AAH57373 PRELIMINARY; PRT; 781 AA.
AC AAH57373;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Cadherin-like 24.
GN CDH24.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
RU Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC057373; AAH57373.1; -
SQ SEQUENCE 781 AA; 84104 MW; 15996D6E6C9835AA CRC64;

Query Match 98.8%; Score 244; DB 2; Length 781;
Best Local Similarity 97.9%; Pred. No. 4.2e-22;
Matches 47; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STVTVTLSDVNDNPKPKFPOSILYQFSVETAGPGLVGRLRADPDIG 48
DB 242 STVTVTLSDVNDNPKPKFPOSILYQFSVETAGPGLVGRLRADPDIG 289

RESULT 6

ID CADB_CHICK STANDARD; PRT; 792 AA.
AC 093319;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-11 precursor.
GN Name=CDH11;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

CC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White leghorn;
 RA Wei J., Dong X.R., Topouzis S., Zimmer W.E., Broders F., Thiery J.P.,
 RA Kotliarsky V., Majesky M.W.;
 RT "Molecular cloning of chick cadherin 11 and its expression during
 RL smooth muscle differentiation and formation of the tunica media.";
 CC Submitted (Mar-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or
 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC DR EMBL; AF055342; AAC33675.1; -;
 CC DR HSSP; P09803; 117W.
 CC DR InterPro; IPR002126; Cadherin.
 CC DR InterPro; IPR000233; Cadherin_C_term.
 CC Pfam; PF01048; Cadherin_5.
 CC Pfam; PF01048; Cadherin_5.
 CC DR PRINTS; PR0205; CADHERIN.
 CC DR SMART; SM00232; CADHERIN_1; 3.
 CC DR PROSITE; PS00232; CADHERIN_1; 3.
 CC DR PROSITE; PS0268; CADHERIN_2; 5.
 CC KW Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 CC Transmembrane.
 CC FT SIGNAL 1 22 Potential.
 CC FT PROPEP 23 53 Potential.
 CC FT CHAIN 54 792 Cadherin-11.
 CC FT DOMAIN 54 613 Extracellular (Potential).
 CC FT TRANSEM 614 634 Cytoplasmic (Potential).
 CC FT DOMAIN 635 792 Potential.
 CC FT DOMAIN 54 159 Cadherin 1.
 CC FT DOMAIN 160 268 Cadherin 2.
 CC FT DOMAIN 269 384 Cadherin 3.
 CC FT DOMAIN 384 486 Cadherin 4.
 CC FT DOMAIN 487 608 Cadherin 5.
 CC FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
 CC FT CARBOHYD 536 536 N-linked (GlcNAc...) (Potential).
 CC FT CARBOHYD 594 594 N-linked (GlcNAc...) (Potential).
 CC SQ SEQUENCE 792 AA; 87572 MW; 3E3498C686731AB CRC64;
 CC -----
 CC Query Match 72.9%; Score 180; DB 1; Length 792;
 CC Best Local Similarity 68.8%; Pred. No. 6e-14;
 CC Matches 33; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
 CC -----
 CC QY 1 STVTYVLSVNDNPKPKFQSLYQFSVETAGCGTLYGRADDPDLG 48
 CC DB 251 TTKVITLTVNDNPKPKFQSLYQFSVETAGCGTLYGRADDPDLG 298
 CC -----
 CC RESULT 7
 CC CADA_MOUSE STANDARD; PRT; 796 AA.
 CC ID P55286;
 CC DT 01-OCT-1996 (Rel. 34, Created)
 CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
 CC DT 05-JUL-2004 (Rel. 44, Last annotation update)
 CC DE Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSF-4).
 CC GN Name=ch11; Synonym=Cad-11;
 CC OS Mus musculus (Mouse)
 CC BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=95269886; PubMed=7750649;
 RA Hoffman I.H., Balling R.;
 RT "Cloning and expression analysis of a novel mesodermally expressed
 RL cadherin.";
 CC Dev. Biol. 169:337-346(1995).
 CC -----
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 RC MEDLINE=95269887; PubMed=7750650;
 RA Kimura Y., Matsunami H., Inoue T., Shimamura K., Uchida N., Ueno T.,
 RA Miyazaki T., Takeichi M.;
 RT "Cadherin-11 expressed in association with mesenchymal morphogenesis
 RL in the head, somite, and limb bud of early mouse embryos.";
 CC Dev. Biol. 169:347-358(1995).
 CC -----
 CC RN [3]
 CC RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Calvaria;
 RX MEDLINE=94216322; PubMed=8163513;
 RA Okazaki M., Takehita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,
 RA Amanai B.;
 RT "Molecular cloning and characterization of OB-cadherin, a new member
 RL of cadherin family expressed in osteoblasts.";
 CC J. Biol. Chem. 269:12092-12098(1994).
 CC -----
 CC RN [4]
 CC RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein W.J., USCIN T.B., Toshitoki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatane P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -----
 CC RN [5]
 CC RP DEVELOPMENTAL STAGE.
 RC STRAIN=C57BL/6; TISSUE=Testis;
 RX MEDLINE=97033837; PubMed=8879495;
 RA Munro S.B., Blaschuk O.W.;
 RT "A comprehensive survey of the cadherins expressed in the testes of
 RL fetal, immature, and adult mice utilizing the polymerase chain
 RT reaction.";
 CC Biol. Reprod. 55:822-827(1996).
 CC -----
 CC RN [6]
 CC RP FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Selectively expressed in osteoblastic cell
 CC lines, precursor cell lines of osteoblasts, and primary
 CC osteoblastic cells from calvaria, as well as in lung, testis, and
 CC brain tissues at low levels.
 CC -1- DEVELOPMENTAL STAGE: In the testis, expression is highest in fetal
 CC gonad and decreases 8-fold in newborn.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----

DR EMBL; X77557; CAAS4674.1; -
DR EMBL; D31863; BA06730.1; -
DR EMBL; D21253; BA04797.1; -
DR EMBL; BC046314; AAH46314.1; -
DR PIR; A53584; A53584.
DR PIR; I48277; I48277.
DR PIR; I49556; I49556.
DR HSSP; P09803; 117M.
DR MGI; 99217; Cdh11.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR00223; Cadherin_C_term.
DR Pfam; PF00028; Cadherin_5.
DR Pfam; PF01049; Cadherin_C_1.
DR PRINTS; PR00205; CADHERIN.
DR PROSITE; PS00232; CADHERIN_1; 3.
DR PROSITE; PS50268; CADHERIN_2; 5.
KW Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 24 potential.
FT PROPEP 25 53 potential.
FT CHAIN 54 796 Cadherin-11.
FT DOMAIN 54 617 Extracellular (Potential).
FT TRANSMEM 618 640 Potential.
FT DOMAIN 641 796 Cytoplasmic (Potential).
FT DOMAIN 160 268 Cadherin 1.
FT DOMAIN 269 383 Cadherin 2.
FT DOMAIN 384 486 Cadherin 3.
FT DOMAIN 487 612 Cadherin 4.
FT DOMAIN 612 612 Cadherin 5.
FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 540 540 N-linked (GlcNAc...) (Potential).
FT CONFLICT 462 462 E -> D (in Ref. 1).
FT CONFLICT 589 589 T -> L (in Ref. 2).
FT CONFLICT 655 655 D -> N (in Ref. 2).
FT CONFLICT 751 751 V -> M (in Ref. 1).
FT CONFLICT 777 777 P -> Q (in Ref. 2).
FT CONFLICT 782 782 L -> P (in Ref. 2).
SQ SEQUENCE 796 AA; 88112 MW; 0D584D24641DD529 CRC64;

Query Match 72.9%; Score 180; DB 1; Length 796;
Best Local Similarity 68.8%; Pred. No. 6, 1e-14;
Matches 33; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

OY 1 STTAVTLDVNDNPPKPSLYQPSVETAGPGLVRLRAOPDGLG 48
DB 251 TTKVITITLDVNDNPPKPSLYQPSVETAGPGLVRLRAOPDGLG 258

RESULT 8
O8C706 PRELIMINARY; PRT; 796 AA.

AC O8C706;
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length
DE enriched library, clone: C530015F15 product: cadherin 11, full insert
DE sequence.
GN Name=Cdh11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=21085660; PubMed=11217651;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
RN [3]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [4]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=20493374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
RN [5]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama U., Nishi K., Kikunishi T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwa K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai U.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer";
RL Genome Res. 10:1757-1771(2000).
RN [6]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA Adachi U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hamagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasaiwa T.,
RA Kato H., Kawai U., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takada Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 5 cadherin domains.

DR EMBL; AK046552; BK33860.1; -
DR HSSP; P09803; 117M.
DR MGI; 99217; Cdh11.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR00223; Cadherin_C_term.
DR Pfam; PF00028; Cadherin_5.
DR Pfam; PF01049; Cadherin_C_1.
DR PRINTS; PR00205; CADHERIN.

DR SMART; SMO0112; CA; 5.
 DR PROSITE; PS0032; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 KW Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 796 AA; 88126 MW; 7196337482E1BE29 CRC64;

Query Match 72.1%; Score 180; DB 2; Length 796;
 Best Local Similarity 68.8%; Pred. No. 6, 1e-11;
 Matches 33; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

CY 1 STTTVTLSVDNPNPKPQSLYQFSVETAGPGLVGLRAQDDPDIG 48
 Db 251 TTKVTITLTDVNDNPKPQSLYQFSVETAGPGLVGLRAQDDPDIG 298

RESULT 9
 CADB_HUMAN STANDARD; PRT; 796 AA.
 AC P55287; Q15065; Q9U093; Q9U094;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSF-4).
 GN Name=CDH11;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN 1;
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=95073006; PubMed=7982033;
 RA Tanihara H., Sano K., Helmark R.L., St John T., Suzuki S.;
 RT "Cloning of five human cadherins classifies characteristic features of
 RT cadherin extracellular domain and provides further evidence for two
 RT structurally different types of cadherin."
 RL Cell Adhes. Commun. 2:1526(1994).
 RN 2;
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Osteosarcoma;
 RX MEDLINE=94216322; PubMed=8163513;
 RA Okazaki M., Takeshita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,
 RA Amano E.;
 RT "Molecular cloning and characterization of OS-cadherin, a new member
 RT of cadherin family expressed in osteoblasts."
 RL J. Biol. Chem. 269:12092-12098(1994).
 RN 3;
 RP SEQUENCE OF 269-796 FROM N.A. (ISOFORM 1).
 RC TISSUE=Fetal brain;
 RX MEDLINE=91283540; PubMed=2059658;
 RA Suzuki S., Sano K., Tanihara H.;
 RT "Diversity of the cadherin family: evidence for eight new cadherins in
 RT nervous tissue."
 RL Cell Regul. 2:261-270(1991).
 RN 4;
 RP SEQUENCE OF 600-668 FROM N.A. (ISOFORMS 1 AND 2).
 RA Kools P.F.J., Hendooorn P.C.W., Boyce J.V.M.G., Van Roy F.;
 RT "Alternative cadherin-11 transcripts encoding truncated adhesion
 RT molecules are detectable in both human cancer and normal cells."
 RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P55287-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P55287-2; Sequence=VSP 000640; VSP 000641;
 CC -1- TISSUE SPECIFICITY: Expressed mainly in brain but also found in
 CC other tissues. Expressed in neuroblasts.

CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.ebi.ac.uk/announcements/>
 CC or send an email to license@ebi.ac.uk).

DR EMBL; I34056; AAA35622.1; -;
 DR EMBL; D1254; BAA04798.1; -;
 DR EMBL; D1255; BAA04798.1; -;
 DR EMBL; AF060370; AAD27755.1; -;
 DR EMBL; AF060369; AAD27755.1; JOINED.
 DR EMBL; AF060370; AAD27755.1; -;
 DR EMBL; AF060369; AAD27755.1; JOINED.
 DR PIR; A38992; A38992.
 DR HSSP; P09803; 117W.
 DR Genew; HGNC:1750; CDH11.
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0007156; P:hemophilic cell adhesion; NAS.
 DR GO; GO:0001303; P:osification; NAS.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C_term.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin_C; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SMO0112; CA; 5.
 DR PROSITE; PS0032; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 KW Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 22 Potential.
 FT PROPEP 23 53 Potential.
 FT CHAIN 54 796 Cadherin-11.
 FT DOMAIN 54 617 Extracellular (Potential).
 FT TRANSMEM 618 640 Potential.
 FT DOMAIN 641 796 Cytoplasmic (Potential).
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.
 FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 612 Cadherin 5.
 FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 540 540 N-linked (GlcNAc...) (Potential).
 FT VARSPLIC 632 693 VIVLFTLIRKCKEPLIVPEEDRENITTYDEGGGEED
 FT TSPADIATLQNDGNGPIRP -> GGPSLMEPSPEDMR
 FT LTVGFQMLFSYKYNRRPCLGVFKPLPLYVATESP
 FT TULSL (in isoform 2).
 FT FTID=VSP_000640.
 FT Missing (in isoform 2).
 FT VARSPLIC 694 796 /FTID=VSP_000641.
 FT FT Missing (in isoform 2).
 FT CONFLICT 271 272 RL -> SV (in Ref. 2).
 FT CONFLICT 275 275 M -> I (in Ref. 2).
 FT CONFLICT 340 340 E -> K (in Ref. 2).
 FT CONFLICT 373 373 S -> A (in Ref. 2).
 FT CONFLICT 471 471 Q -> K (in Ref. 2).
 SQ SEQUENCE 796 AA; 88049 MW; 206704478ADB32E CRC64;

Query Match 72.1%; Score 178; DB 1; Length 796;
 Best Local Similarity 68.8%; Pred. No. 1, 1e-13;
 Matches 33; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

CY 1 STTTVTLSVDNPNPKPQSLYQFSVETAGPGLVGLRAQDDPDIG 48
 Db 251 TTKVTITLTDVNDNPKPQSLYQFSVETAGPGLVGLRAQDDPDIG 298

RESULT 10
 Q96CZ9 PRELIMINARY; PRT; 796 AA.

AC 096C29;
 DT 01-DEC-2001 (TRENBLREL. 19, Created)
 DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
 DE Cadherin 11, type 2, isoform 1 preproprotein.
 GN Name=CDH11;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RX MEDLINE=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Altschuler S.F., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ueda T.B., Tomshiki S., Carninci P., Mullahy S.J.,
 Raha S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullaly S.J.,
 Boak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 Jones S.J., Marra M.A., Skalski U., Smallus D.E., Scheraga A., Schein J.E.,
 Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC EMBL; SC013609; AAI13609.1; -.
 DR HSSP; P09803; 117W.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C-term.
 DR InterPro; IPR001901; SecE.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin_C; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS02668; CADHERIN_2; 5.
 DR PROSITE; PS01067; SECE_SECIG; UNKNOWN_1.
 KW Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 796 AA; 87979 MW; 8497F9B834F7547C CRC64;
 Query Match 70.4%; Score 174; DB 2; Length 796;
 Best Local Similarity 66.7%; Pred. No. 3.5e-13;
 Matches 32; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

AC 093264;
 DT 01-NOV-1998 (TRENBLREL. 08, Created)
 DT 01-NOV-1998 (TRENBLREL. 08, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
 DE Cadherin precursor.
 GN Name=Xcad-11;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 NCBI_TaxID=9335;
 RX MEDLINE=98202517; PubMed=9533956;
 RA Haddad B., Borchers A., Medlich D.;
 RT "Xenopus cadherin-11 (Xcadherin-11) expression requires the Wg/Wnt
 signal.";
 RL Mech. Dev. 72:101-113 (1998).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC EMBL; AF002983; AAC28073.1; -.
 DR HSSP; P09803; 117W.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin_C; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS02668; CADHERIN_2; 5.
 KW Calcium; Calcium-binding; Cell adhesion; Signal; Transmembrane.
 FT SIGNAL 1
 FT CHAIN 54 794 cadherin.
 SQ SEQUENCE 794 AA; 88302 MW; 7221AD4CFA719DB CRC64;
 Query Match 70.0%; Score 173; DB 2; Length 794;
 Best Local Similarity 66.7%; Pred. No. 4.7e-13;
 Matches 32; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

RESULT 12
 CADM_MOUSE STANDARD; PRT; 813 AA.
 ID CADM_MOUSE
 AC 09WTP5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-22 precursor (Pp-cadherin).
 GN Name=Cdh22;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX MEDLINE=9326347; PubMed=10398531;
 RA Kitajima K., Koshimizu U., Nakamura T.;
 RT "Expression of a novel type of classic cadherin, Pp-cadherin in
 developing brain and limb buds.";
 RL Dev. Dyn. 215:206-214 (1999).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic


```

CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types. pb-cadherins may have a role
CC in the morphological organization of pituitary gland and brain
CC tissues.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Predominantly expressed in brain. Abundant in
CC olfactory bulb, cerebellum, and cerebellum, less in pons, medulla,
CC and spinal cord. Low expression in heart. No expression in lung,
CC liver, spleen, kidney, testis, stomach, intestine, colon, and
CC placenta.
CC -1- DEVELOPMENTAL STAGE: Expressed at 9.5 dpc onwards. At 10.5 dpc, in
CC brain (telencephalic vesicles and isthmus), spinal cord and limb
CC buds (in the zone of polarizing activity). At 14.5 dpc, in
CC olfactory bulb and cerebellum.
CC -1- INDUCTION: Down-regulated by thyroid hormone.
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; AB019618; BAA34426.1; -.
CC DR HSSP; P09803; 117W.
CC DR MGD; MGI:1341843; Cdh22.
CC DR InterPro; IPR002126; Cadherin.
CC DR InterPro; IPR002033; Cadherin_C_term.
CC DR Pfam; PF00028; Cadherin_5.
CC DR Pfam; PF01049; Cadherin_C_1.
CC DR PRINTS; PR00205; CADHERIN.
CC DR SMART; SM00112; CA; 5.
CC DR PROSITE; PS00232; CADHERIN_1; 2.
CC DR PROSITE; PS0266; CADHERIN_2; 5.
CC DR Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
CC Transmembrane.
CC KW SIGNAL 1 33 Potential.
CC FT CHAIN 34 813 Cadherin-22.
CC FT DOMAIN 33 621 Extracellular (Potential).
CC FT TRANSMEM 622 642 Potential.
CC FT DOMAIN 643 813 Cytoplasmic (Potential).
CC FT DOMAIN 61 165 Cadherin_1.
CC FT DOMAIN 166 274 Cadherin_2.
CC FT DOMAIN 275 391 Cadherin_3.
CC FT DOMAIN 392 495 Cadherin_4.
CC FT DOMAIN 496 613 Cadherin_5.
CC FT CARBOHYD 159 159 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 609 609 N-linked (GlcNAc...) (Potential).
CC SQ SEQUENCE 813 AA; 88021 MW; 5510F9848D976567 CRC64;
CC -----
CC Query Match 69.6%; Score 172; DB 1; Length 813;
CC Best Local Similarity 62.5%; Pred. No. 6.5e-13;
CC Matches 30; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
CC -----
CC 1 STTYVTLSVDVNDNPKPFQPSLQFQSVETAGCGTLVGRADDPDLG 48
CC Db 257 STTYVTLSVDVNDNPKPFQPSLQFQSVETAGCGTLVGRADDPDLG 304
CC -----
CC RESULT 13
CC CDM_RAT STANDARD; PRT; 813 AA.
CC AC Q63315; Q63561;
CC DT 28-FEB-2003 (Rel. 41, Created)
CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
CC DT 05-JUL-2004 (Rel. 44, Last annotation update)
CC DE Cadherin-22 precursor (PB-cadherin).
CC GN Name=Cdh22;
CC OS Rattus norvegicus (Rat).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CC NCBI_TaxID=10116;
CC RN [1]
CC RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND CHARACTERIZATION.
CC RC STRAIN=Wiistar; TISSUE=Brain, and Pituitary;
CC RX MEDLINE=96212232; PubMed=8626716;
CC RA Sugimoto K., Honda S., Yamamoto T., Ueki T., Mondan M., Kaji A.,
CC RA Matsumoto K., Nakamura T.;
CC RT "Molecular cloning and characterization of a newly identified member
CC of the cadherin family, PB-cadherin.";
CC J. Biol. Chem. 271:11548-11556(1996).
CC -1- FUNCTION: Cadherins are calcium dependent cell-adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types. pb-cadherins may have a role
CC in the morphological organization of pituitary gland and brain
CC tissues.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Name=1;
CC IsoId=Q63315-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q63315-2; Sequence=VSP_000643, VSP_000644;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Strongly expressed in the pituitary gland and
CC the brain (in the inner granular and glomerular layers of the
CC olfactory bulb, anterior olfactory nucleus, primary olfactory
CC cortex, Parkinje cell layer of cerebellum, and pineal gland). Low
CC expression in lung and heart. No expression in submandibular
CC gland, thymus, liver, spleen, adrenal, and kidney.
CC -1- DEVELOPMENTAL STAGE: Expressed strongly in fetal brain.
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; D83348; BAA11894.1; -.
CC DR EMBL; D83349; BAA11895.1; -.
CC DR HSSP; P09803; 117W.
CC DR GSD; 2321; Cdh22.
CC DR InterPro; IPR002126; Cadherin.
CC DR InterPro; IPR002033; Cadherin_C_term.
CC DR Pfam; PF00028; Cadherin_5.
CC DR Pfam; PF01049; Cadherin_C_1.
CC DR PRINTS; PR00205; CADHERIN.
CC DR SMART; SM00112; CA; 5.
CC DR PROSITE; PS00232; CADHERIN_1; 2.
CC DR PROSITE; PS0266; CADHERIN_2; 5.
CC DR Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
CC Repeat; Signal; Transmembrane.
CC KW SIGNAL 1 33 Potential.
CC FT CHAIN 34 813 Cadherin-22.
CC FT DOMAIN 33 621 Extracellular (Potential).
CC FT TRANSMEM 622 642 Potential.
CC FT DOMAIN 643 813 Cytoplasmic (Potential).
CC FT DOMAIN 61 165 Cadherin_1.
CC FT DOMAIN 166 274 Cadherin_2.
CC FT DOMAIN 275 391 Cadherin_3.
CC FT DOMAIN 392 495 Cadherin_4.
CC FT DOMAIN 496 613 Cadherin_5.
CC FT CARBOHYD 159 159 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 609 609 N-linked (GlcNAc...) (Potential).
CC FT VARSPLIC 668 694
CC FT VARSPLIC 695 813
CC Missing (in isoform 2).

```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 19.863 Seconds

(without alignments)
866.886 Million cell updates/sec

US-09-788-051-9

Title: 247
Perfect score: 1 STVTVTLSVDVNDNPKFPQ.....ETAGPGLVGLRLRAPDPDLG 48

Sequence: 1 STVTVTLSVDVNDNPKFPQ.....ETAGPGLVGLRLRAPDPDLG 48

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseqp19808:*
2: Geneseqp19908:*
3: Geneseqp20008:*
4: Geneseqp20018:*
5: Geneseqp20028:*
6: Geneseqp20038:*
7: Geneseqp20048:*
8: Geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	247	100.0	48	ADD29450	Human cad
2	247	100.0	493	AD116946	Human NOV
3	247	100.0	607	ABBS3295	Human pol
4	247	100.0	620	ADD29448	Human cad
5	247	100.0	636	ADD29445	Human pol
6	247	100.0	781	ABBS3296	Human cad
7	247	100.0	781	AAW48736	Human NOV
8	247	100.0	781	ABG34078	Human NOV
9	247	100.0	781	AD116604	Human NOV
10	247	100.0	781	AD116606	Human NOV
11	247	100.0	781	ABR40114	Human cel
12	247	100.0	781	ADA01366	Human PRO
13	247	100.0	781	ADA43795	Human sec
14	247	100.0	781	ADA43563	Human sec
15	247	100.0	781	ADA01238	Human PRO
16	247	100.0	781	ADA01122	Human sec
17	247	100.0	781	ADA43579	Human sec
18	247	100.0	781	ADA06941	Human PRO
19	247	100.0	781	ADA08429	Human hum
20	247	100.0	781	ADBS9722	Human PRO
21	247	100.0	781	ADBS7005	Human PRO
22	247	100.0	781	ADBS6160	Human sec
23	247	100.0	781	ADBS9938	Human PRO
24	247	100.0	781	ADBS99493	Human hum
25	247	100.0	781	ADBS6044	Human sec

26	247	100.0	781	7	ADC23442	ADC23442 Human tra
27	247	100.0	781	7	ADC26135	ADC26135 Human PRO
28	247	100.0	781	7	ADE04962	ADE04962 Human PRO
29	247	100.0	781	7	ADE11268	ADE11268 Human PRO
30	247	100.0	781	7	ADD88199	ADD88199 Human PRO
31	247	100.0	781	7	ADD95494	ADD95494 Human sec
32	247	100.0	781	7	ADE06424	ADE06424 Human PRO
33	247	100.0	781	7	ADE38199	ADE38199 Human PRO
34	247	100.0	781	7	ADE88315	ADE88315 Human PRO
35	247	100.0	781	7	ADD90896	ADD90896 Human sec
36	247	100.0	781	7	ADBS9451	ADBS9451 Human sec
37	247	100.0	781	7	ADG06544	ADG06544 Human PRO
38	247	100.0	781	7	ADG05495	ADG05495 Human PRO
39	247	100.0	781	7	ADG82496	ADG82496 Human PRO
40	247	100.0	781	8	ADE51749	ADE51749 Human sec
41	247	100.0	781	8	ADE51865	ADE51865 Human sec
42	247	100.0	781	8	ADE37723	ADE37723 Human sec
43	247	100.0	781	8	ADBS37607	ADBS37607 Human sec
44	247	100.0	781	8	ADBS3578	ADBS3578 Human sec
45	247	100.0	781	8	ADE38078	ADE38078 Human PRO

ALIGNMENTS

RESULT 1
ADD29450
ID ADD29450 standard; protein; 48 AA.
XX
AC ADD29450:
XX
DT 15-JUN-2004 (first entry)
XX
DE Human cadherin-like protein peptide fragment Seg 109.
XX
XX cadherin-like protein; transmembrane protein; cadherin domain;
KW homotypic cell-cell adhesion; cytostatic; osteopetrosis; cancer;
KW osteopetrosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
KW metastatic tumour; human.
XX
OS Homo sapiens.
XX
PN US2003144491-A1.
XX
PD 31-JUL-2003.
XX
PF 16-FEB-2001; 2001US-00788051.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
XX
PA (GDB/) GDBOLE S D.
PA (KUOC/) KUO C.
PA (ARTE/) ARTERBURN M C.
PA (YEUN/) YEUNG G.
PA (PALE/) PALENCIA S.
PA (TANG/) TANG Y T.
PA (LUC/) LIU C.
PA (DRMA/) DRMANAC R T.
XX
XX Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;
PI Liu C, Drmanac RT;
PI WPI; 2003-829759/77.
XX
XX Novel isolated human secreted cadherin-like polypeptide useful for
PT treating diseases such as cancers, osteopetrosis, Paget's disease,
PT osteomalacia, hyperostosis, osteopetrosis.
XX
XX Claim 11; SEQ ID NO 9; 63bp; English.
XX
XX This invention relates to a novel isolated human secreted cadherin-like
CC protein and the DNA sequence which encodes it. Cadherins are a family of

26-MAR-2001; 2001US-0278778P.
PR 29-MAR-2001; 2001US-0279682P.
PR 29-MAR-2001; 2001US-0279684P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282992P.
PR 11-APR-2001; 2001US-0283063P.
PR 20-APR-2001; 2001US-0285133P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 29-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294173P.
PR 08-JUN-2001; 2001US-0296564P.
PR 18-JUN-2001; 2001US-0298559P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312889P.
PR 16-AUG-2001; 2001US-0312808P.
PR 21-AUG-2001; 2001US-0313390P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323375P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330208P.
PR 14-NOV-2001; 2001US-0332701P.
XX
XX
XX (CURA-) CURAGEN CORP.
XX
XX
XX Tchernev VT, Spytek KA, Zernhusen BD, Patnrajan M, Shinkets RA;
PI Li L, Gangolli EA, Padgug M, Anderson DM, Rastelli L, Miller CE;
PI Gelach VL, Taulper RJ, Gusev VY, Carlson SD, Wolenc AR, Pena CEA,
PI Putrak K, Grosse WM, Aisbrook JP, Lepley DM, Rieger DK, Burgess CE,
XX WPI; 2002-706998/76.
XX
XX
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
PT
PS
PS Disclosure; SEQ ID NO 482; 1496BP, English.
XX
XX
XX This invention relates to a novel nucleic acid, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOVX polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig) nephropathy, cirrhosis,
CC atrichitis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC cytostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
CC haemostatic, anti-HIV, antidiabetic, antiantherosclerotic, anorectic,
CC antistimatic, nephrotoxic, antiarthritic, hepatocytic,
CC neuroprotective, nootropic, antibacterial, vinocide, antiparasitic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
CC of the invention.
XX
XX

Query Match 100.0%; Score 247; DB 5; Length 493;
Best Local Similarity 100.0%; Pred. No. 3, 3e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTAVTSLSDVNDNPKFPQSLYQPSVETAGPGLVGRRAQDPDLG 48
DB 242 STTAVTSLSDVNDNPKFPQSLYQPSVETAGPGLVGRRAQDPDLG 289

RESULT 3
ABBS3295
ID ABBS3295 standard; protein; 607 AA.

AC ABB53295;

DT 12-FEB-2002 (first entry)

DE Human polypeptide #35.

Human; nocotropic; neuroprotective; anticonvulsant; antidepressant;
neuroleptic; tranquilizer; antiarrhythmic; cardiac; antidiabetic;
antiinflammatory; antilipemic; hepatotropic; virocidic; antidiabetic;
neurotrophic; anorectic; cytotactic; vaccine; neurological disease;
cardiovascular disease; respiratory disease; liver disease;
renal disease; skeletal muscle disease; gastrointestinal disease;
placental disease; testicular cancer; male fertility; pancreatic disease.

OS Homo sapiens.

PN WO200181363-A1.

PD 01-NOV-2001.

PF 26-APR-2001; 2001WO-US013360.

PR 27-APR-2000; 2000US-0199963P.

PR 11-MAY-2000; 2000US-0203338P.

PR 25-MAY-2000; 2000US-0207087P.

PR 26-MAY-2000; 2000US-0207546P.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM P.L.C.

PI Agarwal P, Murdock PR, Rizvi SK, Smith RF, Xiang Z, Kahnick KS;

PI Lal Y, Xie Q;

DR N-PSDB; ABA90360.

DR WPI; 2002-041392/05.

DR N-PSDB; ABA90360.

DR WPI; 2002-041392/05.

DR N-PSDB; ABA90360.

DR WPI; 2002-041392/05.

DR N-PSDB; ABA90360.

DR WPI; 2002-041392/05.

DR N-PSDB; ABA90360.

DR WPI; 2002-041392/05.

CC myotonia congenita and intestinal obstruction; lymph diseases including
CC lymphagiectasia; diseases of placenta including choriochorionoma; diseases
CC of testes including testicular cancer, male reproductive diseases
CC including low testosterone and male infertility; and disease of pancreas
CC including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The
CC present sequence is a polypeptide of the invention

CC Sequence 607 AA;

Query Match 100.0%; Score 247; DB 5; Length 607;
Best Local Similarity 100.0%; Pred. No. 4, 2e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTAVTSLSDVNDNPKFPQSLYQPSVETAGPGLVGRRAQDPDLG 48
DB 242 STTAVTSLSDVNDNPKFPQSLYQPSVETAGPGLVGRRAQDPDLG 289

RESULT 4
ADD29448
ID ADD29448 standard; protein; 620 AA.

AC ADD29448;

DT 15-JUN-2004 (first entry)

DE Human cadherin-like mature protein.

Human; cadherin-like protein; transmembrane protein; cadherin domain;
cadherin-like cell-cell adhesion; cytoskeletal; osteopathic; cancer;
osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
metastatic tumour; human.

OS Homo sapiens.

PN US2003144491-A1.

PD 31-JUL-2003.

PF 16-FEB-2001; 2001US-00788051.

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PA (GDB/) GODSOLE S D.

PA (KUC/) KUO C.

PA (ARTE/) ARTERBURN M C.

PA (YEUN/) YEUNG G.

PA (PALE/) PALENCIA S.

PA (TANG/) TANG Y T.

PA (LIUC/) LIU C.

PA (DRMA/) DRMANAC R T.

PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;

PI Liu C, Drmanac RT;

DR WPI; 2003-829799/77.

DR N-PSDB; ABA90360.

DR WPI; 2003-829799/77.

DR N-PSDB; ABA90360.

DR WPI; 2003-829799/77.

Novel isolated human secreted cadherin-like polypeptide useful for
treating diseases such as cancers, osteoporosis, Paget's disease,
osteomalacia, hyperostosis, osteopetrosis.

Claim 11; SEQ ID NO 7; 63bp; English.

This invention relates to a novel isolated human secreted cadherin-like
protein and the DNA sequence which encodes it. Cadherins are a family of
transmembrane proteins which share a common cadherin domain in their
extracellular region. The extracellular portion mediates homotypic cell-
cell adhesion that is calcium dependent. Modulators of the protein of the
invention may have cytoskeletal or osteopathic activity. The invention may
allow development of therapeutics useful for the treatment of diseases
such as cancers, osteoporosis, Paget's disease, osteomalacia,
hyperostosis and osteopetrosis. The protein and DNA sequence of the

CC invention may also be useful as markers for prognosis of metastatic
 CC tumours. The present sequence is that of the mature human secreted
 CC cadherin-like protein which was used during the exemplification of the
 CC invention.

CC SQ Sequence 620 AA;

Query Match 100.0%; Score 247; DB 7; Length 620;
 Best Local Similarity 100.0%; Pred. No. 4.3e-26;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTAVTSLSDVNDNPKRPSLYQFSVETAGPGLVGRRAQDDPDG 48
 Db 226 STTAVTSLSDVNDNPKRPSLYQFSVETAGPGLVGRRAQDDPDG 273

RESULT 5
 ADD29445
 ID ADD29445 standard; protein; 636 AA.

XX AC ADD29445;
 XX DT 15-JAN-2004 (first entry)
 XX DE Human cadherin-like protein amino acid sequence.
 XX KW cadherin-like protein; transmembrane protein; cadherin domain;
 KW homotypic cell-cell adhesion; cytosolic; osteopathic; cancer;
 KW osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
 KW metastatic tumour; human.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Peptide 1..16
 FT /label= Signal peptide
 FT 17..636
 FT /label= Mature_human_cadherin-like_protein

XX US2003144491-A1.
 XX 31-JUL-2003.
 XX PD 16-FEB-2001; 2001US-00788051.
 XX PF 03-FEB-2000; 2000US-00496914.
 XX PR 27-APR-2000; 2000US-00560875.
 XX PA (GODEB) GODEBOLE S D.
 PA (KUCO) KUO C.
 PA (ARTE) ARTERBURN M C.
 PA (YEUN) YEUNG G.
 PA (PALE) PALENCIA S.
 PA (TANG) TANG Y T.
 PA (LIUC) LIU C.
 PA (DRMA) DRMANAC R T.
 XX PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;
 PI Liu C, Drmanac RT;
 XX DR WPI; 2003-829799/77.
 DR N-PSDB; ADD29445, ADD29446.
 XX PT Novel isolated human secreted cadherin-like polypeptide useful for
 PT treating diseases such as cancers, osteoporosis, Paget's disease,
 PT osteomalacia, hyperostosis, osteopetrosis.
 XX PS Claim 11; SEQ ID NO 4; 636p; English.
 XX CC This invention relates to a novel isolated human secreted cadherin-like
 CC protein and the DNA sequence which encodes it. Cadherins are a family of
 CC transmembrane proteins which share a common cadherin domain in their
 CC extracellular region. The extracellular portion mediates homotypic cell-

CC cell adhesion that is calcium dependent. Modulators of the protein of the
 CC invention may have cytostatic or osteopathic activity. The invention may
 CC allow development of therapeutics useful for the treatment of diseases
 CC such as cancers, osteoporosis, Paget's disease, osteomalacia,
 CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
 CC invention may also be useful as markers for prognosis of metastatic
 CC tumours. The present sequence is that of the human secreted cadherin-like
 CC protein of the invention.

CC SQ Sequence 636 AA;

Query Match 100.0%; Score 247; DB 7; Length 636;
 Best Local Similarity 100.0%; Pred. No. 4.3e-26;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTAVTSLSDVNDNPKRPSLYQFSVETAGPGLVGRRAQDDPDG 48
 Db 242 STTAVTSLSDVNDNPKRPSLYQFSVETAGPGLVGRRAQDDPDG 289

RESULT 6
 ABB53296
 ID ABB53296 standard; protein; 781 AA.

XX AC ABB53296;
 XX DT 12-FEB-2002 (first entry)
 XX DE Human polypeptide #36.
 XX KW Human; nootropic; neuroprotective; anticonvulsant; antidepressant;
 KW neuroleptic; tranquilizer; antiarrhythmic; cardiant; antiasthmatic;
 KW antidiabetic; antihypertensive; hepatotropic; virucide; antidiabetic;
 KW nephrotoxic; anorectic; cytosolic; vaccine; neurological disease;
 KW cardiovascular disease; respiratory disease; liver disease;
 KW renal disease; skeletal muscle disease; gastrointestinal disease;
 KW placental disease; testicular cancer; male fertility; pancreatic disease.
 XX OS Homo sapiens.
 XX FH WO200181363-A1.
 XX PD 01-NOV-2001.
 XX PF 26-APR-2001; 2001WO-US013360.
 XX PR 27-APR-2000; 2000US-0199963P.
 XX PR 11-MAY-2000; 2000US-0203336P.
 XX PR 25-MAY-2000; 2000US-0207087P.
 XX PR 26-MAY-2000; 2000US-0207546P.
 XX PA (SMIX) SMITHLINE BECHAM CORP.
 PA (SMIK) SMITHLINE BECHAM PLC.
 XX PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z, Kabnick KS;
 PI Lai Y, Xie Q;
 XX DR WPI; 2002-041392/05.
 DR N-PSDB; ABA90361.
 XX PT Novel polypeptides and polynucleotides useful as a vaccine for preventing
 PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.
 XX PS Claim 1; Page 108-109; 116pp; English.
 XX CC The invention relates to an isolated polypeptide comprising a 277, 480,
 CC 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
 CC 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,
 CC 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
 CC given in the specification. The polypeptides, modulators of the
 CC polypeptides and antibodies against the polypeptides are useful for
 CC treating diseases such as neurological and psychiatric diseases including

CC Alzheimer's, parasupranuclear palsy, Huntington's disease, myotonic
 CC dystrophy, anorexia and depression; cardiovascular diseases including
 CC congestive heart failure, Hodgkin's disease and myocardial infarction;
 CC respiratory diseases including asthma, chronic obstructive pulmonary
 CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
 CC diseases including hypercholesterolaemia, cirrhosis, viral and nonviral
 CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
 CC renal disease including renal failure, acute tubular necrosis and
 CC glomerulonephritis; skeletal muscle diseases including Eulenburg's
 CC disease, hypoglycaemia and obesity; gastrointestinal diseases including
 CC myocenta congenita and intestinal obstruction; lymph diseases including
 CC lymphoedema; diseases of placenta including choriocarcinoma; diseases
 CC of testes including testicular cancer, male reproductive diseases
 CC including low testosterone and male infertility; and disease of pancreas
 CC including diabetic ketocidosis, Type 1 and 2 diabetes and obesity. The
 CC present sequence is a polypeptide of the invention

CC Sequence 781 AA;

Query Match 100.0%; Score 247; DB 5; Length 781;
 Best Local Similarity 100.0%; Pred. No. 5.7e-26;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTVTVTLSDVNDNPKPFQSLYQFSVETAGPGLVGRRAQDDPLG 48
 |||||
 DB 242 STTVTVTLSDVNDNPKPFQSLYQFSVETAGPGLVGRRAQDDPLG 289

RESULT 7
 AAM48736
 ID AAM48736 standard; protein; 781 AA.

AC AAM48736;

DT 28-MAR-2002 (first entry)

DE Human cadherin family member 57805 protein SEQ ID NO 2.

XX Human; cadherin 57805; osteopathic; hepatotropic; antibacterial;
 KW antidiabetic; neuroprotective; antiarthritic; antirheumatic;
 KW dermatological; immunosuppressive; antiinflammatory; antipruritic;
 KW antiasthmatic; antiallergic; antileptotic; haemostatic; antipruritic;
 KW antihypertoid; hypotensive; antiatherosclerotic; cardiant; antiaerhythmic;
 KW anorectic; immunomodulatory; vasotropic; vitruide; cytosstatic; liver;
 KW thrombolytic; analgesic; anabolic; immune disorder; cardiovascular;
 KW viral; pain; metabolism; osteoporosis; diabetes mellitus; arthritis;
 KW osteoarthritis; multiple sclerosis; Crohn's disease; asthma; allergy;
 KW thrombus; inflammation; infection; ischaemia; irritable bowel syndrome;
 KW gene therapy.

XX Homo sapiens.

XX WO200190145-A2.

PD 29-NOV-2001.

PF 18-MAY-2001; 2001WO-US016013.

PR 19-MAY-2000; 2000US-0205674P.

PA (MILL-) MILLENNIUM PHARM INC.

PI Curtis RAJ;

XX WPI; 2002-083082/11.

DR N-PSDB; ABA96406, ABA96407.

PT New human cadherin family protein and polynucleotides, useful for
 PT diagnosing and treating disorders e.g. obstructive jaundice, multiple
 PT sclerosis, encephalomyelitis and atherosclerosis and to identify
 PT modulators of therapeutic use.

PS Claim 9; Page 105; 119pp; English

XX The invention relates to human cadherin family polypeptide designated
 CC 57805 with osteopathic, hepatotropic, antibacterial, antiallergic,
 CC neuroprotective, antiarthritic, antirheumatic, dermatological,
 CC immunosuppressive, antiinflammatory, antipruritic, antiaerhythmic,
 CC antiallergic, antileptotic, haemostatic, antipruritic, antihypertoid,
 CC hypotensive, antiatherosclerotic, cardiant, antiarrhythmic, anorectic,
 CC immunomodulatory, vasotropic, vitruide, cytosstatic, thrombolytic,
 CC analgesic and anabolic activity. The 57805 molecules are useful for
 CC diagnosing and treating disorders which include disorders associated with
 CC bone metabolism, immune disorders, cardiovascular disorders, liver
 CC disorders, viral diseases, pain or metabolic disorders. Especially bone
 CC metabolism including osteoporosis, rickets, osteosclerosis, cirrhosis;
 CC immune disorders including autoimmune diseases including diabetes mellitus
 CC arthritis, including rheumatoid arthritis and osteoarthritis, multiple
 CC sclerosis, systemic lupus, dermatitis, psoriasis, Crohn's disease,
 CC asthma, thrombocytopenia, Graves' disease, graft-versus-host disease,
 CC allergy; cardiovascular disorders, thrombus, hypertension,
 CC atherosclerosis, arrhythmias and cardiomyopathy; liver disorders,
 CC glycogen storage disease, vascular disorders, chronic heart failure,
 CC portal vein thrombosis; viral diseases; metabolic or pain disorders
 CC include obesity, anorexia nervosa and diabetes, inflammation, infection
 CC and ischaemia, irritable bowel syndrome. The polynucleotides are also
 CC useful in gene therapy

XX Sequence 781 AA;

Query Match 100.0%; Score 247; DB 5; Length 781;
 Best Local Similarity 100.0%; Pred. No. 5.7e-26;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTVTVTLSDVNDNPKPFQSLYQFSVETAGPGLVGRRAQDDPLG 48
 |||||
 DB 242 STTVTVTLSDVNDNPKPFQSLYQFSVETAGPGLVGRRAQDDPLG 289

RESULT 8
 AEG34078
 ID AEG34078 standard; protein; 781 AA.

AC AEG34078;

DT 15-JUL-2002 (first entry)

DE Human Pro peptide #49.

XX Human; PRO; secreted protein; transmembrane protein; genetic disorder;
 KW tumour; cancer.

XX Homo sapiens.

XX WO200224888-A2.

PD 28-MAR-2002.

PF 29-AUG-2001; 2001WO-US027099.

PR 01-SEP-2000; 2000US-0229896P.

PR 05-SEP-2000; 2000US-0230621P.

PR 22-SEP-2000; 2000US-0235147P.

PR 10-NOV-2000; 2000WO-US030873.

PR 12-JAN-2001; 2001US-0261878P.

PR 16-JAN-2001; 2001US-0261810P.

PR 16-JAN-2001; 2001US-0261939P.

PR 25-JAN-2001; 2001US-0262150P.

PR 02-FEB-2001; 2001US-0264395P.

PR 09-FEB-2001; 2001US-0266421P.

PR 28-FEB-2001; 2001WO-US006520.

PR 09-MAR-2001; 2001US-0274359P.

PR 03-APR-2001; 2001US-0280982P.

PR 04-APR-2001; 2001US-0282129P.

PR 04-APR-2001; 2001US-0282199P.

PR 09-MAY-2001; 2001US-0290569P.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi UC,
PI Guirney AL, Smith V, Stephan J, Matanabe CK, Wood WI, Zhang Z,
PI Fong S;
XX
XX WPI; 2002-362426/39.
DR N-PSDB; ABX70009.
XX
XX New PRO polypeptides and polynucleotides encoding the polypeptides,
PT useful in gene therapy, chromosome identification, tissue typing, or for
PT genetic analysis of individuals with genetic disorders.
XX
XX
XX Claim 11; Fig 98; 218pp; English.
XX
XX This invention relates to the cDNA and protein sequences of novel
CC secreted and transmembrane polypeptides PRO polypeptides. The invention
CC also comprises a method for producing the proteins of the invention by
CC recombinant means and antibodies specific for the protein of the
CC invention. The antibody may be used for detecting the PRO proteins of the
CC invention and may be used to modify their activity. Polynucleotides may
CC be used as hybridisation probes for a cDNA library to isolate the full-
CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation
CC probes for mapping the gene which encodes that PRO and for genetic
CC analysis of individuals with genetic disorders, in assays to identify
CC other proteins or molecules involved in binding reaction, to generate
CC transgenic animals or knock-out animals which in turn are useful in the
CC development and screening of therapeutically useful reagents, for
CC chromosome identification, and tissue typing. The PRO polypeptides are
CC useful in gene therapy, and as molecular weight markers for protein
CC electrophoresis purposes. The sequences may also be used to detect
CC overexpression on PRO polypeptides in cancerous tumours and for screening
CC for differentially expressed genes using microarray technology. The
CC present sequence represents a human PRO protein of the invention
XX
XX Sequence 781 AA;
SQ
Query Match 100.0%; Score 247; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 5; 7e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 STVTVTLSVDNDNPKFPGSLYQFSVETAGFGLTGVGRAPDPDG 48
Db 242 STVTVTLSVDNDNPKFPGSLYQFSVETAGFGLTGVGRAPDPDG 269
RESULT 9
AD116604
ID AD116604 standard; protein; 781 AA.
XX
XX
XX AD116604;
AC
XX
XX 15-APR-2004 (first entry)
DT
XX
XX Human NOVX protein to treat human pathological conditions SegID140.
DE
XX
XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
KW inflammation; autoimmune disorder; allergy; blood disorder;
KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
KW Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
KW cytostatic; cardant; antiinflammatory; immunosuppressive; antiallergic;
KW haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;
KW antiashtmatic; nephrotoxic; antiarthritic; hepatotoxic;
KW neuroprotective; nootropic; antibacterial; vinorel; antiparastic;
KW relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
KW

KW chromosome mapping; tissue typing; pharmacogenomic; SNP;
KW single nucleotide polymorphism.
XX
XX Homo sapiens.
OS
XX
XX WO200268649-A2.
EN
XX
XX 06-SEP-2002.
PD
XX
XX 31-JAN-2002; 2002WO-US002785.
PF
XX
XX 31-JAN-2001; 2001US-0265395P.
PR 31-JAN-2001; 2001US-0265412P.
PR 31-JAN-2001; 2001US-0265514P.
PR 31-JAN-2001; 2001US-0265517P.
PR 02-FEB-2001; 2001US-0266406P.
PR 05-FEB-2001; 2001US-0266767P.
PR 07-FEB-2001; 2001US-0266975P.
PR 07-FEB-2001; 2001US-0267057P.
PR 09-FEB-2001; 2001US-0267459P.
PR 09-FEB-2001; 2001US-0267823P.
PR 15-FEB-2001; 2001US-0268974P.
PR 26-FEB-2001; 2001US-0271664P.
PR 27-FEB-2001; 2001US-0271839P.
PR 27-FEB-2001; 2001US-0271855P.
PR 02-MAR-2001; 2001US-0272788P.
PR 02-MAR-2001; 2001US-0273046P.
PR 14-MAR-2001; 2001US-0275925P.
PR 14-MAR-2001; 2001US-0275947P.
PR 14-MAR-2001; 2001US-0275950P.
PR 14-MAR-2001; 2001US-0275989P.
PR 15-MAR-2001; 2001US-0276448P.
PR 15-MAR-2001; 2001US-0276450P.
PR 16-MAR-2001; 2001US-0276397P.
PR 16-MAR-2001; 2001US-0276768P.
PR 20-MAR-2001; 2001US-0276552P.
PR 26-MAR-2001; 2001US-0278775P.
PR 26-MAR-2001; 2001US-0278778P.
PR 29-MAR-2001; 2001US-0278882P.
PR 29-MAR-2001; 2001US-0278884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282992P.
PR 11-APR-2001; 2001US-0283083P.
PR 23-APR-2001; 2001US-0285133P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 29-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296564P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312889P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313390P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0333701P.
XX
XX (CUBA-) CUBAGEN CORP.
XX
XX Tchernev VT, Spytek KA, Zernusen BD, Paturajan M, Shinkets RA;
PI Li L, Gangoli EA, Patisaru M, Anderson DW, Rastelli L, Miller CE;
PI Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CE;
PI Furek K, Grosse WM, Alsebrook JP, Lepley DM, Rieger DX, Burgess CB;
XX

DR WPI: 2002-706998/76.
DR N-PSDB; ADI16603.
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.

XX Claim 1; SEQ ID NO 140; 1498bp; English.

XX This invention relates to a novel nucleic acid, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOVX polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC cyostatic, cardiac, antiinflammatory, immunosuppressive, antiallergic,
CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
CC antiasthmatic, nephrotropic, antiarthritic, hepatotropic,
CC neuroprotective, nootropic, antibacterial, vincicid, antiparasitic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a human NOVX protein of the
CC invention.

XX Sequence 781 AA;

Query Match 100.0%; Score 247; DB 5; Length 781;
Best local Similarity 100.0%; Pred. No. 5.7e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STTAVTTLSDVNDNPKPFQSLYQSVETAGPGLTVGRRLAQPDDIG 48
Db 242 STTAVTTLSDVNDNPKPFQSLYQSVETAGPGLTVGRRLAQPDDIG 289

RESULT 10

ADI16606
ID ADI16606 standard; protein; 781 AA.

AC ADI16606;

DT 15-APR-2004 (first entry)

DE Human NOVX protein to treat human pathological conditions SeqID142.

XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
KW inflammation; autoimmune disorder; allergy; blood disorder;
KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
KW Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
KW cyostatic; cardiac; antiinflammatory; immunosuppressive; antiallergic;
KW haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;
KW antiasthmatic; nephrotropic; antiarthritic; hepatotropic;
KW neuroprotective; nootropic; antibacterial; vincicid; antiparasitic;
KW relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
KW chromosome mapping; tissue typing; pharmacogenomic.

XX Homo sapiens.

XX WO200268649-A2.

XX 06-SEP-2002.
XX 31-JAN-2002; 2002WO-US002785.
XX 31-JAN-2001; 2001US-0265395P.
XX 31-JAN-2001; 2001US-0265412P.
XX 31-JAN-2001; 2001US-0265514P.
XX 31-JAN-2001; 2001US-0265517P.
XX 02-FEB-2001; 2001US-0265406P.
XX 05-FEB-2001; 2001US-0266767P.
XX 07-FEB-2001; 2001US-0266975P.
XX 07-FEB-2001; 2001US-0267057P.
XX 08-FEB-2001; 2001US-0267459P.
XX 09-FEB-2001; 2001US-0267823P.
XX 15-FEB-2001; 2001US-0268974P.
XX 26-FEB-2001; 2001US-0271664P.
XX 27-FEB-2001; 2001US-0271839P.
XX 27-FEB-2001; 2001US-0271855P.
XX 02-MAR-2001; 2001US-0272788P.
XX 02-MAR-2001; 2001US-0273046P.
XX 14-MAR-2001; 2001US-0275925P.
XX 14-MAR-2001; 2001US-0275947P.
XX 14-MAR-2001; 2001US-0275950P.
XX 14-MAR-2001; 2001US-0275989P.
XX 15-MAR-2001; 2001US-0276448P.
XX 15-MAR-2001; 2001US-0276450P.
XX 16-MAR-2001; 2001US-0276397P.
XX 16-MAR-2001; 2001US-0276768P.
XX 20-MAR-2001; 2001US-0278652P.
XX 26-MAR-2001; 2001US-0278775P.
XX 26-MAR-2001; 2001US-0278778P.
XX 29-MAR-2001; 2001US-0279882P.
XX 29-MAR-2001; 2001US-0279884P.
XX 30-MAR-2001; 2001US-0280147P.
XX 11-APR-2001; 2001US-0282892P.
XX 11-APR-2001; 2001US-0283083P.
XX 20-APR-2001; 2001US-0285133P.
XX 23-APR-2001; 2001US-0285749P.
XX 03-MAY-2001; 2001US-0288327P.
XX 03-MAY-2001; 2001US-0288504P.
XX 28-MAY-2001; 2001US-0294473P.
XX 30-MAY-2001; 2001US-0294473P.
XX 08-JUN-2001; 2001US-0296964P.
XX 18-JUN-2001; 2001US-0298599P.
XX 19-JUN-2001; 2001US-0299324P.
XX 13-AUG-2001; 2001US-0312020P.
XX 16-AUG-2001; 2001US-0312889P.
XX 16-AUG-2001; 2001US-0312889P.
XX 21-AUG-2001; 2001US-0313390P.
XX 28-AUG-2001; 2001US-0315470P.
XX 31-AUG-2001; 2001US-0316447P.
XX 07-SEP-2001; 2001US-0318115P.
XX 07-SEP-2001; 2001US-0318115P.
XX 12-SEP-2001; 2001US-0318740P.
XX 19-SEP-2001; 2001US-0323379P.
XX 18-OCT-2001; 2001US-0330245P.
XX 18-OCT-2001; 2001US-0330308P.
XX 14-NOV-2001; 2001US-0332701P.
XX (CURA-) CURAGEN CORP.
XX Therneer VT, Spyrek KA, Zernusen BD, Patturajan M, Shinkels RA,
XX Li L, Gangoli EA, Padgug M, Anderson DM, Rastelli L, Miller CB,
XX Gerlich VL, Tupper RJ, Gusev VV, Colman SD, Wolenc AR, Pena CB,
XX Futrak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE,
XX WPI: 2002-706998/76.
XX N-PSDB; ADI16605.
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or

PT pharmacogenomics.
XX
PS Claim 1; SEQ ID NO 142; 1498bp; English.
XX
CC This invention relates to a novel nucleic acid, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOVX polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig) A nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC cytostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
CC haemostatic, anti-HIV, antidiabetic, antihypertensive, anorectic,
CC antiaesthetic, nephroprotective, antibacterial, hepatotropic,
CC neuroprotective, neurotropic, antiparasitic, vitruide, antiparasitic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a human NOVX protein of the
CC invention.
CC
XX
SQ Sequence 781 AA;
Query Match 100.0%; Score 247; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 5.7e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 STTVTVTLSDVNDNPKPKFQSLVQFSVETAGPGLVGRRAADPDIG 48
ID ABR40114 standard; protein; 781 AA.
XX
AC ABR40114;
XX
DT 04-JUL-2003 (first entry)
XX
DE Human cell adhesion and extracellular matrix protein, CADECM-11.
XX
KW Human: anti-HIV; antiallergic; cerebroprotective; antiparkinsonian;
KW anticonvulsant; neurotropic; neuroprotective; immunosuppressive;
KW dermatological; anti-inflammatory; cytostatic; antiarteriosclerotic;
KW gene therapy; cell adhesion; extracellular matrix; CADECM;
KW immune system disorder; AIDS; allergy; neurological disorder; stroke;
KW Parkinson's disease; epilepsy; developmental disorder; Down's syndrome;
KW cerebral palsy; connective tissue disorder; systemic lupus erythematosus;
KW genetic disorder; Alport's syndrome; cell proliferative disorder; cancer;
KW atherosclerosis.
XX
OS Homo sapiens.
XX
PN WO2003027230-A2.
XX
PD 03-APR-2003.
XX
PF 02-AUG-2002; 2002MO-US024649.
XX
PR 03-AUG-2001; 2001US-030964P.
XX
PR 03-AUG-2001; 2001US-031011P.
XX
PR 17-AUG-2001; 2001US-031091P.

PR 31-AUG-2001; 2001US-0316771P.
PR 07-SEP-2001; 2001US-031786P.
PR 21-SEP-2001; 2001US-0324781P.
PR 05-OCT-2001; 2001US-0327606P.
PR 12-OCT-2001; 2001US-0328960P.
PR 09-NOV-2001; 2001US-0344471P.
PR 17-MAY-2002; 2002US-0381291P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Burford N, Warren BA, Duggan BM, Mason FM, Richardson TM, Yue H;
PI Forsyth J, Elliott VS, Griffin DA, Gozard AE, Azimzai Y;
PI Kallack DA, Xu Y, Honchell CD, Baughn MR, Gietzen KU, Lee S;
PI Walla NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Ramkumar J;
DR MPI; 2003-354645/33.
DR N-PSDB; ACC00402.
XX
XX
PT New human cell adhesion and extracellular matrix proteins (CADECM),
PT useful for diagnosing, treating or preventing disorders associated with
PT aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies
PT or stroke.
XX
PS Claim 1; Page 192-194; 234pp; English.
XX
CC The present invention relates to novel human cell adhesion and
CC extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding
CC sequences (ACC00392-ACC00413 and ABR40104-ABR40125). The coding sequences
CC and proteins are useful in diagnosing, treating and preventing disorders
CC associated with aberrant expression of CADECM, such as immune system
CC disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,
CC Parkinson's disease or epilepsy), developmental disorders (e.g. Down's
CC syndrome or cerebral palsy), connective tissue disorders (e.g. systemic
CC lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell
CC proliferative disorders (e.g. cancer or atherosclerosis)
CC
XX
SQ Sequence 781 AA;
Query Match 100.0%; Score 247; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 5.7e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 STTVTVTLSDVNDNPKPKFQSLVQFSVETAGPGLVGRRAADPDIG 48
ID ABR40114 standard; protein; 781 AA.
XX
AC ABR40114;
XX
DT 04-JUL-2003 (first entry)
XX
DE Human PRO polypeptide #49.
XX
KW Human: PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
KW microvascular endothelial cell; endothelial cell tube formation;
KW sports-related joint problem; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.
XX
OS Homo sapiens.
XX
PN US2003068779-A1.
XX
PD 10-APR-2003.
XX
PF 16-SEP-2002; 2002US-00245107.
XX
PR 09-MAY-2001; 2001US-0290589P.

PR 29-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX (GENTH) GENENTECH INC.
 PA Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S;
 DR WPI: 2003-625484/59.
 DR N-PSDB; ADA01365.
 XX Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
 PT stimulating proliferation of human microvascular endothelial cells, and
 PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
 PT cells.
 XX Claim 11; Fig 98; 307pp; English.
 PS The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
 CC colon, breast, prostate, rectal, cervical and liver tumours). The
 CC polynucleotides are useful in molecular biology, including uses as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
 CC be used in preparing PRO polypeptides by recombinant techniques and in
 CC generating either transgenic animals or knock-out animals which are
 CC useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides or antibodies are used in preparing a
 CC medicament for treating a condition responsive to the polypeptides or
 CC antibodies, such as tumours, for stimulating and inhibiting proliferation
 CC of human microvascular endothelial cells, for inducing endothelial cell
 CC tube formation and for treating sports-related joint problems, articular
 CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
 CC represents a human PRO polypeptide of the invention.
 CC
 SO Sequence 781 AA;
 Query Match 100.0%; Score 247; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 5,7e-26;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 STTAVTTLSDVNDNPKFPOSILYQFSVETAGPGLVGRRAQDPDLG 48
 DB 242 STTAVTTLSDVNDNPKFPOSILYQFSVETAGPGLVGRRAQDPDLG 289
 RESULT 13
 ID ADA43795 standard; protein; 781 AA.
 AC ADA43795;
 XX 20-NOV-2003 (first entry)
 DT Human secreted/transmembrane polypeptide PRO34009.
 DE Human; PRO; secreted protein; transmembrane protein;
 XX microvascular endothelial cell formation; chondrocyte cell differentiation;
 KM microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KM breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KM liver tumour; cyclostatic; vaccine.
 XX Homo sapiens.
 OS US2003064474-A1.
 XX 03-APR-2003.

XX 16-SEP-2002; 2002US-00245859.
 PF 29-AUG-2001; 2001WO-US027099.
 XX 18-JUL-2002; 2002US-00197942.
 PR (GENTH) GENENTECH INC.
 PA Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S;
 DR WPI: 2003-605867/57.
 DR N-PSDB; ADA43794.
 XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
 PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
 PT generating antisense RNA and DNA, and in gene therapy.
 XX Claim 11; Fig 98; 308pp; English.
 PS The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acids deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide. Also included are vectors,
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
 CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
 CC and PRO21383 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumour in a mammal, including tumours of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence represents a PRO protein.
 CC
 SO Sequence 781 AA;
 Query Match 100.0%; Score 247; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 5,7e-26;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 STTAVTTLSDVNDNPKFPOSILYQFSVETAGPGLVGRRAQDPDLG 48
 DB 242 STTAVTTLSDVNDNPKFPOSILYQFSVETAGPGLVGRRAQDPDLG 289
 RESULT 14
 ID ADA43563 standard; protein; 781 AA.
 AC ADA43563;
 XX 20-NOV-2003 (first entry)
 DT Human secreted/transmembrane polypeptide PRO34009.
 DE Human; PRO; secreted protein; transmembrane protein;
 XX microvascular endothelial cell formation; chondrocyte cell differentiation;
 KM microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KM breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KM liver tumour; cyclostatic; vaccine.
 XX Homo sapiens.
 OS US2003064474-A1.
 XX 03-APR-2003.

DE Human secreted/transmembrane polypeptide PRO34009.
 XX Human; PRO; secreted protein; transmembrane protein;
 KW endothelial cell tube formation; chondrocyte cell differentiation;
 KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KW liver tumour; cytoskeletal; vaccine.
 XX Homo sapiens.
 OS
 XX US2003073196-A1.
 PN
 XX 17-APR-2003.
 PD
 XX 18-SEP-2002; 2002US-00246210.
 PF
 XX 04-APR-2001; 2001US-0282199P.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX (GENTH) GENENTECH INC.
 PA Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S;
 XX WPI, 2003-743614/70.
 DR N-PsDB; ADA43562.
 XX
 PT New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
 PT PRO21383 useful for stimulating the proliferation or differentiation of
 PT chondrocyte cells and detecting the presence of a tumor in a mammal.
 XX
 PS Claim 11; Fig 98; 307pp; English.
 XX
 CC The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acids deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide. Also included are vectors,
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO189, PRO499, PRO308, PRO600,
 CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
 CC and PRO21383 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6071, PRO487 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumour in a mammal, including tumours of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO499, PRO6008, PRO6000, PRO10275, PRO21207, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence represents a PRO protein.
 XX
 SO Sequence 781 AA.

Query Match 100.0%; Score 247; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 5,7e-26;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTVVTLSDVNDNPKPKPSQSLYQFSVYETAGPGLTVRLRAQDPDLG 48
 ID |||||
 DB 242 STTVVTLSDVNDNPKPKPSQSLYQFSVYETAGPGLTVRLRAQDPDLG 289
 ID |||||
 RESULT 15
 ID ADA01238
 ID ADA01238 standard; protein; 781 AA.
 AC ADA01238;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human PRO polypeptide #49.
 XX
 KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
 KW cancer; lung; colon; breast; prostate; rectum; kidney; liver;
 KW microvascular endothelial cell; endothelial cell tube formation.
 XX
 OS Homo sapiens.
 XX
 PN US2003068782-A1.
 PD 10-APR-2003.
 XX
 PF 16-SEP-2002; 2002US-00245851.
 XX
 PR 27-APR-1999; 99US-0131271P.
 PR 29-OCT-1999; 99US-0162506P.
 PR 02-DEC-1999; 99WO-US028551.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX
 PA (GENTH) GENENTECH INC.
 PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S;
 XX WPI, 2003-625487/59.
 DR N-PsDB; ADA01237.
 XX
 PT Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
 PT preparation of a medicament for treating a condition responsive to PRO
 PT polypeptide, and as therapeutic agents e.g. vaccines.
 XX
 PS Claim 11; Fig 98; 308pp; English.
 XX
 CC The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
 CC prostate, rectal, kidney and liver tumours). The polynucleotides are
 CC useful in molecular biology, including uses as hybridisation probes, in
 CC chromosome and gene mapping, in generating antisense RNA and DNA and in
 CC gene therapy. The polynucleotides may also be used in preparing PRO
 CC polypeptides by recombinant techniques and in generating either
 CC transgenic animals or knock-out animals which are useful in the
 CC development and screening of therapeutically useful reagents. The PRO
 CC polypeptides or antibodies are used in preparing a medicament for
 CC treating a condition responsive to the polypeptides or antibodies, such
 CC as tumours, for stimulating and inhibiting proliferation of human
 CC microvascular endothelial cells and for inducing endothelial cell tube
 CC formation. This sequence represents a human PRO polypeptide of the
 CC invention.
 XX
 SO Sequence 781 AA;

Wed Dec 8 11:46:36 2004

us-09-788-051-9.rag

Page 11

Query Match 100.0%; Score 247; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 5.7e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 STVTVTLSVDYNDNPPKFPQSLYQFSVETAGPGLVGRRLRAQDPDLG 48
242 STVTVTLSVDYNDNPPKFPQSLYQFSVETAGPGLVGRRLRAQDPDLG 289
Db
Search completed: December 8, 2004, 10:13:05
Job time : 19.863 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 10:13:18 ; Search time 49.0484 Seconds
(without alignments)
349.544 Million cell updates/sec

Title: US-09-788-051-9

Perfect score: 247
Sequence: 1 STVTYTLSDVNDNPKFPQ.....ETAGPGLVGRLEAQPDLG 48

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1585576 segs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	247	100.0	48	US-09-788-051-9	Sequence 9, Appl
2	247	100.0	493	US-10-072-012-482	Sequence 482, Appl
3	247	100.0	607	US-10-258-851-74	Sequence 74, Appl
4	247	100.0	620	US-08-788-051-7	Sequence 7, Appl
5	247	100.0	636	US-09-788-051-4	Sequence 4, Appl
6	247	100.0	781	US-09-860-868-2	Sequence 2, Appl
7	247	100.0	781	US-10-245-752-98	Sequence 98, Appl
8	247	100.0	781	US-10-245-859-98	Sequence 98, Appl
9	247	100.0	781	US-10-245-103-98	Sequence 98, Appl
10	247	100.0	781	US-10-245-107-98	Sequence 98, Appl
11	247	100.0	781	US-10-245-143-98	Sequence 98, Appl
12	247	100.0	781	US-10-245-771-98	Sequence 98, Appl
13	247	100.0	781	US-10-245-851-98	Sequence 98, Appl

14	247	100.0	781	14	US-10-245-883-98	Sequence 98, Appl
15	247	100.0	781	14	US-10-237-535-98	Sequence 98, Appl
16	247	100.0	781	14	US-10-238-183-98	Sequence 98, Appl
17	247	100.0	781	14	US-10-238-283-98	Sequence 98, Appl
18	247	100.0	781	14	US-10-238-370-98	Sequence 98, Appl
19	247	100.0	781	14	US-10-245-055-98	Sequence 98, Appl
20	247	100.0	781	14	US-10-245-147-98	Sequence 98, Appl
21	247	100.0	781	14	US-10-245-730-98	Sequence 98, Appl
22	247	100.0	781	14	US-10-245-739-98	Sequence 98, Appl
23	247	100.0	781	14	US-10-246-210-98	Sequence 98, Appl
24	247	100.0	781	14	US-10-239-156-98	Sequence 98, Appl
25	247	100.0	781	14	US-10-245-024-98	Sequence 98, Appl
26	247	100.0	781	14	US-10-245-409-98	Sequence 98, Appl
27	247	100.0	781	14	US-10-245-621-98	Sequence 98, Appl
28	247	100.0	781	14	US-10-245-880-98	Sequence 98, Appl
29	247	100.0	781	14	US-10-245-033-98	Sequence 98, Appl
30	247	100.0	781	14	US-10-245-095-98	Sequence 98, Appl
31	247	100.0	781	14	US-10-245-185-98	Sequence 98, Appl
32	247	100.0	781	14	US-10-245-427-98	Sequence 98, Appl
33	247	100.0	781	14	US-10-245-473-98	Sequence 98, Appl
34	247	100.0	781	14	US-10-245-770-98	Sequence 98, Appl
35	247	100.0	781	14	US-10-245-877-98	Sequence 98, Appl
36	247	100.0	781	14	US-10-246-976-98	Sequence 98, Appl
37	247	100.0	781	14	US-10-245-320-98	Sequence 98, Appl
38	247	100.0	781	14	US-10-162-435-13	Sequence 13, Appl
39	247	100.0	781	14	US-10-242-743-98	Sequence 98, Appl
40	247	100.0	781	14	US-10-242-845-98	Sequence 98, Appl
41	247	100.0	781	14	US-10-237-636-98	Sequence 98, Appl
42	247	100.0	781	14	US-10-238-325-98	Sequence 98, Appl
43	247	100.0	781	14	US-10-238-346-98	Sequence 98, Appl
44	247	100.0	781	14	US-10-238-411-98	Sequence 98, Appl
45	247	100.0	781	14	US-10-245-124-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-09-788-051-9
Sequence 9, Application US/09788051
Publication No. US2003014491A1
GENERAL INFORMATION:
APPLICANT: Codbole, Shubhada D
APPLICANT: Kuo, Chaoyun
APPLICANT: Ateburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Dmanac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES A
FILE REFERENCE: HYS-39
CURRENT APPLICATION NUMBER: US/09/788,051
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 48
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-9

Query Match 100.0%; Score 247; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 6.8e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 STVTYTLSDVNDNPKFPQSLYQFVETAGPGLVGRLEAQPDLG 48
|||||

Db 1 STTWTVLSDVNDNPKPKFQSLYQFSVETAGPGLVGRRAQDPDLG 48

```
RESULT 2
US-10-072-012-482
; Sequence 482, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zethusen, Bryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Shimkova, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangoli, Esna
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grose, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US/10/072,012
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 482
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-482

Query Match 100.0%; Score 247; DB 15; Length 493;
Best Local Similarity 100.0%; Pred. No. 1.2e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Db 1 STTWTVLSDVNDNPKPKFQSLYQFSVETAGPGLVGRRAQDPDLG 48
242 STTWTVLSDVNDNPKPKFQSLYQFSVETAGPGLVGRRAQDPDLG 289

RESULT 3
US-10-258-951-74

```
; Sequence 74, Application US/10258951
; Publication No. US20040033504A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kadnick, Karen
; APPLICANT: Lai, Ying-Ta
; APPLICANT: Xie, Qing
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GPE50025
; CURRENT APPLICATION NUMBER: US/10/258,951
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/13360
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/199,963
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/203,336
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 60/207,087
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/207,546
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-951-74
```

Query Match 100.0%; Score 247; DB 15; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.5e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 STTWTVLSDVNDNPKPKFQSLYQFSVETAGPGLVGRRAQDPDLG 48
242 STTWTVLSDVNDNPKPKFQSLYQFSVETAGPGLVGRRAQDPDLG 289

```
RESULT 4
US-09-788-051-7
; Sequence 7, Application US/09788051
; Publication No. US20030144491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dymnac, Radjoie T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES
; FILE REFERENCE: HYS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent version 3.0
; SEQ ID NO 7
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-7
```


Query Match 100.0%; Score 247; DB 10; Length 620;
 Best Local Similarity 100.0%; Pred. No. 1.6e-24;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STTVTLSDVNDNPKFPQSLYQFSVETAGPGLVGRRLRAQDDPLG 48
 |||||
 DB 226 STTVTLSDVNDNPKFPQSLYQFSVETAGPGLVGRRLRAQDDPLG 273

RESULT 5
 US-09-788-051-4
 ; Sequence 4, Application US/09788051
 ; Publication No. US2003014491A1
 ; GENERAL INFORMATION:

APPLICANT: Godbole, Shubhada D
 APPLICANT: Kuo, Chiaoyun
 APPLICANT: Atterburn, Matthew C
 APPLICANT: Yeung, George
 APPLICANT: Palencia, Servando
 APPLICANT: Tang, Y. Tom
 APPLICANT: Liu, Chenghua
 APPLICANT: Dimnac, Radoje T
 TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN
 ; TITLE OF INVENTION: POLYNUCLEOTIDES
 ; FILE REFERENCE: HVS-39
 ; CURRENT APPLICATION NUMBER: US/09/788,051
 ; CURRENT FILING DATE: 2001-02-16
 ; PRIOR APPLICATION NUMBER: US 09/560,875
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: US 09/496,914
 ; PRIOR FILING DATE: 2000-02-03
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 636
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-788-051-4

Query Match 100.0%; Score 247; DB 10; Length 636;
 Best Local Similarity 100.0%; Pred. No. 1.6e-24;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STTVTLSDVNDNPKFPQSLYQFSVETAGPGLVGRRLRAQDDPLG 48
 |||||
 DB 242 STTVTLSDVNDNPKFPQSLYQFSVETAGPGLVGRRLRAQDDPLG 289

RESULT 6
 US-09-860-868-2
 ; Sequence 2, Application US/09860868
 ; Patent No. US20020076757A1
 ; GENERAL INFORMATION:

APPLICANT: Curtis, Rory A.J.
 TITLE OF INVENTION: 57805, A NOVEL HUMAN CADHERIN FAMILY
 ; TITLE OF INVENTION: MEMBER AND USES THEREOF
 ; FILE REFERENCE: 10448-050001
 ; CURRENT APPLICATION NUMBER: US/09/860,868
 ; CURRENT FILING DATE: 2001-05-18
 ; PRIOR APPLICATION NUMBER: 60/205,674
 ; PRIOR FILING DATE: 2000-05-19
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 781
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; US-09-860-868-2

Query Match 100.0%; Score 247; DB 9; Length 781;
 Best Local Similarity 100.0%; Pred. No. 2.1e-24;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STTVTLSDVNDNPKFPQSLYQFSVETAGPGLVGRRLRAQDDPLG 48
 |||||
 DB 242 STTVTLSDVNDNPKFPQSLYQFSVETAGPGLVGRRLRAQDDPLG 289

RESULT 7

US-10-245-752-98
 ; Sequence 98, Application US/10245752
 ; Publication No. US20030064473A1
 ; GENERAL INFORMATION:

APPLICANT: Baker, Kevin
 APPLICANT: Baton, Dan
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurley, Austin
 APPLICANT: Smith, Victoria
 APPLICANT: Stephan, Jean-Philippe
 APPLICANT: Watanabe, Colin
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 APPLICANT: Fong, Sherman
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3630R1C66
 ; CURRENT APPLICATION NUMBER: US/10/245,752
 ; CURRENT FILING DATE: 2002-09-16
 ; PRIOR APPLICATION NUMBER: 10/197942
 ; PRIOR FILING DATE: 2002-07-18
 ; PRIOR APPLICATION NUMBER: 60/059114
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/063046
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/065027
 ; PRIOR FILING DATE: 1997-11-10
 ; PRIOR APPLICATION NUMBER: 60/079689
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/086478
 ; PRIOR FILING DATE: 1998-05-22
 ; PRIOR APPLICATION NUMBER: 60/087607
 ; PRIOR FILING DATE: 1998-06-02
 ; PRIOR APPLICATION NUMBER: 60/089801
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/090557
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090689
 ; PRIOR FILING DATE: 1998-06-25
 ; Remaining Prior Application data removed - See file wrapper or PAM.
 ; NUMBER OF SEQ ID NOS: 116
 ; SEQ ID NO 98
 ; LENGTH: 781
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-245-752-98

Query Match 100.0%; Score 247; DB 14; Length 781;
 Best Local Similarity 100.0%; Pred. No. 2.1e-24;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STTVTLSDVNDNPKFPQSLYQFSVETAGPGLVGRRLRAQDDPLG 48
 |||||
 DB 242 STTVTLSDVNDNPKFPQSLYQFSVETAGPGLVGRRLRAQDDPLG 289

RESULT 8

US-10-245-859-98
 ; Sequence 98, Application US/10245859
 ; Publication No. US20030064474A1
 ; GENERAL INFORMATION:

APPLICANT: Baker, Kevin
 APPLICANT: Baton, Dan
 APPLICANT: Filvaroff, Ellen

```

/ APPLICANT: Goddard,Audrey
/ APPLICANT: Grimaldi,J. Christopher
/ APPLICANT: Gurney,Austin
/ APPLICANT: Smith,Victoria
/ APPLICANT: Stephan,Jean-Philippe
/ APPLICANT: Matembe,Colin
/ APPLICANT: Wood,William
/ APPLICANT: Zhang,Zemin
/ APPLICANT: Fong,Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C78
/ CURRENT APPLICATION NUMBER: US/10/245, 859
/ PRIOR FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
/ US-10-245-859-98

Query Match      100.0%; Score 247; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1  STVTVTLSDVNDNPKPKFQSLYQFSVETAGPGLVGRRAQPDPLG 48
Db      242 STVTVTLSDVNDNPKPKFQSLYQFSVETAGPGLVGRRAQPDPLG 289

RESULT 9
/ US-10-245-103-98
/ Sequence 98, Application US/10245103
/ Publication No. US20030068778A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Baton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Matembe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C12
/ CURRENT APPLICATION NUMBER: US/10/245, 103
/ PRIOR FILING DATE: 2002-09-17
```

```

/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
/ US-10-245-103-98

Query Match      100.0%; Score 247; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1  STVTVTLSDVNDNPKPKFQSLYQFSVETAGPGLVGRRAQPDPLG 48
Db      242 STVTVTLSDVNDNPKPKFQSLYQFSVETAGPGLVGRRAQPDPLG 289

RESULT 10
/ US-10-245-107-98
/ Sequence 98, Application US/10245107
/ Publication No. US20030068779A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Baton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Matembe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C71
/ CURRENT APPLICATION NUMBER: US/10/245, 107
/ PRIOR FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
```

PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-107-98

Query Match 100.0%; Score 247; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2,1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTVTVTLSDVNDNPPKPFQSLYQFSVETAGPGLVGRRAQDDPLG 48
|||||
Db 242 STTVTVTLSDVNDNPPKPFQSLYQFSVETAGPGLVGRRAQDDPLG 289

RESULT 11

US-10-245-143-98
Sequence 98, Application US/10245143
Publication No. US20030068780A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C98
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-143-98

Query Match 100.0%; Score 247; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2,1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTVTVTLSDVNDNPPKPFQSLYQFSVETAGPGLVGRRAQDDPLG 48
|||||
Db 242 STTVTVTLSDVNDNPPKPFQSLYQFSVETAGPGLVGRRAQDDPLG 289

RESULT 12

US-10-245-771-98
Sequence 98, Application US/10245771
Publication No. US20030068781A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C98
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-771-98

Query Match 100.0%; Score 247; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2,1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTVTVTLSDVNDNPPKPFQSLYQFSVETAGPGLVGRRAQDDPLG 48
|||||
Db 242 STTVTVTLSDVNDNPPKPFQSLYQFSVETAGPGLVGRRAQDDPLG 289

RESULT 13

US-10-245-851-98
Sequence 98, Application US/10245851
Publication No. US20030068782A1
GENERAL INFORMATION:

```

/ APPLICANT: Baker, Kevin
/ APPLICANT: Eaton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Phillippe
/ APPLICANT: Watanabe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C93
/ CURRENT APPLICATION NUMBER: US/10/245,851
/ PRIOR FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-851-98

Query Match      100.0%; Score 247; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 STTATVTLSDVNDNPKPKFPOSLSYQFSVETAGAGETLVGRRAADPDLG 48
Db      242 STTATVTLSDVNDNPKPKFPOSLSYQFSVETAGAGETLVGRRAADPDLG 289

RESULT 14
US-10-245-883-98
/ Sequence 98, Application US/10245883
/ Publication No. US20030068783A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Eaton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Phillippe
/ APPLICANT: Watanabe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C93
/ CURRENT APPLICATION NUMBER: US/10/245,851
/ PRIOR FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-883-98

Query Match      100.0%; Score 247; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 STTATVTLSDVNDNPKPKFPOSLSYQFSVETAGAGETLVGRRAADPDLG 48
Db      242 STTATVTLSDVNDNPKPKFPOSLSYQFSVETAGAGETLVGRRAADPDLG 289

RESULT 15
US-10-237-535-98
/ Sequence 98, Application US/10237535
/ Publication No. US20030073188A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Eaton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Phillippe
/ APPLICANT: Watanabe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C93
/ CURRENT APPLICATION NUMBER: US/10/237,535
/ PRIOR FILING DATE: 2002-09-06
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
```

```

/ FILE REFERENCE: P3630R1C70
/ CURRENT APPLICATION NUMBER: US/10/245,883
/ CURRENT FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-883-98

Query Match      100.0%; Score 247; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 STTATVTLSDVNDNPKPKFPOSLSYQFSVETAGAGETLVGRRAADPDLG 48
Db      242 STTATVTLSDVNDNPKPKFPOSLSYQFSVETAGAGETLVGRRAADPDLG 289

RESULT 15
US-10-237-535-98
/ Sequence 98, Application US/10237535
/ Publication No. US20030073188A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Eaton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Phillippe
/ APPLICANT: Watanabe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C93
/ CURRENT APPLICATION NUMBER: US/10/237,535
/ PRIOR FILING DATE: 2002-09-06
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
```

Wed Dec 8 11:46:37 2004

us-09-788-051-9.rapb

Page 7

```

PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091358
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/098803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/106932
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/115554
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119342
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/123957
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123972
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: 60/127372
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/131271
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/133459
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/135725
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135729
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135750
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/138385
PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: 60/140653
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144732
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144790
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145228
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146843
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/148188
PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/148513
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/149327
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149395
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/150114
PRIOR FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: 60/151700
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/151734
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29

PRIOR APPLICATION NUMBER: 60/170262
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/177118
PRIOR FILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: 60/179851
PRIOR FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 60/180921
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: 60/187202
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/198587
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 60/199614
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 60/206330
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206368
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/209832
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 60/218371
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/222695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/229896
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/230621
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/232887
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/235147
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/261878
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/261910
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/261939
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/262150
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/264395
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/266421
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/267623
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/274399
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/280382
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/282129
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/282199
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/290589
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 09/180997
PRIOR FILING DATE: 1998-11-19
PRIOR APPLICATION NUMBER: 09/267213
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 09/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/403297
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 09/423741
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: 09/709238
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 09/802706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 09/872035
```

; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/924419
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/927796
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/923404
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/931836
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 09/941992
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/946374
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 10/001054
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 10/081056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 10/119480
; PRIOR FILING DATE: 2002-04-09

Query Match 100.0%; Score 247; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 STVTVLSDVNDNPKKPOSTVQFSVETAGPCTVGRRAQDDPDG 48
Db 242 STVTVLSDVNDNPKKPOSTVQFSVETAGPCTVGRRAQDDPDG 289

Search completed: December 8, 2004, 11:34:28
Job time : 49.0484 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 : Search time 5.72373 Seconds
(without alignments)
556.152 Million cell updates/sec

Title: US-09-788-051-9

Perfect score: 247
Sequence: 1 STVTVTLSVDNDNPKFPQ.....ETAGPGLVGRLRAPDPLG 48

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTus.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	180	72.9	693	2	US-08-738-349-6
2	180	72.9	693	2	US-09-919-497-55
3	180	72.9	796	2	US-08-738-349-2
4	180	72.9	796	2	US-08-738-349-4
5	178	72.1	796	1	US-08-188-228-58
6	178	72.1	796	1	US-08-332-643-52
7	178	72.1	796	1	US-08-332-638-58
8	178	72.1	796	4	US-09-654-328-2
9	169.5	68.6	615	2	US-08-738-349-12
10	163	66.0	532	1	US-08-188-228-44
11	163	66.0	532	1	US-08-332-638-44
12	163	66.0	793	1	US-08-188-228-54
13	163	66.0	793	1	US-08-332-643-48
14	163	66.0	793	1	US-08-332-638-54
15	163	66.0	799	1	US-08-188-228-42
16	163	66.0	799	1	US-08-332-638-42
17	144	58.3	794	1	US-08-188-228-60
18	144	58.3	794	1	US-08-332-643-54
19	144	58.3	794	1	US-08-332-638-50
20	137	55.5	653	1	US-08-188-228-46
21	137	55.5	653	1	US-08-332-638-46
22	110	44.5	780	1	US-08-188-228-50
23	110	44.5	780	1	US-08-332-643-44
24	110	44.5	780	1	US-08-332-638-50
25	109	44.1	348	4	US-09-270-767-46673
26	104	42.1	616	1	US-08-453-695A-115
27	104	42.1	616	1	US-08-268-161A-115

28	104	42.1	616	2	US-08-453-702A-115	Sequence 115, App
29	104	42.1	616	3	US-09-099-639-115	Sequence 115, App
30	104	42.1	616	5	PCT-US95-08071-115	Sequence 115, App
31	104	42.1	747	3	US-09-035-648-18	Sequence 18, App
32	104	42.1	747	3	US-09-001-951-18	Sequence 18, App
33	104	42.1	747	4	US-08-818-829-18	Sequence 18, App
34	100	40.5	797	1	US-08-453-695A-112	Sequence 112, App
35	100	40.5	797	1	US-08-268-161A-112	Sequence 112, App
36	100	40.5	797	2	US-08-453-702A-112	Sequence 112, App
37	100	40.5	797	3	US-09-099-639-112	Sequence 112, App
38	100	40.5	797	5	PCT-US95-08071-112	Sequence 112, App
39	100	40.5	1184	4	US-10-140-002-394	Sequence 394, App
40	99	40.1	884	2	US-08-474-067-8	Sequence 8, App
41	99	40.1	884	2	US-08-474-068A-8	Sequence 8, App
42	99	40.1	884	2	US-08-472-481-7	Sequence 7, App
43	98	39.7	148	1	US-07-998-003A-36	Sequence 36, App
44	98	39.7	148	1	US-08-453-274B-36	Sequence 36, App
45	98	39.7	148	1	US-08-453-695A-36	Sequence 36, App

ALIGNMENTS

RESULT 1
US-08-738-349-6
Sequence 6, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Kawasaki, Makoto
APPLICANT: Tsujimura, Aetsushi
APPLICANT: Amann, Egon
TITLE OF INVENTION: Bone-Related Cadherin-like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 06/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 693 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-6

APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-58

Query Match 72.1%; Score 178; DB 1; Length 796;
Best Local Similarity 68.8%; Pred. No. 9e-17; Mismatches 8; Indels 0; Gaps 0;
Matches 33; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 STVTVTLSVDNDNPPKFPQSLYQFSVETAGPGLVGRRAADPDIG 48
Db 251 TTKVTITLTDVNDNPPKFPQSLYQMSVSAVPGEEVGRVAKDPDID 298

RESULT 8
US-09-654-328-2
Sequence 2, Application US/09654328
Patent No. 6787136
GENERAL INFORMATION:
APPLICANT: Brenner, Michael B.
APPLICANT: Valencia, Xavier
TITLE OF INVENTION: Methods and Compositions for Treatment
TITLE OF INVENTION: Of Inflammatory Disease Using Cadherin-11 Modulating Agents
FILE REFERENCE: B0801/7187/ERP/MAT
CURRENT APPLICATION NUMBER: US/09/654,328
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/152,456
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: US 60/153,490
PRIOR FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 796
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-654-328-2

Query Match 72.1%; Score 178; DB 4; Length 796;
Best Local Similarity 68.8%; Pred. No. 8e-17; Mismatches 8; Indels 0; Gaps 0;
Matches 33; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 STVTVTLSVDNDNPPKFPQSLYQFSVETAGPGLVGRRAADPDIG 48
Db 251 TTKVTITLTDVNDNPPKFPQSLYQMSVSAVPGEEVGRVAKDPDID 298

RESULT 9
US-08-738-349-12
Sequence 12, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amano, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and

TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-738-349-12

Query Match 68.6%; Score 169.5; DB 2; Length 615;
Best Local Similarity 68.8%; Pred. No. 9.5e-16; Mismatches 6; Indels 1; Gaps 1;
Matches 33; Conservative 8; Mismatches 6; Indels 1; Gaps 1;

Qy 1 STVTVTLSVDNDNPPKFPQSLYQFSVETAGPGLVGRRAADPDIG 48
Db 244 TTKVTITLTDVNDNPPKFPQSVQ-SVSEAVPGEEVGRVAKDPDID 290

RESULT 10
US-08-188-228-44
Sequence 44, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/049,460
; FILING DATE: 19 APR 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 559772sand, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELETYPE: 25-3856
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-188-228-44

Query Match      66.0%; Score 163; DB 1; Length 532;
Best Local Similarity 64.6%; Pred. No. 6,8e-15;
Matches 31; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY      1 STTVTVLSDVNDNPKPKFQSLYQFSVYETAGPGLVGRRAQDPDLG 48
Db      259 TTTLVTVLTDVNDNPKPKFQSLYHFSVPEVDVLTGTAIGRVKANDDIDG 306

RESULT 11
US-08-332-638-44
; Sequence 44, Application US/08332638
; Patent No. 5646250
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,638
; FILING DATE: 01-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; APPLICATION NUMBER: US/08/049,460
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5646250and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELETYPE: 25-3856
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
```

```

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-332-638-44

Query Match      66.0%; Score 163; DB 1; Length 532;
Best Local Similarity 64.6%; Pred. No. 6,8e-15;
Matches 31; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY      1 STTVTVLSDVNDNPKPKFQSLYQFSVYETAGPGLVGRRAQDPDLG 48
Db      259 TTTLVTVLTDVNDNPKPKFQSLYHFSVPEVDVLTGTAIGRVKANDDIDG 306

RESULT 12
US-08-188-228-54
; Sequence 54, Application US/08188228
; Patent No. 5597725
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,228
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/049,460
; FILING DATE: 19 APR 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 559772sand, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELETYPE: 25-3856
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 793 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-188-228-54

Query Match      66.0%; Score 163; DB 1; Length 793;
Best Local Similarity 64.6%; Pred. No. 1.1e-14;
Matches 31; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY      1 STTVTVLSDVNDNPKPKFQSLYQFSVYETAGPGLVGRRAQDPDLG 48
Db      252 TTTLVTVLTDVNDNPKPKFQSLYHFSVPEVDVLTGTAIGRVKANDDIDG 299

RESULT 13
US-08-332-643-48
; Sequence 48, Application US/08332634
; Patent No. 5639634
```

GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-643-48

Query Match 66.0%; Score 163; DB 1; Length 793;
Best Local Similarity 64.6%; Pred. No. 1.1e-14;
Matches 31; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Db 1 STTVTVLSDVNDNPKPKFPOSLYQFSVETAGPGLVGRRAODPDUG 48
252 TTTLFTVLTVDNPNPKFAQSLYHFVSPEVDVLTALGRVANDODIG 299

RESULT 14
US-08-332-638-54
Sequence 54, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638

FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-54

Query Match 66.0%; Score 163; DB 1; Length 793;
Best Local Similarity 64.6%; Pred. No. 1.1e-14;
Matches 31; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Db 1 STTVTVLSDVNDNPKPKFPOSLYQFSVETAGPGLVGRRAODPDUG 48
252 TTTLFTVLTVDNPNPKFAQSLYHFVSPEVDVLTALGRVANDODIG 299

RESULT 15
US-08-188-228-42
Sequence 42, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:

Wed Dec 8 11:46:36 2004

us-09-788-051-9.rai

Page 7

```

; LENGTH: 799 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-188-228-42

```

Query Match	66.0%	Score 163;	DB 1;	Length 799;
Best local similarity	64.6%	Pred No 1	1e-14.	

Best Local Similarity 64.6%; Pred: No. 1, 1e-14;
Matches 31; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

```

Qy      1 STTATVTLSDVNDNPCKFPOSILYQFSVETAGPGLVGRRAQDDPLG 48
      :||:||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      259 TTTTLVTLLTDVNDNPCKFAQSLYHFSVPEDVVLGTAIGRVKANDQDIG 306

```

```
Search completed: December  8, 2004, 10:01:13
Job time : 6.72373 secs
```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 / Search time 2.66883 Seconds
(without alignments)
1189.717 Million cell updates/sec

Title: US-09-788-051-10
Perfect score: 180
Sequence: 1 LILTRRSWMNQFVIEEYAGPEPVLIGKLHSD 33

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	152	84.4	796 2	A38992
2	152	84.4	796 2	cadherin-11 - precu
3	152	84.4	796 2	cadherin-11 - mous
4	152	84.4	796 2	OB-cadherin precu
5	142	78.9	785 2	cadherin-7 - chick
6	140	77.8	790 2	F-cadherin - Affic
7	139	77.2	793 2	cadherin 8 - huma
8	133	73.9	794 2	cadherin 12 - huma
9	127	70.6	790 2	cadherin-14 - huma
10	122	67.8	789 2	K-cadherin - rat
11	122	67.8	790 2	cadherin-6B - chic
12	121	67.2	790 2	cadherin-6 - huma
13	121	67.2	790 2	cadherin 5 precu
14	56	31.1	822 1	cadherin precu
15	52.5	29.2	1466 2	CLIAA protein - ra
16	52.5	29.2	1467 2	latrophilin-1, bra
17	52.5	29.2	1471 2	CLIBA protein - ra
18	52.5	29.2	1472 2	latrophilin-1, bra
19	52.5	29.2	1510 2	CLIBB protein - ra
20	52.5	29.2	1515 2	CLIBB protein - ra
21	51.5	28.6	651 2	probable purple ac
22	51	28.3	209 2	hypothetical prote
23	51	28.3	209 2	hypothetical 24k p
24	50	27.8	179 2	conserved hypothet
25	50	27.8	147 2	hypothetical prote
26	50	27.8	847 2	periplasmic glucan
27	50	27.8	847 2	glucan biosynthesi
28	50	27.8	857 2	membrane glycosyl
29	50	27.8	878 2	lipoxygenase (EC 1

30	50	27.8	887 1	IUCHCL
31	49.5	27.5	445 2	P90562
32	49.5	27.5	598 2	gamma-aminobutyric
33	49.5	27.5	1006 2	hypothetical prote
34	49	27.2	244 2	precortin-2 C20-me
35	49	27.2	305 2	probable phosphogl
36	49	27.2	515 2	protein Cl3A10.3 l
37	49	27.2	513 2	mannosyl-Oligosacc
38	49	27.2	687 1	glycine-tRNA ligas
39	49	27.2	1	myosin I heavy cha
40	49	27.2	1	SS2517
41	49	27.2	1109 2	myosin-IC Isimilar
42	48.5	26.9	1254 1	DNA-directed DNA p
43	48	26.7	394 2	hypothetical prote
44	48	26.7	570 2	glycyl-tRNA synthet
45	48	26.7	637 2	beta-N-acetylhexos
			655 2	protein Y32FeA.3 l

ALIGNMENTS

RESULT 1
A38992
cadherin 11 precursor - human
N/Alternate names: OB-cadherin, osteoblast
C/Species: Homo sapiens (man)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: A38992
R/Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous
A/Reference number: 824305; PMID:91283540; PMID:2059658
A/Accession: A38992
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-796 <SUZ>
A/Cross-references: UNIPROT:P55287; GB:U34056; NID:9506403; PIDN:AAA5622.1; PID:950640
C/Genetics:
A/Gene: GDB:CDH11; OB
A/Cross-references: GDB:512891; OMIM:600023
A/Map position: 16q22.1-16q22.1
C/Superfamily: cadherin; cadherin repeat homology
C/Keywords: calcium binding; cell adhesion; duplication
F/56-159/Domain: cadherin repeat homology <CR1>
F/162-268/Domain: cadherin repeat homology <CR2>
F/271-383/Domain: cadherin repeat homology <CR3>
F/386-488/Domain: cadherin repeat homology <CR4>

Query Match 84.4%; Score 152; DB 2; Length 796;
Best Local Similarity 75.8%; Pred. No. 8, 9e-14;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 LILTRRSWMNQFVIEEYAGPEPVLIGKLHSD 33
DB 48 LQSKRGWVWVNFVIEEYAGPEPVLIGKLHSD 80

RESULT 2
148277
cadherin-11 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 148277
R/Hoffmann, I.; Bailling, R.
Dev. Biol. 169, 337-346, 1995
A/Title: Cloning and expression analysis of a novel mesodermally expressed cadherin.
A/Reference number: 148277; PMID:95269886; PMID:7750649
A/Accession: 148277
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-796 <RES>
A/Cross-references: UNIPROT:P55288; EMBL:X77557; NID:9642796; PIDN:CAA54674.1; PID:9666
C/Genetics:

A:Gene: cad-11
C:Superfamily: cadherin; cadherin repeat homology
F:156-159/Domain: cadherin repeat homology <CDH>

Query Match
Best Local Similarity 75.8%; Score 152; DB 2; Length 796;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLRTSRWVWVNOFFVIEEYAGPEPVLIGKLHSD 33
Db 48 LQSRKRGVWVNOFFVIEEYAGPEPVLIGKLHSD 80

RESULT 3

cadherin-11 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: U19556

R:Kimura, Y.; Matsunami, H.; Inoue, T.; Shimamura, K.; Uchida, N.; Ueno, T.; Miyazaki, T.
Dev. Biol. 169, 347-358, 1995
A>Title: Cadherin-11 expressed in association with mesenchymal morphogenesis in the head
A:Reference number: U19556; MUID:95269887; PMID:7750650
A:Accession: U19556

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-796 <RBS>
A:Cross-references: UNIPROT:P55288; GB:D11963; NID:G974190; PIDN:BA06730.1; PID:G974191
C:Superfamily: cadherin; cadherin repeat homology
F:156-159/Domain: cadherin repeat homology <CDH>

Query Match
Best Local Similarity 75.8%; Score 152; DB 2; Length 796;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLRTSRWVWVNOFFVIEEYAGPEPVLIGKLHSD 33
Db 48 LQSRKRGVWVNOFFVIEEYAGPEPVLIGKLHSD 80

RESULT 4

OB-cadherin precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: A53584

R:Okazaki, M.; Takeshita, S.; Kawai, S.; Kikuno, R.; Tsujimura, A.; Kudo, A.; Mann, E.
J. Biol. Chem. 269, 12092-12098, 1994
A>Title: Molecular cloning and characterization of OB-cadherin, a new member of cadherin
A:Reference number: A53584; MUID:94216322; PMID:8163513
A:Accession: A53584

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-796 <OKA>

A:Cross-references: UNIPROT:P55288; GB:D11253; NID:G994774; PIDN:BA04797.1; PID:G994775
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: transmembrane protein
F:156-159/Domain: cadherin repeat homology <CR1>
F:162-268/Domain: cadherin repeat homology <CR2>
F:1386-488/Domain: cadherin repeat homology <CR4>

Query Match
Best Local Similarity 75.8%; Score 152; DB 2; Length 796;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLRTSRWVWVNOFFVIEEYAGPEPVLIGKLHSD 33
Db 48 LQSRKRGVWVNOFFVIEEYAGPEPVLIGKLHSD 80

RESULT 5

150180
cadherin-7 - chicken

C:Species: Gallus gallus (chicken)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: U150180

R:Nakagawa, S.; Takeichi, M.
Development 121, 1321-1337, 1995
A>Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spec

A:Reference number: U150178; MUID:95309115; PMID:7540531
A:Accession: U150180

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-785 <NAX>

A:Cross-references: UNIPROT:Q90763; GB:D42150; NID:G868000; PIDN:BA07721.1; PID:G868000
C:Superfamily: cadherin; cadherin repeat homology
F:156-262/Domain: cadherin repeat homology <CDH>

Query Match
Best Local Similarity 74.2%; Score 142; DB 2; Length 785;
Matches 23; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RTRRSWVWVNOFFVIEEYAGPEPVLIGKLHSD 33
Db 44 RTRRSWVWVNOFFVIEEYAGPEPVLIGKLHSD 74

RESULT 6
151638
F-cadherin - African clawed frog

C:Species: Xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: U151638; S55391
R:Espeseth, A.; Johnson, E.; Kintner, C.
Mol. Cell. Neurosci. 6, 199-212, 1995

A>Title: Xenopus F-cadherin, a novel member of the cadherin family of cell adhesion mole
A:Reference number: U151638; MUID:96035533; PMID:7456627
A:Accession: U151638
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-790 <ESP>

A:Cross-references: UNIPROT:Q91838; EMBL:X85330; NID:G854634; PIDN:CA059679.1; PID:G854634
C:Superfamily: cadherin; cadherin repeat homology
F:161-267/Domain: cadherin repeat homology <CR2>

Query Match
Best Local Similarity 77.8%; Score 140; DB 2; Length 790;
Matches 23; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 3 RTRRSWVWVNOFFVIEEYAGPEPVLIGKLHSD 33
Db 49 RTRRSWVWVNOFFVIEEYAGPEPVLIGKLHSD 79

RESULT 7
D38992
cadherin 8 - human

C:Species: Homo sapiens (man)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
C:Accession: D38992
R:Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991

A>Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t
A:Reference number: S24305; MUID:91283540; PMID:12059658
A:Accession: D38992
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-793 <STZ>

A:Cross-references: GB:L14060; NID:G506411; PIDN:AAA35628.1; PID:G506412
C:Genetics:
A:Gene: CDB8

A:Cross-references: GDB:5822911
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication
F:163-269/Domain: cadherin repeat homology <CDH>

A:Gene: GDB:CDH6
A:Cross-references: GDB:5822908
C:Superfamily: cadherin, cadherin repeat homology
F:162-268/Domain: cadherin repeat homology <CDH>
Query Match 67.2%; Score 121; DB 2; Length 790;
Best Local Similarity 60.6%; Pred. No. 2.7e-09;
Matches 20; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
QY 1 LRTSRWVWNOFPVIEYAGPEPVILGKLSHD 33
DB 48 LRRSRGSMWNOFPVIEYAGPEPVILGKLSHD 80
RESULT 13
IGHUC5
cadherin 5 precursor - human
N:Alternate names: 7B4 antigen; cadherin, endothelial-specific; VE-cadherin
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1993 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: S49893; S24305; A43418
R:Bravario, F.; Cavada, L.; Corada, M.; Martin-Padura, I.; Golay, J.; Introna, M.; Lamp
submitted to the EMBL Data Library, June 1994
A:Description: Molecular and functional properties of VE-cadherin (7B4/cadherin-5) a nov
A:Reference number: S49893
A:Accession: S49893
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-784

A:Cross-references: UNIPROT:P3151; EMBL:X79981; NID:G599833; PIDN:CA56306.1; PID:G5998
R:Sunuk, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t
A:Reference number: S24305; MUID:91283540; PMID:2059658
A:Accession: S24305
A:Molecule type: mRNA
A:Residues: 5-516, 'I', 518-784 <SU>
A:Cross-references: EMBL:X59796; NID:G639976; PIDN:CA442468.1; PID:G29593
R:Lampugnani, M.G.; Resnati, M.; Raiteri, M.; Pigott, R.; Pisacane, A.; Houen, G.; Ruco,
J. Cell Biol. 118, 1511-1522, 1992
A:Title: A novel endothelial-specific membrane protein is a marker of cell-cell contacts
A:Reference number: A43418; MUID:92394977; PMID:1522121
A:Accession: A43418
A:Molecule type: Protein
A:Residues: 48-60, 'X', 62, 'X', 64, 108-116, 'X', 118-123, 237-238, 'X', 240, 'X', 242-252, 'X', 254-
A:Experimental source: cultured endothelial cells
A:Note: Sequence extracted from NCBI backbone (NCBI:P:113040, NCBI:P:113045, NCBI:P:113047,
C:Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought b
C:Genetics:
A:Gene: GDB:CDH5
A:Cross-references: GDB:134230; OMIM:601120
A:Map position: 16q22.1-16q22.1
C:Superfamily: cadherin, cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane pro
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-47/Domain: propeptide #status predicted <PRO>
F:48-784/Domain: extracellular #status predicted <EXT>
F:50-151/Domain: cadherin repeat homology <CR1>
F:154-258/Domain: cadherin repeat homology <CR2>
F:261-312/Domain: cadherin repeat homology <CR3>
F:375-479/Domain: cadherin repeat homology <CR4>
F:481-587/Domain: cadherin repeat homology <CR5>
F:594-650/Domain: transmembrane #status predicted <TM>
F:621-784/Domain: intracellular #status predicted <INT>
F:726-753/Region: serine-rich
F:61,112,157,362,442,523,533/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 36.7%; Score 66; DB 1; Length 784;
Best Local Similarity 40.0%; Pred. No. 0.24;
Matches 12; Conservative 5; Mismatches 13; Indels 0; Gaps 0;
QY 3 RTRSRWVWNOFPVIEYAGPEPVILGKLSHD 32

DB 44 ROKRDMWNOFPVIEYAGPEPVILGKLSHD 73
RESULT 14
IUMSCP
P-cadherin precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: S03163; S34458
R:Nose, A.; Nagatuchi, A.; Takeichi, M.
EMBO J. 6, 3655-3661, 1987
A:Title: Isolation of placental cadherin cDNA: identification of a novel gene family of
A:Reference number: S03163; MUID:8811554; PMID:3428270
A:Accession: S03163
A:Molecule type: mRNA
A:Residues: 1-822 <NOS>
A:Cross-references: UNIPROT:P10287; EMBL:X06340
R:Faraldo, M.L.M.; Cano, A.
J. Mol. Biol. 231, 935-941, 1993
A:Title: The 5' flanking sequences of the mouse P-cadherin gene. Homologies to 5' sequen
A:Reference number: S34458; MUID:93294853; PMID:8515462
A:Accession: S34458
A:Molecule type: DNA
A:Residues: 1-55 <PAR>
A:Cross-references: EMBL:X68057
C:Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought t
C:Genetics:
A:Intron: 16/3
C:Superfamily: cadherin, cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication; glycoprotein; placenta; transme
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-99/Domain: propeptide #status predicted <PRO>
F:100-822/Product: P-cadherin #status predicted <MNT>
F:100-645/Domain: extracellular #status predicted <EXT>
F:102-207/Domain: cadherin repeat homology <CR1>
F:210-320/Domain: cadherin repeat homology <CR2>
F:323-432/Domain: cadherin repeat homology <CR3>
F:433-540/Domain: cadherin repeat homology <CR4>
F:541-645/Domain: cadherin repeat homology <CR5>
F:646-670/Domain: transmembrane #status predicted <TM>
F:671-822/Domain: intracellular #status predicted <INT>
F:778-793/Region: serine-rich
F:192,558/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 31.1%; Score 56; DB 1; Length 822;
Best Local Similarity 39.4%; Pred. No. 7.1;
Matches 13; Conservative 4; Mismatches 16; Indels 0; Gaps 0;
QY 1 LRTSRWVWNOFPVIEYAGPEPVILGKLSHD 33
DB 94 LRRRGWVMPPIFVPEWKGKPPFRLNQLKSN 126
RESULT 15
TI138
CLIAA protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T17138
R:Kranopcevic, V.G.; Bitner, M.A.; Davis, R.; Kuang, Y.; Salnikow, K.V.; Chepurny, O.C.
Neuron 18, 925-937, 1997
A:Title: Alpha-latrotoxin stimulates exocytosis by the interaction with a neuronal G-pro
A:Reference number: Z18710; MUID:97352465; PMID:9208860
A:Accession: T17138
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-1466 <KRA>
A:Cross-references: UNIPROT:O88917; EMBL:AF081144; NID:G3695114; PID:G3695115; PIDN:AAACG
C:Superfamily: alpha-latrotoxin receptor, calcium-independent
Query Match 29.2%; Score 52.5; DB 2; Length 1466;
Best Local Similarity 36.0%; Pred. No. 44;

Wed Dec 8 11:46:19 2004

us-09-788-051-10.rpr

Page 5

	Matches	9;	Conservative	6;	Mismatches	7;	Indels	3;	Gaps	1;
QY	3	RTSRWYNQFFVYE---	ETAGPEP	24						
		: : : : :	: :							
Db	372	RDNLVYWNVNFVRYSL	ETGPPDP	396						

```
Search completed: December 8, 2004, 10:27:07
Job time : 3.66883 secs
```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd

OM protein - protein search, using sw model

```
Run on:      December 8, 2004, 09:16:13 ; Search time 13.2273 Seconds
              (without alignments)
              1435.471 Million cell updates/sec
```

Title: US-09-788-051-10
Perfect score: 180
Sequence: 1 LRLRRSWVNNQFVIEEYAGPEPYILGKLHSD 33

Scoring table: BLOSUM62

Searched: 1825181 seqs, 57537466 residues

Total number of hits satisfying chosen parameters: 1825181

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*
```

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB	ID	Description	
1	180	100.0	241	2	086f758	086f58 homo sapien
2	180	100.0	493	2	096d07	096d17 homo sapien
3	180	100.0	819	1	CAD0_HUMAN	086d90 homo sapien
4	177	98.3	781	2	06PfX6	06PfX6 mus musculi
5	177	98.3	781	2	AAH57373	Aah57373 mus musculi
6	152	84.4	796	1	CAD8_HUMAN	P55287 homo sapien
7	152	84.4	796	1	CAD8_MOUSE	P55288 mus musculi
8	152	84.4	796	2	096cZ9	096cZ9 homo sapien
9	152	84.4	796	2	08C706	08C706 mus musculi
10	151	83.9	792	1	CAD8_CHICK	093339 gallus galli
11	151	83.9	794	2	093264	093264 xenopus lae
12	143	79.4	801	1	CADK_HUMAN	09b1c6 homo sapien
13	142	78.9	340	2	08B1L74	08b1L4 mus musculi
14	142	78.9	630	2	08AWM2	08awM2 gallus galli
15	142	78.9	551	2	08IY78	08iY78 homo sapien
16	142	78.9	785	1	CAD7_CHICK	090763 gallus galli
17	142	78.9	785	1	CAD7_HUMAN	09ul55 homo sapien
18	142	78.9	785	2	08BW82	08bw82 mus musculi
19	140	77.8	247	2	08C9N7	08c9N7 mus musculi
20	140	77.8	508	2	06PAN4	06pan4 mus musculi
21	140	77.8	508	2	AAH60200	Aah60200 mus muscu
22	140	77.8	716	2	08C449	08c449 mus musculi
23	140	77.8	716	2	AAH57581	Aah57581 mus muscu
24	140	77.8	754	2	08BRK4	08brK4 mus musculi
25	140	77.8	790	2	P91838	C91838 xenopus lae
26	140	77.8	799	1	CAD8_MOUSE	P91791 mus musculi
27	139	77.2	799	1	CAD8_HUMAN	P55286 homo sapien
28	139	77.2	799	1	CAD8_RAT	054800 rattus norv
29	137	77.2	801	2	QZ0M3	Qz0m3 mus musculi
30	137	76.1	798	2	07Z1V7	07z1V7 gallus galli
31	137	76.1	798	2	06QGh3	06qgh3 gallus galli

33	136	75.6	139	2	Q6PD33	Q6PD33	mus musculus
32	136	75.6	139	2	AAS58969	AAS58969	mus muscu
34	136	75.6	813	1	CADM_MOUSE	Q9WPS5	mus musculus
35	136	75.6	813	1	CADM_RAT	Q9WJ15	ratu
36	136	75.6	828	1	CADM_HUMAN	P55299	homo sapien
37	134	74.4	794	1	CADCD_HUMAN	P55289	homo sapien
38	134	74.4	794	2	Q6UD02	Q6UD02	homo sapien
39	132	73.3	716	2	Q8C375	Q8C375	mus musculus
40	127	70.6	337	2	Q8BLB5	Q8BLB5	mus musculus
41	127	70.6	790	1	CADI_HUMAN	Q13644	homo sapien
42	127	70.6	790	2	Q8N5Z2	Q8N5Z2	homo sapien
43	122	67.8	789	1	CAD6_RAT	P55280	ratu
44	122	67.8	790	1	CAD6_CHICK	Q90762	gallu
45	121	67.2	76	2	Q9BLT5	Q9BLT5	mus musculus

ALIGNMENTS

[illegible]

FT VMPYCGVLPs (in isoform 3).
 FT /FTId=VSP_008719.
 SQ SEQUENCE 819 AA; 87751 MW; 9083034F18BA7E8A CRC64;
 Query Match 100.0%; Score 180; DB 1; Length 819;
 Best Local Similarity 100.0%; Pred. No. 1.5e-16;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKTRRSWVWNOFVIEEYAGPEPVILGKLHSD 33
 Db 39 LKTRRSWVWNOFVIEEYAGPEPVILGKLHSD 71

RESULT 4
 Q6PFX6 PRELIMINARY; PRT; 781 AA.
 ID Q6PFX6
 AC Q6PFX6
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Cadherin-like 24.
 GN Name=Cdh24.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RX MEDLINE=22386257; PubMed=12477932.
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ue din T.B., Roshyuk S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Faley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butlerfield Y.S.,
 Krzywinski M.I., Skalska U., Small D.E., Scherch A., Schein J.E.,
 Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL; BC057373; AAH57373.1; -
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR002233; Cadherin.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 4.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 KM Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 781 AA; 84104 MW; 15996DE6C9835AA CRC64;

Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKTRRSWVWNOFVIEEYAGPEPVILGKLHSD 33
 Db 39 LKTRRSWVWNOFVIEEYAGPEPVILGKLHSD 71

RESULT 5
 AAH57373 PRELIMINARY; PRT; 781 AA.
 ID AAH57373
 AC AAH57373
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Cadherin-like 24.
 GN Cdh24.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RX MEDLINE=22386257; PubMed=12477932.
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ue din T.B., Roshyuk S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Faley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butlerfield Y.S.,
 Krzywinski M.I., Skalska U., Small D.E., Scherch A., Schein J.E.,
 Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC057373; AAH57373.1; -
 SQ SEQUENCE 781 AA; 84104 MW; 15996DE6C9835AA CRC64;

Query Match 98.3%; Score 177; DB 2; Length 781;
 Best Local Similarity 97.0%; Pred. No. 3.8e-16;
 Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKTRRSWVWNOFVIEEYAGPEPVILGKLHSD 33
 Db 39 LKTRRSWVWNOFVIEEYAGPEPVILGKLHSD 71

RESULT 6
 CADD_HUMAN STANDARD; PRT; 796 AA.
 ID CADD_HUMAN
 AC P55287; Q15065; Q15066; Q9UG93; Q9UG94;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSF-4).
 GN Name=CDH11;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OK NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RP TISSUE=Brain;
 RC MEDLINE=95073006; PubMed=7982033;
 RA Tanhara H., Sano K., Heimerl R.L., St John T., Suzuki S.,
 RT "Cloning of five human cadherins cDNAs characterizes features of
 RT cadherin extracellular domain and provides further evidence for two
 RT structurally different types of cadherin."
 RT Cell Adhes. Commun. 2:15-26(1994).
 RN [2]
 RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RP TISSUE=Osteosarcoma;
 RC MEDLINE=94216322; PubMed=8163513;
 RA Okazaki M., Takeshita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,
 RA Mann B.,
 RT "Molecular cloning and characterization of OB-cadherin, a new member
 RT of cadherin family expressed in osteoblasts."
 RT J. Biol. Chem. 269:12092-12098(1994).
 RN [3]
 RN SEQUENCE OF 269-796 FROM N.A. (ISOFORM 1).
 RC TISSUE=fetal brain;
 RA MEDLINE=91283540; PubMed=2059658;
 RA Suzuki S., Sano K., Tanhara H.,
 RT "Diversity of the cadherin family: evidence for eight new cadherins in
 RT nervous tissue."
 RT Cell Regul. 2:261-270(1991).
 RN [4]
 RN SEQUENCE OF 600-668 FROM N.A. (ISOFORMS 1 AND 2).
 RA Koolis P.F., Hogendoorn P.C.W., Boyce J.V.M.G., Van Roy F.,
 RT "Alternative cadherin-11 transcripts encoding truncated adhesion
 RT molecules are detectable in both human cancer and normal cells."
 RT Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P55287-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P55287-2; Sequence=VSP_000640; VSP_000641;
 CC -1- TISSUE SPECIFICITY: Expressed mainly in brain but also found in
 CC other tissues. Expressed in neuroblasts.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.jsb-sib.ch/announce/>
 CC or send an email to license@lsb-sib.ch).
 CC -----
 DR EMBL; LJ4056; AAA35622.1; -;
 DR EMBL; D21254; BA04798.1; -;
 DR EMBL; D21255; BA04799.1; -;
 DR EMBL; AF060370; AAD27755.1; -;
 DR EMBL; AF060369; AAD27755.1; JOINED.
 DR EMBL; AF060370; AAD27756.1; -;
 DR EMBL; AF060369; AAD27756.1; JOINED.
 DR PIR; A38992; A38992.
 DR HSSP; P09803; 117W.
 DR Genew; HGNC:1750; CDP11.
 DR MIM; 600023; -;
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0007156; P:homophilic cell adhesion; NAS.
 DR GO; GO:0001503; P:cell-cell adhesion; NAS.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin; 5.

DR Pfam; PF01049; Cadherin_C; 1.
 DR PRINTS; PRO0205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS00268; CADHERIN_2; 5.
 KM Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 22
 FT PROPEP 23 53
 FT CHAIN 54 796
 FT TRANSMEM 54 617
 FT DOMAIN 618 640
 FT DOMAIN 641 796
 FT DOMAIN 54 159
 FT DOMAIN 160 268
 FT DOMAIN 269 383
 FT DOMAIN 384 486
 FT DOMAIN 487 612
 FT CARBOHYD 455 455
 FT CARBOHYD 540 540
 FT VARSPLIC 632 693
 FT
 FT VARSPLIC 694 796
 FT
 FT CONFLICT 271 272
 FT CONFLICT 275 275
 FT CONFLICT 340 340
 FT CONFLICT 373 373
 FT CONFLICT 471 471
 SQ SEQUENCE 796 AA; 88049 MW; 2C67044C78ADBB2E CXC64;
 Query Match 84.4%; Score 152; DB 1; Length 796;
 Best Local Similarity 75.8%; Pred. No. 1,3e-12;
 Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LRTSRWVWVQFVIEVEYAGPEVPLICKLSD 33
 DB 48 LQSRGKGVWVQFVIEVEYTGPDVVGRLMSD 80
 RESULT 7
 CADB_MOUSE STANDARD; PRT; 796 AA.
 ID CADB_MOUSE P55288;
 AC P55288;
 DT 01-OCT-1996 (rel. 34, Created)
 DT 01-OCT-1996 (rel. 34, Last sequence update)
 DT 05-JUL-2004 (rel. 44, Last annotation update)
 DE Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSF-4).
 GN Name=Cdh11; Synonyms=Cad-11;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=95269887; PubMed=7750649;
 RA Kimura Y., Matsunami H., Inoue T., Shimamura K., Uchida N., Ueno T.,
 RA Miyazaki T., Takeichi M.,
 RT "Cadherin-11 expressed in association with mesenchymal morphogenesis
 RT in the head, somite, and limb bud of early mouse embryos."
 RT Dev. Biol. 169:347-358(1995).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=95269887; PubMed=7750650;
 RA Kimura Y., Matsunami H., Inoue T., Shimamura K., Uchida N., Ueno T.,
 RA Miyazaki T., Takeichi M.,
 RT "Cadherin-11 expressed in association with mesenchymal morphogenesis
 RT in the head, somite, and limb bud of early mouse embryos."
 RT Dev. Biol. 169:347-358(1995).
 RN [3]
 RN SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Calvaria;
 RX MEDLINE=94216322; PubMed=816313;
 RA Okazaki M., Takeshita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,
 Amano E.,
 RT "Molecular cloning and characterization of OB-cadherin, a new member
 of cadherin family expressed in osteoblasts.";
 RL J. Biol. Chem. 269:12092-12098 (1994).
 RP [4]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stadelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman U.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood U., Schmutz J., Myers R.W.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16839-16903 (2002).
 RN [5]
 RP DEVELOPMENTAL STAGE.
 RC STRAIN=C57BL/6; TISSUE=Testis;
 RX MEDLINE=97033837; PubMed=8879495;
 RA Munro S.B., Blaschuk O.W.,
 RT "A comprehensive survey of the cadherins expressed in the testes of
 fetal, immature, and adult mice utilizing the polymerase chain
 reaction.";
 RL Biol. Reprod. 55:822-827 (1996).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Selectively expressed in osteoblastic cell
 CC lines, precursor cell lines of osteoblasts, and primary
 CC osteoblastic cells from calvaria, as well as in lung, testis, and
 CC brain tissues at low levels.
 CC -1- DEVELOPMENTAL STAGE: In the testis, expression is highest in fetal
 CC gonad and decreases 8-fold in newborn.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X77557; CAA54674.1; -
 DR EMBL; D31563; BAA06730.1; -
 DR EMBL; D21253; BAA04797.1; -
 DR EMBL; BC046314; AAH46314.1; -
 DR PIR; A53584; A53584;
 DR PIR; I48277; I48277;
 DR PIR; I49556; I49556;
 DR HSSP; P09803; I17W.
 DR MGD; MGI:99217; Cdh11.
 DR GO; GO:0005737; Cytoplasm; IDA.
 DR GO; GO:000586; Cytoplasmic membrane; IDA.
 DR InterPro; IPR002126; Cadherin.

DR InterPro; IPR000233; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin_C; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 KW Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 24 Potential.
 FT PROPEP 25 53 Potential.
 FT CHAIN 54 796 Cadherin-11.
 FT DOMAIN 54 617 Extracellular (Potential).
 FT TRANSMEM 618 640 Potential.
 FT DOMAIN 641 796 Cytoplasmic (Potential).
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.
 FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 612 Cadherin 5.
 FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 540 540 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 462 462 E -> D (in Ref. 1).
 FT CONFLICT 589 589 T -> L (in Ref. 2).
 FT CONFLICT 655 655 D -> N (in Ref. 2).
 FT CONFLICT 751 751 V -> M (in Ref. 1).
 FT CONFLICT 777 777 P -> Q (in Ref. 2).
 FT CONFLICT 782 782 L -> P (in Ref. 2).
 SQ SEQUENCE 796 AA; 88112 MW; 0D584D2464ID529 CRC64;
 Query Match 84.4%; Score 152; DB 1; Length 796;
 Best Local Similarity 75.8%; Pred. No. 1.3e-12;
 Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LKTRRSWVWNPFEVIEYAGPEVILIGLHSD 33
 Db 48 LQSKRGWVWNPFEVIEYAGPEVILIGLHSD 80
 RESULT 8
 Q96C29 PRELIMINARY; PRT; 796 AA.
 AC Q96C29;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Cadherin 11, type 2, isoform 1 preproprotein.
 GN Name=Cdh11;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stadelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman U.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood U., Schmutz J., Myers R.W., Butcherfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human

```
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC Tissue=Brain;
RA Strusberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC EMBL: BC013609; AAH13609.1; -.
DR HSSP: P09803; 117W.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:000509; F:calcium ion binding; IEA.
DR GO: GO:0007156; F:homophilic cell adhesion; IEA.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR00233; Cadherin.
DR InterPro: IPR001901; SecE.
DR Pfam: PF00028; Cadherin_C_1.
DR Pfam: PF01049; Cadherin_C_1.
DR PRINTS: PR0205; CADHERIN.
DR SMART: SMO0112; CA; 5.
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS0268; CADHERIN_2; 5.
DR PROSITE: PS01067; SRCR SEC61G; UNKNOWN 1.
DR Calcium-binding; Cell adhesion; Transmembrane.
KW SEQUENCE 796 AA; 87979 MW; 8497F9B834F7547C CRC64;
SQ

Query Match 84.4%; Score 152; DB 2; Length 796;
Best Local Similarity 75.8%; Pred. No. 1.3e-12;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Cy 1 LLRTSRWVWVNFVIEYAGPEPVLLIGKXHS 33
Db 48 LQSRKRGVWVNFVIEYTCPEVLTGRLHSD 80

RESULT 9
ID 08C706 PRELIMINARY; PRT; 796 AA.
AC 08C706.
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length
DE enriched library, clone: C530015F15 product: cadherin 11, full insert
DE sequence.
GN Name=ch11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
```

```
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujisawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe K.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka Y., Matsura S., Kawai U.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA Adachi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohnato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 5 cadherin domains.
DR EMBL: AK049652; BAC33860.1; -.
DR HSSP: P09803; 117W.
DR MGD: MGI:99217; Cdh11.
DR GO: GO:0005737; C:cytoplasm; IEA.
DR GO: GO:0005886; C:plasma membrane; IEA.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR00233; Cadherin_C-term.
DR Pfam: PF00028; Cadherin_5.
DR Pfam: PF01049; Cadherin_C_1.
DR PRINTS: PR0205; CADHERIN.
DR SMART: SMO0112; CA; 5.
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS0268; CADHERIN_2; 5.
KW Calcium-binding; Cell adhesion; Transmembrane.
KW SEQUENCE 796 AA; 88126 MW; 71963374B2E1BE29 CRC64;
SQ

Query Match 84.4%; Score 152; DB 2; Length 796;
Best Local Similarity 75.8%; Pred. No. 1.3e-12;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Cy 1 LLRTSRWVWVNFVIEYAGPEPVLLIGKXHS 33
Db 48 LQSRKRGVWVNFVIEYTCPEVLTGRLHSD 80

RESULT 10
CABD_CHICK STANDARD; PRT; 792 AA.
ID CABD_CHICK
AC 093319;
```

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-11 precursor.
 GN Name=CDH11;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White Leghorn;
 RA Wei J., Dong X.R., Topouzis S., Zimmer W.E., Broders F., Thierry J.P.,
 RA Koreliansky V., Majesky M.W.;
 RT "Molecular cloning of chick cadherin 11 and its expression during
 RT smooth muscle differentiation and formation of the tunica media";
 RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL; AF055342; AAC33675.1; -
 DR HSSP; P09803; 117M.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; P50268; Cadherin_C_term.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin_C; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SMO0112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 DR KX Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 22 Potential.
 FT PROPEP 23 53 Potential.
 FT CHAIN 54 792 Cadherin-11.
 FT DOMAIN 54 613 Extracellular (Potential).
 FT TRANSVM 614 634 Potential.
 FT DOMAIN 635 792 Cytoplasmic (Potential).
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.
 FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 608 Cadherin 5.
 FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 536 536 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 594 594 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 792 AA; 87572 MW; 3E3488C666731AB CRC64;

AC 093264;
 DT 01-NOV-1998 (TRENDSrel. 08, Created)
 DT 01-NOV-1998 (TRENDSrel. 08, Last sequence update)
 DT 01-MAR-2004 (TRENDSrel. 26, Last annotation update)
 DE Cadherin precursor.
 GN Name=Cad-11;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 CC Xenopodinae; Xenopus.
 CX NCBI_TaxID=6355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eggs;
 RA MEDLINE=98202517; PubMed=9533956;
 RA Hagedall B., Borchers A., Medlich D.;
 RT "Xenopus cadherin-11 (Xcadherin-11) expression requires the Wg/Wnt
 RT signal";
 RL Mech. Dev. 72:101-113 (1998).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -----
 CC EMBL; AF002983; AAC28073.1; -
 DR HSSP; P09803; 117M.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C_term.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin_C; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SMO0112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 DR KX Calcium; Calcium-binding; Cell adhesion; Signal; Transmembrane.
 FT SIGNAL 1 53 Potential.
 FT CHAIN 54 794 cadherin.
 SQ SEQUENCE 794 AA; 88302 MW; 7221AD4CFEA719DB CRC64;

Query Match 83.9%; Score 151; DB 2; Length 794;
 Best Local Similarity 75.8%; Pred. No. 1.8e-12;
 Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 LKTRSWYWNQPFVIEEYAGPEPVLIGLHSD 33
 DB 48 LKRSKRWYWNQPFVIEEYAGPEPVLIGLHSD 80

RESULT 12
 CADK_HUMAN STANDARD; PRT; 801 AA.
 ID CADK_HUMAN
 AC 09HPTG;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-20 precursor.
 GN Name=CDH20; Synonyms=CDH7L3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euteleostomi; Primates; Catarrhini; Hominiidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20453188; PubMed=10995570;
 RA Kools P., Van Imschoot G., van Roy F.;
 RT "Characterization of three novel human cadherin genes (CDH7, CDH9, and CDH20) clustered on chromosome 18q22-q23 and with high homology to chicken cadherin-7";
 RL Genomics 68:283-295 (2000).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic

manner in connecting cells; cadherins may thus contribute to the sorting of heterogeneous cell types.

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- TISSUE SPECIFICITY: Expressed in placenta, adult brain, and fetal brain.

-1- SIMILARITY: Contains 5 cadherin domains.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: AF217289; AAC23739.1; -.

CC HSSP: P09803; 117X.

CC Genew: H8NC:1760; CDH20.

CC MIN: 605807; -.

CC GO: GO:0016021; C: integral to membrane; NAS.

CC GO: GO:0007156; P: homophilic cell adhesion; NAS.

CC InterPro: IPR002126; Cadherin.

CC InterPro: IPR000233; Cadherin_C-term.

CC Pfam: PF00028; Cadherin_5.

CC Pfam: PF01049; Cadherin_1.

CC PRINTS: PR00205; CADHERIN.

CC SMART: SM00112; CA; 5.

CC PROSITE: PS00232; CADHERIN_1; 3.

CC PROSITE: PS0268; CADHERIN_2; 5.

CC KX Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal; Transmembrane.

CC KW SIGNAL.

CC FT PROPEP 1 7 Potential.

CC FT CHAIN 1 59 Potential.

CC FT DOMAIN 1 60 801 Cadherin-20.

CC FT TRANSMEM 1 619 Extracellular (Potential).

CC FT DOMAIN 620 640 Potential.

CC FT DOMAIN 641 801 Cytoplasmic (Potential).

CC FT DOMAIN 61 165 Cadherin_1.

CC FT DOMAIN 166 274 Cadherin_2.

CC FT DOMAIN 275 389 Cadherin_3.

CC FT DOMAIN 390 494 Cadherin_4.

CC FT DOMAIN 494 610 Cadherin_5.

CC FT CARBOHYD 261 261 N-linked (GlcNAc...) (Potential).

CC FT CARBOHYD 420 420 N-linked (GlcNAc...) (Potential).

CC FT CARBOHYD 461 461 N-linked (GlcNAc...) (Potential).

CC FT CARBOHYD 542 542 N-linked (GlcNAc...) (Potential).

CC SQ SEQUENCE 801 AA; 89104 MW; F8SDC53B1631866 CRC64;

Query Match 79.4%; Score 143; DB 1; Length 801;

Best Local Similarity 74.2%; Pred. No. 2.5e-11;

Matches 23; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

CC 3 RTSRWVWNOFFVIEEYAGPEPVYIGTLHSD 33.

CC Db 56 RTKRSWVWNOFFVIEEYTGDPYVGLKLSHSD 86

RESULT 13

CCBLT4 PRELIMINARY; PRT; 340 AA.

CC ID CCBLT4.

CC DT 01-MAR-2003 (TrEMBLrel. 23, Created)

CC DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

CC DT 01-MAR-2004 (TrEMBLrel. 25, Last annotation update)

CC DE Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone: A730013p10 product: CADHERIN-7 homologue.

CC GN Name: cdh7.

CC OS Mus musculus (Mouse).

CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

CC OX NCBI_TaxID=10090;

CC RN [1]

CC RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RX MEDLINE=99279253; PubMed=10349636;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44 (1999).

CC SEQUENCE FROM N.A.

CC RP STRAIN=C57BL/6J; TISSUE=Cerebellum;

CC RX MEDLINE=21085660; PubMed=11217851;

CC RA RIKEN FANTOM Consortium;

CC RT "Functional annotation of a full-length mouse cDNA collection.";

CC RL Nature 409:685-690 (2001).

CC RN [3]

CC RP SEQUENCE FROM N.A.

CC RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

CC RA The FANTOM Consortium;

CC RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

CC RL Nature 420:563-573 (2002).

CC RN [4]

CC RP SEQUENCE FROM N.A.

CC RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

CC RX MEDLINE=20499374; PubMed=11042159;

CC RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

CC RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";

CC RL Genome Res. 10:1617-1630 (2000).

CC RN [5]

CC RP SEQUENCE FROM N.A.

CC RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

CC RX MEDLINE=20530913; PubMed=11076861;

CC RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P., Kono H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsubiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuda S., Kawal U., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

CC RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";

CC RL Genome Res. 10:1757-1771 (2000).

CC RN [6]

CC RP SEQUENCE FROM N.A.

CC RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

CC RA Aichi U., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirokane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ono M., Ohnato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Takagawa A., Takahashi F., Takaku-Akita S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

CC RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Contains 3 cadherin domains.

CC CC EMBL: AK042657; BAC31323.1; -.

CC DR HSSP: P15116; INCI.

CC DR WGI: 2442792; Cdh7.

CC DR GO: GO:0016020; C: membrane; IEA.

CC DR GO: GO:0005509; F: calcium ion binding; IEA.

CC DR GO: GO:0007156; P: homophilic cell adhesion; IEA.

CC DR InterPro: IPR002126; Cadherin.

CC Pfam: PF00028; Cadherin_3.

CC PRINTS: PR00205; CADHERIN.

CC SMART: SM00112; CA; 2.

CC PROSITE: PS00232; CADHERIN_1; 2.

CC PROSITE: PS0268; CADHERIN_2; 3.

CC KX Calcium-binding.

CC KW SEQUENCE 340 AA; 37654 MW; DBA9DCA05F7527 CRC64;

Query Match 78.9%; Score 142; DB 2; Length 340;
 Best Local Similarity 74.2%; Pred. No. 1.5e-11;
 Matches 23; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 RTFRSWVWNOFFVIEYAGPEPVILGKXHS 33
 DB 44 RTFRSWVWNOFFVIEYAGSDPLVYGKXHS 74

RESULT 14

Q8AWM2 PRELIMINARY; PRT; 551 AA.
 AC Q8AWM2;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Cadherin-7
 OS Gallus gallus (Chicken)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22344707; PubMed=13364338;
 RA Kawano R., Matsuo N., Tanaka H., Nasu M., Yoshioka H., Shirabe K.,
 RT "Identification and characterization of a soluble cadherin-7 isoform
 RT produced by alternative splicing."
 RL J. Biol. Chem. 277:47679-47685(2002).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL; AY15555; AAM55476.1; -.
 DR HSRP; P15116; INCI.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00028; Cadherin; 5.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 4.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 DR KX Calcium-binding.
 KW SEQUENCE 551 AA; 60862 MW; ABBAC26B42D65B7C CRC64;

Query Match 78.9%; Score 142; DB 2; Length 551;
 Best Local Similarity 74.2%; Pred. No. 2.4e-11;
 Matches 23; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 RTFRSWVWNOFFVIEYAGPEPVILGKXHS 33
 DB 44 RTFRSWVWNOFFVIEYAGSDPLVYGKXHS 74

RESULT 15

Q8IY78 PRELIMINARY; PRT; 630 AA.
 AC Q8IY78;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE CDH7 protein.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywicki M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.,
 RT Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL; BC036786; AAK36786.1; -.
 DR HSRP; P15116; INCI.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00028; Cadherin; 5.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 DR KX Calcium-binding.
 KW SEQUENCE 630 AA; 69217 MW; 1BB6FD87A21A61D3 CRC64;

Query Match 78.9%; Score 142; DB 2; Length 630;
 Best Local Similarity 74.2%; Pred. No. 2.7e-11;
 Matches 23; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 RTFRSWVWNOFFVIEYAGPEPVILGKXHS 33
 DB 44 RTFRSWVWNOFFVIEYAGSDPLVYGKXHS 74

Search completed: December 8, 2004, 10:24:38
 Job time: 13.2273 secs

This Page Blank (usp10)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd

OM protein - protein search, using sw model

```
Run on:      December 8, 2004, 09:16:13 ; Search time 13.6558 Seconds
              (without alignments)
              866.886 Million cell updates/sec
```

Title: US-09-788-051-10

Perfect score: 180
Sequence: 1 LLRTSRSWVNQFVIEEYAGPEVLIGKTHSD 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%

```

A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	180	100.0	33	7	ADD29451	Add29451 Human cat
2	180	100.0	493	5	AD116946	Ad116946 Human NOV
3	180	100.0	607	5	ABBS53295	Abbs53295 Human pol
4	180	100.0	620	7	ADD29448	Add29448 Human cat
5	180	100.0	636	7	ADD29445	Add29445 Human cat
6	180	100.0	781	5	ABBS3296	Abbs3296 Human pol
7	180	100.0	781	5	AA48736	Aa48736 Human cat
8	180	100.0	781	5	ABG34078	Abg34078 Human Proc
9	180	100.0	781	5	AD116604	Ad116604 Human NOV
10	180	100.0	781	5	AD116606	Ad116606 Human NOV
11	180	100.0	781	6	ABR40114	AbR40114 Human cel
12	180	100.0	781	6	ADAO1366	Ada01366 Human Proc
13	180	100.0	781	6	ADAA3795	Ada43795 Human sec
14	180	100.0	781	6	ADAA3563	Ada43563 Human sec
15	180	100.0	781	6	ADAO1238	Ada01238 Human Proc
16	180	100.0	781	7	ADA01122	Ada01122 Human sec
17	180	100.0	781	7	ADA43679	Ada43679 Human sec
18	180	100.0	781	7	ADAO6941	Ada06941 Human Proc
19	180	100.0	781	7	ADA08422	Ada08422 Novel
20	180	100.0	781	7	ADBS9722	Adbs9722 Human Proc
21	180	100.0	781	7	ADBS8705	Adbs8705 Human Proc
22	180	100.0	781	7	ADBS6160	Adbs6160 Human sec
23	180	100.0	781	7	ADBS9838	Adbs9838 Human Proc
24	180	100.0	781	7	ADBS9493	Adbs9493 Novel
25	180	100.0	781	7	ADB66044	ADB66044 Human sec

45	180	100.0	781	8	AD838078	Human	PRO
44	180	100.0	781	8	AD838078	Human	sec
43	180	100.0	781	8	AD838078	Human	sec
42	180	100.0	781	8	AD838078	Human	sec
41	180	100.0	781	8	AD838078	Human	sec
40	180	100.0	781	8	AD838078	Human	sec
39	180	100.0	781	8	AD838078	Human	sec
38	180	100.0	781	7	AD838078	Human	PRO
37	180	100.0	781	7	AD838078	Human	PRO
36	180	100.0	781	7	AD838078	Human	PRO
35	180	100.0	781	7	AD838078	Human	PRO
34	180	100.0	781	7	AD838078	Human	PRO
33	180	100.0	781	7	AD838078	Human	PRO
32	180	100.0	781	7	AD838078	Human	PRO
31	180	100.0	781	7	AD838078	Human	PRO
30	180	100.0	781	7	AD838078	Human	PRO
29	180	100.0	781	7	AD838078	Human	PRO
28	180	100.0	781	7	AD838078	Human	PRO
27	180	100.0	781	7	AD838078	Human	PRO
26	180	100.0	781	7	AD838078	Human	PRO
25	180	100.0	781	7	AD838078	Human	PRO
24	180	100.0	781	7	AD838078	Human	PRO
23	180	100.0	781	7	AD838078	Human	PRO
22	180	100.0	781	7	AD838078	Human	PRO
21	180	100.0	781	7	AD838078	Human	PRO
20	180	100.0	781	7	AD838078	Human	PRO
19	180	100.0	781	7	AD838078	Human	PRO
18	180	100.0	781	7	AD838078	Human	PRO
17	180	100.0	781	7	AD838078	Human	PRO
16	180	100.0	781	7	AD838078	Human	PRO
15	180	100.0	781	7	AD838078	Human	PRO
14	180	100.0	781	7	AD838078	Human	PRO
13	180	100.0	781	7	AD838078	Human	PRO
12	180	100.0	781	7	AD838078	Human	PRO
11	180	100.0	781	7	AD838078	Human	PRO
10	180	100.0	781	7	AD838078	Human	PRO
9	180	100.0	781	7	AD838078	Human	PRO
8	180	100.0	781	7	AD838078	Human	PRO
7	180	100.0	781	7	AD838078	Human	PRO
6	180	100.0	781	7	AD838078	Human	PRO
5	180	100.0	781	7	AD838078	Human	PRO
4	180	100.0	781	7	AD838078	Human	PRO
3	180	100.0	781	7	AD838078	Human	PRO
2	180	100.0	781	7	AD838078	Human	PRO
1	180	100.0	781	7	AD838078	Human	PRO

ALIGNMENTS

RESULT 1	
ADD29451	
ID	ADD29451 standard; protein; 33 AA.
XX	
AC	ADD29451;
XX	
DT	15-JAN-2004 (first entry)
XX	
DE	Human cadherin-like protein peptide fragment Seq ID10.
XX	
KW	cadherin-like protein; transmembrane protein; cadherin domain;
KW	homotypic cell-cell adhesion; cytotactic; osteoparitic; cancer;
KW	osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis
KW	metastatic tumour; human.
XX	
OS	Homo sapiens.
XX	
PN	US2003144491-A1.
XX	
PD	31-JUL-2003.
XX	
PF	16-FEB-2001; 2001US-00788051.
XX	
XX	03-FEB-2000; 2000US-00496914.
PR	27-APR-2000; 2000US-00560875.
XX	
PA	(GDB//) GODBOLE S D.
PA	(KIOC//) KUO C.
PA	(ARTE//) ARTERBURN M C.
PA	(YEUN//) YEUNG G.
PA	(PALE//) PALENCIA S.
PA	(TANG//) TANG Y T.
PA	(LIUC//) LIU C.
PA	(DRMA//) DRMANAC R T.
XX	
PI	Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;
PI	Liu C, Drmanac RT;
XX	
DR	WPI: 2003-829799/77.
XX	
PT	Novel isolated human secreted cadherin-like polypeptide useful for
PT	treating diseases such as cancers, osteoporosis, Paget's disease,
PT	osteomalacia, hyperostosis, osteopetrosis.
XX	
PS	Claim 11; SEQ ID NO 10; 63bp; English.
XX	
CC	This invention relates to a novel isolated human secreted cadherin-like
	protein and the DNA sequence which encodes it. Cadherins are a family of

transmembrane proteins which share a common cadherin domain in their extracellular region. The extracellular portion mediates homotypic cell-cell adhesion that is calcium dependent. Modulators of the protein of the invention may have cytostatic or osteopathic activity. The invention may allow development of therapeutic useful for the treatment of diseases such as cancers, osteoporosis, Paget's disease, osteomalacia, hyperostosis and osteopetrosis. The protein and DNA sequence of the invention may also be useful as markers for prognosis of metastatic tumours. The present sequence is that of a peptide fragment of the human secreted cadherin-like protein which was used during the exemplification of the invention.

CC Sequence 33 AA;

Query Match 100.0%; Score 180; DB 7; Length 33;
Best Local Similarity 100.0%; Pred. No. 3,5e-21;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 LLRTRRSWWVWVQFVIEVYAGPEPVLGKLSHD 33
Db 1 LLRTRRSWWVWVQFVIEVYAGPEPVLGKLSHD 33

RESULT 2
AD16946
ID AD16946 standard; protein: 493 AA.
XX AC AD16946;
XX DT 15-APR-2004 (first entry)
XX DE Human NOVX protein homologue SegID 482.
XX KW human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
KW inflammation; autoimmune disorder; allergy; blood disorder;
KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
KW Alzheimer's disease; infection; str.
XX OS Homo sapiens.
XX PN W0200268649-A2.
XX PD 06-SEP-2002.
XX PF 31-JAN-2002; 2002WC-US002785.
XX PR 31-JAN-2001; 2001US-02653355.
PR 31-JAN-2001; 2001US-02654122.
PR 31-JAN-2001; 2001US-02655142.
PR 31-JAN-2001; 2001US-02655176.
PR 02-FEB-2001; 2001US-02664062.
PR 05-FEB-2001; 2001US-02667672.
PR 07-FEB-2001; 2001US-02669752.
PR 07-FEB-2001; 2001US-02670572.
PR 08-FEB-2001; 2001US-02674592.
PR 09-FEB-2001; 2001US-02678232.
PR 15-FEB-2001; 2001US-02689742.
PR 26-FEB-2001; 2001US-02716642.
PR 27-FEB-2001; 2001US-02718392.
PR 27-FEB-2001; 2001US-02718552.
PR 02-MAR-2001; 2001US-02727882.
PR 02-MAR-2001; 2001US-02730462.
PR 14-MAR-2001; 2001US-02732522.
PR 14-MAR-2001; 2001US-02759472.
PR 14-MAR-2001; 2001US-02759502.
PR 14-MAR-2001; 2001US-02759892.
PR 15-MAR-2001; 2001US-02764482.
PR 15-MAR-2001; 2001US-02764502.
PR 15-MAR-2001; 2001US-02763972.
PR 16-MAR-2001; 2001US-02767682.
PR 20-MAR-2001; 2001US-02786522.
PR 26-MAR-2001; 2001US-02787752.

26-MAR-2001; 2001US-02787762.
PR 29-MAR-2001; 2001US-02788832.
PR 29-MAR-2001; 2001US-02788842.
PR 30-MAR-2001; 2001US-02801472.
PR 11-APR-2001; 2001US-02829522.
PR 11-APR-2001; 2001US-02830832.
PR 20-APR-2001; 2001US-02851332.
PR 23-APR-2001; 2001US-02857492.
PR 03-MAY-2001; 2001US-02883272.
PR 03-MAY-2001; 2001US-02885042.
PR 29-MAY-2001; 2001US-02940472.
PR 30-MAY-2001; 2001US-02944732.
PR 08-JUN-2001; 2001US-02969642.
PR 18-JUN-2001; 2001US-02989592.
PR 19-JUN-2001; 2001US-02993242.
PR 13-AUG-2001; 2001US-03120202.
PR 16-AUG-2001; 2001US-03128892.
PR 16-AUG-2001; 2001US-03128992.
PR 21-AUG-2001; 2001US-03133902.
PR 28-AUG-2001; 2001US-03154702.
PR 31-AUG-2001; 2001US-03164472.
PR 07-SEP-2001; 2001US-03181152.
PR 07-SEP-2001; 2001US-03181182.
PR 12-SEP-2001; 2001US-03187402.
PR 19-SEP-2001; 2001US-03233792.
PR 18-OCT-2001; 2001US-03302452.
PR 18-OCT-2001; 2001US-03303082.
PR 14-NOV-2001; 2001US-03327012.
(CURA-) CURAGEN CORP.

XX PA
XX PI Tchermey VT, Spytek KA, Zernusen BD, Patturajan M, Shinkes RA;
PI Li L, Gangoli EA, Padigar M, Anderson DW, Rastell L, Miller CE;
PI Gerlach V, Taupier R, Gusev VY, Colman SD, Wolenc AR, Pena CE;
PI Furtak K, Grose WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CB;
PI WPI, 2002-706998/76.
XX DR
XX PT New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX PS
XX PS Disclosure; SEQ ID NO 482; 1498bp; English.

XX CC This invention relates to a novel nucleic acids, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOVX polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC cyostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
CC antiasthmatic, nephrotropic, antiarrhythmic, hepatotropic,
CC neuroprotective, nootropic, antibacterial, virucide, antiparasitic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
CC of the invention.

XX SQ Sequence 493 AA;

Query Match 100.0%; Score 180; DB 5; Length 493;
 Best Local Similarity 100.0%; Pred. No. 8.5e-20;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTRRSWMWNOFFVEEYAGPEPVLTGKLHSD 33
 |||
 DB 39 LTRRSWMWNOFFVEEYAGPEPVLTGKLHSD 71

RESULT 3
 ABB53295
 ID ABB53295 standard; protein: 607 AA.
 AC ABB53295;
 XX
 DT 12-FEB-2002 (first entry)
 DE Human polypeptide #35.

Human; nootropic; neuroprotective; anticonvulsant; antidepressant;
 neuroleptic; tranquilizer; antirhythmic; cardiac; antidiabetic;
 antiinflammatory; antihypertensive; hepatotropic; vitruclide; antidiabetic;
 nephrotropic; anorectic; cytostatic; vaccine; neurological disease;
 cardiovascular disease; respiratory disease; liver disease;
 renal disease; skeletal muscle disease; gastrointestinal disease;
 placental disease; testicular cancer; male fertility; pancreatic disease.

XX Homo sapiens.
 OS
 XX MO200181363-A1.
 PN
 PD 01-NOV-2001.
 PF 26-APR-2001; 2001WO-US013360.
 PR 27-APR-2000; 2000US-0199963P.
 PR 11-MAY-2000; 2000US-0203336P.
 PR 25-MAY-2000; 2000US-0207087P.
 PR 26-MAY-2000; 2000US-0207546P.

XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA

PI Agarwal P, Murdock PR, Rizvi SK, Smith RF, Xiang Z, Kabinick KS;
 PI Lai Y, Xie Q;
 XX

DR WPI; 2002-04392/05.
 DR N-PSDB; ABA90360.

PT Novel polypeptides and polynucleotides useful as a vaccine for preventing
 PT and treating diseases associated the polypeptide, e.g. Alzheimer's
 PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesias.
 PS Claim 1; Page 106-108; 116pp; English.

XX The invention relates to an isolated polypeptide comprising a 277, 480,
 CC 581, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
 CC 844, 782, 262, 394, 471, 485, 286, 533, 495, 619, 490, 462, 255,
 CC 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
 CC given in the specification. The polypeptides, modulators of the
 CC polypeptides and antibodies against the polypeptides are useful for
 CC treating diseases such as neurological and psychiatric diseases including
 CC Alzheimer's, parasupranuclear palsy, Huntington's disease, myotonic
 CC dystrophy, anorexia and depression; cardiovascular diseases including
 CC congestive heart failure, Hodgkin's disease and myocardial infarction;
 CC respiratory diseases including asthma, chronic obstructive pulmonary
 CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
 CC disease, including hypercholesterolaemia, cirrhosis, viral and nonviral
 CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
 CC renal disease including renal failure, acute tubular necrosis and
 CC glomerulonephritis; skeletal muscle diseases including Eulenburg's
 CC disease, hypoglycaemia and obesity; gastrointestinal diseases including

CC myotonia congenita and intestinal obstruction; lymph diseases including
 CC lymphagiectasia; diseases of placenta including choriochorionoma; diseases
 CC of testes including testicular cancer, male reproductive diseases
 CC including low testosterone and male infertility; and disease of pancreas
 CC including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The
 CC present sequence is a polypeptide of the invention
 XX Sequence 607 AA;
 SQ

Query Match 100.0%; Score 180; DB 5; Length 607;
 Best Local Similarity 100.0%; Pred. No. 1.1e-19;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTRRSWMWNOFFVEEYAGPEPVLTGKLHSD 33
 |||
 DB 39 LTRRSWMWNOFFVEEYAGPEPVLTGKLHSD 71

RESULT 4
 ADD29448
 ID ADD29448 standard; protein: 620 AA.
 AC ADD29448;
 XX
 DT 15-JAN-2004 (first entry)
 DE Human cadherin-like mature protein.

Human cadherin-like mature protein.
 XX cadherin-like protein; transmembrane protein; cadherin domain;
 XX homotypic cell-cell adhesion; cytostatic; osteopetrosis; cancer;
 XX osteopetrosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
 XX metastatic tumour; human.
 XX

OS Homo sapiens.
 XX
 XX US2003144491-A1.
 XX
 XX 31-JUL-2003.
 PD
 PD 16-FEB-2001; 2001US-00788051.
 PF
 PF 03-FEB-2000; 2000US-00496934.
 PR 27-APR-2000; 2000US-00560875.
 PR

XX (GODR/) GODBOLE S D.
 PA (KUOC/) KUO C.
 PA (ARTE/) ARTERBURN M C.
 PA (VEIN/) YEUNG G.
 PA (PALE/) PALENCIA S.
 PA (TANG/) TANG Y T.
 PA (LITC/) LIT C.
 PA (DRMA/) DRMANAC R T.

XX Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;
 PI Liu C, Drmanac RT;
 PI
 XX WPI; 2003-829799/77.
 DR
 XX Novel isolated human secreted cadherin-like polypeptide useful for
 PT treating diseases such as cancers, osteopetrosis, Paget's disease,
 PT osteomalacia, hyperostosis, osteopetrosis.
 PT

XX Claim 11; SEQ ID NO 7; 63pp; English.

XX This invention relates to a novel isolated human secreted cadherin-like
 CC protein and the DNA sequence which encodes it. Cadherins are a family of
 CC transmembrane proteins which share a common cadherin domain in their
 CC extracellular region. The extracellular portion mediates homotypic cell-
 CC cell adhesion that is calcium dependent. Modulators of the protein of the
 CC invention may have cytostatic or osteopathic activity. The invention may
 CC allow development of therapeutics useful for the treatment of diseases
 CC such as cancers, osteopetrosis, Paget's disease, osteomalacia,
 CC hyperostosis and osteopetrosis. The protein and DNA sequence of the

CC invention may also be useful as markers for prognosis of metastatic
CC tumours. The present sequence is that of the mature human secreted
CC cadherin-like protein which was used during the exemplification of the
CC invention.
XX
SQ Sequence 620 AA;
Query Match 100.0%; Score 180; DB 7; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LRTRRSWWVWVNFVIEEYAGPEPVLIGKLSHD 33
Db 23 LRTRRSWWVWVNFVIEEYAGPEPVLIGKLSHD 55
RESULT 5
ADD29445
ID ADD29445 standard; protein, 636 AA.
XX
XX ADD29445;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human cadherin-like protein amino acid sequence.
XX
XX cadherin-like protein; transmembrane protein; cadherin domain;
XX homotypic cell adhesion; cytosolic; osteopathic; cancer;
XX osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
XX metastatic tumour; human.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..16
XX FT /label= Signal_peptide
XX FT 17..636
XX FT Protein /label= Mature_human_cadherin-like_protein
XX
XX US2003144491-A1.
XX
XX 31-JUL-2003.
XX
XX 16-FEB-2001; 2001US-0078051.
XX
XX 03-FEB-2000; 2000US-00496914.
XX 27-APR-2000; 2000US-00560875.
XX
XX (GODB/) GODBOLE S D.
XX (KUOC/) KUO C.
XX (ARTE/) ARTERBURN M C.
XX (YEUN/) YEUNG G.
XX (PALE/) PALENCIA S.
XX (TANG/) TANG Y T.
XX (LIUC/) LIU C.
XX (DEMA/) DRMANAC R T.
XX
XX Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;
XX Liu C, Drmanac RT;
XX
XX WPI: 2003-828799/77.
XX DR N-PSDB: ADD29461, ADD29446.
XX
XX Novel isolated human secreted cadherin-like polypeptide useful for
XX treating diseases such as cancers, osteoporosis, Paget's disease,
XX osteomalacia, hyperostosis, osteopetrosis.
XX
XX Claim 11; SEQ ID NO 4; 636p; English.
XX
XX This invention relates to a novel isolated human secreted cadherin-like
XX protein and the DNA sequence which encodes it. Cadherins are a family of
XX transmembrane proteins which share a common cadherin domain in their
XX extracellular region. The extracellular portion mediates homotypic cell-

CC cell adhesion that is calcium dependent. Modulators of the protein of the
CC invention may have cytostatic or osteoprotic activity. The invention may
CC allow development of therapeutic useful for the treatment of diseases
CC such as cancers, osteoporosis, Paget's disease, osteomalacia,
CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
CC invention may also be useful as markers for prognosis of metastatic
CC tumours. The present sequence is that of the human secreted cadherin-like
CC protein of the invention.
XX
SQ Sequence 636 AA;
Query Match 100.0%; Score 180; DB 7; Length 636;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LRTRRSWWVWVNFVIEEYAGPEPVLIGKLSHD 33
Db 39 LRTRRSWWVWVNFVIEEYAGPEPVLIGKLSHD 71
RESULT 6
ABB53296
ID ABB53296 standard; protein, 781 AA.
XX
XX ABB53296;
XX
XX 12-FEB-2002 (first entry)
XX
XX Human polypeptide #36.
XX
XX Human; nocotropic; neuroprotective; anticonvulsant; antidepressant;
XX neuroleptic; tranquiliser; antiarrhythmic; cardiant; antiasthmatic;
XX antiinflammatory; antihypertensive; hepatotropic; vitruide; antidiabetic;
XX nephrotropic; anorectic; cytosolic; vaccine; neurological disease;
XX cardiovascular disease; respiratory disease; liver disease;
XX renal disease; skeletal muscle disease; gastrointestinal disease;
XX placental disease; testicular cancer; male fertility; pancreatic disease.
XX
XX Homo sapiens.
XX
XX WO200181363-A1.
XX
XX 01-NOV-2001.
XX
XX 26-APR-2001; 2001WO-US013360.
XX
XX 27-APR-2000; 2000US-0199963P.
XX 11-MAY-2000; 2000US-0203336P.
XX 25-MAY-2000; 2000US-0207087P.
XX 26-MAY-2000; 2000US-0207546P.
XX
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX
XX Agarwal P, Murdock PR, Rizvi SK, Smith RF, Xiang Z, Kabnick KS;
XX Lai Y, Xie Q;
XX
XX WPI: 2002-041392/05.
XX DR N-PSDB: ABA90361.
XX
XX Novel polypeptides and polynucleotides useful as a vaccine for preventing
XX disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesias.
XX
XX Claim 1; Page 108-109; 116pp; English.
XX
XX The invention relates to an isolated polypeptide comprising a 277, 480,
XX 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 886, 1026,
XX 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,
XX 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
XX given in the specification. The polypeptides, modulators of the
XX polypeptides and antibodies against the polypeptides are useful for
XX treating diseases such as neurological and psychiatric diseases including

```
CC Alzheimer's, parasupranuclear palsy, Huntington's disease, myotonic
CC dystrophy, anorexia and depression, cardiovascular diseases including
CC congestive heart failure, Hodgkin's disease and myocardial infarction;
CC respiratory diseases including asthma, chronic obstructive pulmonary
CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
CC diseases including hypercholesterolaemia, cirrhosis, viral and nonviral
CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
CC renal disease including renal failure, acute tubular necrosis and
CC glomerulonephritis; skeletal muscle diseases including Eulenburg's
CC disease, hypoglycaemia and obesity; gastrointestinal diseases including
CC myotonia congenita and intestinal obstruction; lymph diseases including
CC lymphogranuloma; diseases of placenta including choriocarcinoma; diseases
CC of testes including testicular cancer, male reproductive diseases
CC including low testosterone and male infertility; and disease of pancreas
CC including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The
CC present sequence is a polypeptide of the invention
CC
XX Sequence 781 AA:
SQ
Query Match 100.0%; Score 180; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-19;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LRLTRRSWVWVNFVIEEYAGPEPVLIQKLHSD 33
DB 39 LRLTRRSWVWVNFVIEEYAGPEPVLIQKLHSD 71
RESULT 7
ID AAM48736 standard; protein; 781 AA.
XX AAM48736;
AC
XX 28-MAR-2002 (first entry)
DT
XX
DE Human cadherin family member 57805 protein SEQ ID NO 2.
XX
KW Human; cadherin 57805; osteopathic; hepatotropic; antibacterial;
KW antidiabetic; neuroprotective; antiarthritic; antitumoural;
KW dermatological; immunosuppressive; antiinflammatory; antiproliferative;
KW antiaesthetic; antiallergic; antileptotic; haemostatic; antipruritic;
KW antihypertensive; antihypertensive; antihypertensive; antihypertensive;
KW anorectic; immunomodulatory; vasotropic; virucide; cytostatic; liver;
KW thrombolytic; analgesic; anabolic; immune disorder; cardiovascular;
KW vital; pain; metabolism; osteoporosis; diabetes mellitus; arthritis;
KW osteoarthritis; multiple sclerosis; Crohn's disease; asthma; allergy;
KW thrombus; inflammation; infection; ischaemia; irritable bowel syndrome;
KW gene therapy.
XX
OS Homo sapiens.
XX
XX WO200190145-A2.
XX
XX 29-NOV-2001.
XX
XX 18-MAY-2001; 2001WO-US016013.
XX
XX 19-MAY-2000; 2000US-0205674P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Curtis RAJ;
XX
XX WPI; 2002-083082/11.
XX
XX N-P8DB; ABA96406; ABA96407.
XX
XX New human cadherin family protein and polynucleotides, useful for
XX diagnosing and treating disorders e.g. obstructive jaundice, multiple
XX sclerosis, encephalomyelitis and atherosclerosis and to identify
XX modulators of therapeutic use.
XX
PS Claim 9; Page 105; 11pp; English.
```

```
XX The invention relates to human cadherin family polypeptide designated
CC 57805 with osteopathic, hepatotropic, antibacterial, antidiabetic,
CC neuroprotective, antiarthritic, antitumoural, dermatological,
CC immunosuppressive, antiinflammatory, antiproliferative, antisthmatic,
CC antiallergic, antileptotic, haemostatic, antipruritic, antihypertensive,
CC antihypertensive, antihypertensive, antihypertensive, anorectic,
CC immunomodulatory, vasotropic, virucide, cytostatic, thrombolytic,
CC analgesic and anabolic activity. The 57805 molecule are useful for
CC diagnosing and treating disorders which include disorders associated with
CC bone metabolism, immune disorders, cardiovascular disorders, liver
CC disorders, viral diseases, pain or metabolic disorders. Especially bone
CC metabolism including osteoporosis, rickets, osteosclerosis, cirrhosis;
CC immune disorders including autoimmune disease including diabetes mellitus
CC arthritis, including rheumatoid arthritis and osteoarthritis, multiple
CC sclerosis, systemic lupus, dermatitis, psoriasis, Crohn's disease,
CC asthma, thrombocytopenia, Graves' disease, graft-versus-host disease,
CC allergy; cardiovascular disorders, thrombus, hypertension,
CC atherosclerosis, arrhythmias and cardiomyopathy; liver disorders,
CC glycogen storage disease, vascular disorders, chronic heart failure,
CC portal vein thrombosis; viral diseases; metabolic or pain disorders
CC include obesity, anorexia nervosa and diabetes, inflammation, infection
CC and ischaemia, irritable bowel syndrome. The polynucleotides are also
CC useful in gene therapy
CC
XX Sequence 781 AA:
SQ
Query Match 100.0%; Score 180; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-19;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LRLTRRSWVWVNFVIEEYAGPEPVLIQKLHSD 33
DB 39 LRLTRRSWVWVNFVIEEYAGPEPVLIQKLHSD 71
RESULT 8
ID ABG34078 standard; protein; 781 AA.
XX ABG34078;
AC
XX 15-JUL-2002 (first entry)
DT
XX
DE Human Pro peptid 49.
XX
KW Human; PRO; secreted protein; transmembrane protein; genetic disorder;
KW tumour; cancer.
XX
XX Homo sapiens.
XX
XX WO200224888-A2.
XX
XX 28-MAR-2002.
XX
XX 29-AUG-2001; 2001WO-US027099.
XX
XX 01-SEP-2000; 2000US-0229896P.
XX
XX 05-SEP-2000; 2000US-0230621P.
XX
XX 22-SEP-2000; 2000US-023547P.
XX
XX 10-NOV-2000; 2000WO-US03087P.
XX
XX 12-JAN-2001; 2001US-0261878P.
XX
XX 16-JAN-2001; 2001US-0261910P.
XX
XX 16-JAN-2001; 2001US-0261939P.
XX
XX 16-JAN-2001; 2001US-0262150P.
XX
XX 25-JAN-2001; 2001US-0264395P.
XX
XX 02-FEB-2001; 2001US-0266421P.
XX
XX 09-FEB-2001; 2001US-0267623P.
XX
XX 28-FEB-2001; 2001WO-US006520.
XX
XX 09-MAR-2001; 2001US-0274399P.
XX
XX 03-APR-2001; 2001US-0280982P.
XX
XX 04-APR-2001; 2001US-0282129P.
XX
XX 04-APR-2001; 2001US-0282199P.
```

PR 09-MAY-2001; 2001US-0290589P.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
XX (GETH) GENENTECH INC.
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z,
PI Fong S;
XX WPI; 2002-362426/39.
XX N-PSDB; ABR70009.
XX
XX New PRO polypeptides and polynucleotides encoding the polypeptides,
XX PT useful in gene therapy, chromosome identification, tissue typing, or for
XX genetic analysis of individuals with genetic disorders.
XX
XX Claim 11, Fig 98, 218pp: English.
XX
XX This invention relates to the cDNA and protein sequences of novel
XX secreted and transmembrane polypeptides PRO polypeptides. The invention
XX also comprises a method for producing the proteins of the invention by
XX recombinant means and antibodies specific for the protein of the
XX invention. The antibody may be used for detecting the PRO proteins of the
XX invention and may be used to modify their activity. Polynucleotides may
XX be used as hybridisation probes for a cDNA library to isolate the full-
XX length PRO cDNA or to isolate other cDNAs, to construct hybridisation
XX probes for mapping the gene which encodes that PRO and for genetic
XX analysis of individuals with genetic disorders, in assays to identify
XX other proteins or molecules involved in binding reaction, to generate
XX transgenic animals or knock-out animals which in turn are useful in the
XX development and screening of therapeutically useful reagents, for
XX chromosome identification, and tissue typing. The PRO polypeptides are
XX useful in gene therapy, and as molecular weight markers for protein
XX electrophoresis purposes. The sequences may also be used to detect
XX overexpression on PRO polypeptides in cancerous tumours and for screening
XX for differentially expressed genes using microarray technology. The
XX present sequence represents a human PRO protein of the invention
XX
XX Sequence 781 AA:
SQ
Query Match 100.0%; Score 180; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-19;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLRTSRWVWVQPFVIEYAGPEVLLIGKLSHD 33
Db 39 LLRTSRWVWVQPFVIEYAGPEVLLIGKLSHD 71
RESULT 9
AD116604
ID AD116604 standard; protein; 781 AA.
XX
XX AD116604;
AC
XX
XX 15-APR-2004 (first entry)
DE Human NOXV protein to treat human pathological conditions SeqID140.
XX
XX human; NOXV; cardiomyopathy; atherosclerosis; cancer; diabetes;
XX inflammation; autoimmune disorder; allergy; blood disorder;
XX acquired immunodeficiency syndrome; AIDS; obesity; asthma;
XX immunoglobulin (Ig) A nephropathy; cirrhosis; arthritis;
XX Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
XX cyclostatic; cardiac; antiinflammatory; immunosuppressive; antiallergic;
XX hamostatic; anti-HIV; antidiabetic; antiarteriosclerotic; antiparasitic;
XX antitumour; nephrotropic; antitachycardic; hepatotropic;
XX neuroprotective; nootropic; antibacterial; virucide; antiparasitic;
XX relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
XX

XX chromosome mapping; tissue typing; pharmacogenomic; SNP;
XX single nucleotide polymorphism.
XX
XX Homo sapiens.
XX
XX WO20026649-A2.
XX
XX 06-SEP-2002.
XX
XX 31-JAN-2002; 2002WO-US002785.
XX
XX
XX 31-JAN-2001; 2001US-0265395P.
XX 31-JAN-2001; 2001US-0265412P.
XX 31-JAN-2001; 2001US-0265514P.
XX 31-JAN-2001; 2001US-0265517P.
XX 02-FEB-2001; 2001US-0266406P.
XX 05-FEB-2001; 2001US-0266767P.
XX 07-FEB-2001; 2001US-0266975P.
XX 07-FEB-2001; 2001US-0267057P.
XX 08-FEB-2001; 2001US-0267459P.
XX 09-FEB-2001; 2001US-0267823P.
XX 15-FEB-2001; 2001US-0268974P.
XX 26-FEB-2001; 2001US-0271664P.
XX 27-FEB-2001; 2001US-0271839P.
XX 27-FEB-2001; 2001US-0271855P.
XX 02-MAR-2001; 2001US-0272788P.
XX 02-MAR-2001; 2001US-0273046P.
XX 14-MAR-2001; 2001US-0275925P.
XX 14-MAR-2001; 2001US-0275947P.
XX 14-MAR-2001; 2001US-0275950P.
XX 14-MAR-2001; 2001US-0275989P.
XX 15-MAR-2001; 2001US-0276448P.
XX 15-MAR-2001; 2001US-0276450P.
XX 16-MAR-2001; 2001US-0276397P.
XX 16-MAR-2001; 2001US-0276768P.
XX 20-MAR-2001; 2001US-0278652P.
XX 26-MAR-2001; 2001US-0278775P.
XX 26-MAR-2001; 2001US-0278778P.
XX 29-MAR-2001; 2001US-0279882P.
XX 29-MAR-2001; 2001US-0279884P.
XX 30-MAR-2001; 2001US-0280147P.
XX 11-APR-2001; 2001US-0282929P.
XX 11-APR-2001; 2001US-0283083P.
XX 20-APR-2001; 2001US-0285133P.
XX 23-APR-2001; 2001US-0285749P.
XX 03-MAY-2001; 2001US-0288327P.
XX 03-MAY-2001; 2001US-0288504P.
XX 29-MAY-2001; 2001US-0294047P.
XX 30-MAY-2001; 2001US-0294473P.
XX 08-JUN-2001; 2001US-0296464P.
XX 18-JUN-2001; 2001US-0298959P.
XX 19-JUN-2001; 2001US-0299324P.
XX 13-AUG-2001; 2001US-0312020P.
XX 16-AUG-2001; 2001US-0312889P.
XX 16-AUG-2001; 2001US-0312908P.
XX 21-AUG-2001; 2001US-0313390P.
XX 28-AUG-2001; 2001US-0315470P.
XX 31-AUG-2001; 2001US-0316447P.
XX 07-SEP-2001; 2001US-0318115P.
XX 07-SEP-2001; 2001US-0318118P.
XX 12-SEP-2001; 2001US-0318740P.
XX 19-SEP-2001; 2001US-0323379P.
XX 18-OCT-2001; 2001US-0330245P.
XX 18-OCT-2001; 2001US-0330308P.
XX 14-NOV-2001; 2001US-0332701P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Tchernav VT, Snytek KA, Zernusen BD, Parturajan M, Shinkets RA;
XX Li H, Gargoli EA, Padigar M, Anderson DW, Rastelli L, Miller CE;
XX Gerlach VL, Taupier R, Gusev VY, Colman SD, Wolenc AR, Pena CE;
XX Furtak K, Grosse WM, Alsbrook JP, Lepley DM, Rieger DK, Burgess CE;
XX

DR WPI; 2002-706998/76.
DR N-PSDB; AD116603.
XX
PT New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
PS Claim 1; SEQ ID NO 140; 1498bp; English.
XX
CC This invention relates to a novel nucleic acid, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOVX polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC cytoskeletal, cardiac, antiinflammatory, immunosuppressive, antiallergic,
CC hemostatic, anti-HIV, antidiabetic, antiatherosclerotic, anorectic,
CC antiaesthetic, nephroprotective, antiairway, antiparasitic,
CC neuroprotective, neurotropic, antibacterial, virucide, antiparasitic,
CC relaxant and anticoagulant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a human NOVX protein of the
CC invention.
XX
XX Sequence 781 AA;
SQ
Query Match 100.0%; Score 180; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-19;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LLRTSRGWNQFVIEYAGPEVPLIGKLHSD 33
Db 39 LLRTSRGWNQFVIEYAGPEVPLIGKLHSD 71
RESULT 10
AD116606
ID AD116606 standard; protein; 781 AA.
XX
AC AD116606;
XX
DT 15-APR-2004 (first entry)
XX
DS Human NOVX protein to treat human pathological conditions SeqID142.
XX
KW human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
KW inflammation; autoimmune disorder; allergy; blood disorder;
KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
KW Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
KW cytoskeletal; cardiac; antiinflammatory; immunosuppressive; antiallergic;
KW haemostatic; anti-HIV; antidiabetic; antiatherosclerotic; anorectic;
KW antiaesthetic; nephroprotective; antiairway; hepatotropic;
KW neuroprotective; neurotropic; antibacterial; virucide; antiparasitic;
KW relaxant; anticoagulant; neurogenesis; wound healing; angiogenesis;
KW chromosome mapping; tissue typing; pharmacogenomic.
XX
XX Homo sapiens.
OS
XX
XX WO200268649-A2.

XX
PD 06-SEP-2002.
XX
XX 31-JAN-2002; 2002W0-US002785.
XX
XX 31-JAN-2001; 2001US-0265395P.
XX 31-JAN-2001; 2001US-0265412P.
XX 31-JAN-2001; 2001US-0265514P.
XX 31-JAN-2001; 2001US-0265517P.
XX 02-FEB-2001; 2001US-0266406P.
XX 03-FEB-2001; 2001US-0266767P.
XX 07-FEB-2001; 2001US-0266975P.
XX 07-FEB-2001; 2001US-0267057P.
XX 08-FEB-2001; 2001US-0267459P.
XX 09-FEB-2001; 2001US-0267823P.
XX 15-FEB-2001; 2001US-0268974P.
XX 26-FEB-2001; 2001US-0271664P.
XX 27-FEB-2001; 2001US-0271839P.
XX 27-FEB-2001; 2001US-0271855P.
XX 02-MAR-2001; 2001US-0272788P.
XX 02-MAR-2001; 2001US-0273046P.
XX 14-MAR-2001; 2001US-0275925P.
XX 14-MAR-2001; 2001US-0275947P.
XX 14-MAR-2001; 2001US-0275950P.
XX 14-MAR-2001; 2001US-0275989P.
XX 15-MAR-2001; 2001US-0276448P.
XX 15-MAR-2001; 2001US-0276450P.
XX 15-MAR-2001; 2001US-0276397P.
XX 15-MAR-2001; 2001US-0276768P.
XX 20-MAR-2001; 2001US-0278652P.
XX 26-MAR-2001; 2001US-0278775P.
XX 26-MAR-2001; 2001US-0278778P.
XX 29-MAR-2001; 2001US-0279882P.
XX 29-MAR-2001; 2001US-0279884P.
XX 30-MAR-2001; 2001US-0280147P.
XX 11-APR-2001; 2001US-0280292P.
XX 11-APR-2001; 2001US-0280383P.
XX 20-APR-2001; 2001US-0285113P.
XX 23-APR-2001; 2001US-0285749P.
XX 03-MAY-2001; 2001US-0288327P.
XX 03-MAY-2001; 2001US-0288504P.
XX 29-MAY-2001; 2001US-0294047P.
XX 30-MAY-2001; 2001US-0294473P.
XX 08-JUN-2001; 2001US-0296644P.
XX 18-JUN-2001; 2001US-0298959P.
XX 19-JUN-2001; 2001US-0299324P.
XX 13-AUG-2001; 2001US-0312020P.
XX 16-AUG-2001; 2001US-0312889P.
XX 16-AUG-2001; 2001US-0312908P.
XX 21-AUG-2001; 2001US-0313390P.
XX 28-AUG-2001; 2001US-0315470P.
XX 31-AUG-2001; 2001US-0315447P.
XX 07-SEP-2001; 2001US-0318115P.
XX 07-SEP-2001; 2001US-0318118P.
XX 12-SEP-2001; 2001US-0318740P.
XX 19-SEP-2001; 2001US-0323379P.
XX 18-OCT-2001; 2001US-0330245P.
XX 18-OCT-2001; 2001US-0330308P.
XX 14-NOV-2001; 2001US-0332701P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Tcheney VT, Spytek KA, Zethusen BD, Patrujan M, Shimkets RA;
XX Li L, Gangoli EA, Padigaru M, Anderson DM, Rastelli L, Miller CE;
XX Gertlach VL, Tauber RJ, Gusev VY, Coleman SD, Wolenc AR, Pena CBA;
XX Furrick K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
XX
XX WPI; 2002-706998/76.
XX N-PSDB; AD116605.
XX
XX New NOVX polypeptides and nucleic acids, useful for preventing or
XX treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
XX atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or

PT pharmacogenomics.

XX Claim 1; SEQ ID NO 142; 1498bp; English.

CC This invention relates to a novel nucleic acid, and encoded polypeptides

CC thereof, which have properties related to the stimulation of biochemical

CC or physiological responses in a cell, tissue, organ or organism.

CC Specifically, it refers to the use of biologically active fragments for

CC diagnostic and prognostic assays and furthermore in the treatment of

CC diverse pathological conditions. The present invention describes novel

CC human and murine NOVX proteins, as well as methods to modulate their

CC expression using antisense oligos, ribozymes and peptide nucleic acids.

CC The NOVX polypeptides, polynucleotides and antibodies are useful in

CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,

CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in

CC treating or preventing diseases such as inflammation, autoimmune

CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome

CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,

CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy

CC and epilepsy. Accordingly, these molecules have many activities including

CC haemostatic, cardiac, anti-inflammatory, immunosuppressive, antiallergic,

CC antiasthmatic, antidiabetic, antihypertensive, anorectic,

CC neuroprotective, neurotropic, antibacterial, virucide, antiparasitic,

CC relaxant and anticonvulsant. In addition, they are useful in screening

CC assays to identify small molecules that modulate or inhibit, for example,

CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also

CC used as in chromosome mapping, tissue typing, preventive medicine and

CC pharmacogenomics. This polypeptide is a human NOVX protein of the

CC invention.

XX

XX

XX Sequence 781 AA:

Query Match 100.0%; Score 180; DB 5; Length 781;

Best Local Similarity 100.0%; Pred. No. 1.5e-19;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTRTRSMWNQFFVIEYAGPEPVILGKLHSD 33

DB 39 LTRTRSMWNQFFVIEYAGPEPVILGKLHSD 71

RESULT 11

ABR40114

ID ABR40114 standard; protein; 781 AA.

XX

AC ABR40114;

DT 04-JUL-2003 (first entry)

XX

DE Human cell adhesion and extracellular matrix protein, CADECM-11.

XX

KW Human; anti-HIV; anti-allergic; cerebroprotective; antiparkinsonian;

KW anticonvulsant; neurotropic; neuroprotective; immunosuppressive;

KW dermatological; anti-inflammatory; cytostatic; antiarteriosclerotic;

KW gene therapy; cell adhesion; extracellular matrix; CADECM;

KW immune system disorder; AIDS; allergy; neurological disorder; stroke;

KW Parkinson's disease; epilepsy; developmental disorder; Down's syndrome;

KW cerebral palsy; connective tissue disorder; systemic lupus erythematosus;

KW genetic disorder; Alport's syndrome; cell proliferative disorder; cancer;

KW atherosclerosis.

XX

OS Homo sapiens.

XX

PN WO2003027230-A2.

XX

PD 03-APR-2003.

XX

PF 02-AUG-2002; 2002WO-US024649.

XX

PR 03-AUG-2001; 2001US-0309964P.

PR 03-AUG-2001; 2001US-0310119P.

PR 17-AUG-2001; 2001US-0313091P.

PR 31-AUG-2001; 2001US-0316771P.

PR 07-SEP-2001; 2001US-0317896P.

PR 21-SEP-2001; 2001US-0324781P.

PR 05-OCT-2001; 2001US-0327606P.

PR 12-OCT-2001; 2001US-0328960P.

PR 09-NOV-2001; 2001US-0344471P.

PR 17-MAY-2002; 2002US-0381291P.

XX

XX (INCY-) INCYTE GENOMICS INC.

XX

PI Burford N, Warren BA, Dugan BM, Mason PM, Richardson TW, Yue H;

PI Forsythe J, Elliott VS, Griffin JA, Gorvad AE, Azimzai Y;

PI Kallik Da, Xu Y, Honchell CD, Baughn MR, Gietzen KT, Lee S;

PI Walla NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Rammumar U;

XX

XX WPI: 2003-354645/33.

DR N-PSDB; ACC000402.

DR

XX

XX

PS Claim 1; Page 192-194; 234pp; English.

XX

CC The present invention relates to novel human cell adhesion and

CC extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding

CC sequences (ACC000392-ACC00413 and ABR40104-ABR40125). The coding sequences

CC and proteins are useful in diagnosing, treating and preventing disorders

CC associated with aberrant expression of CADECM, such as immune system

CC disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,

CC Parkinson's disease or epilepsy), developmental disorders (e.g. Down's

CC syndrome or cerebral palsy), connective tissue disorders (e.g. systemic

CC lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell

CC proliferative disorders (e.g. cancer or atherosclerosis)

XX

XX Sequence 781 AA:

Query Match 100.0%; Score 180; DB 6; Length 781;

Best Local Similarity 100.0%; Pred. No. 1.5e-19;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTRTRSMWNQFFVIEYAGPEPVILGKLHSD 33

DB 39 LTRTRSMWNQFFVIEYAGPEPVILGKLHSD 71

RESULT 12

ADA01366

ID ADA01366 standard; protein; 781 AA.

XX

AC ADA01366;

DT 06-NOV-2003 (first entry)

XX

DE Human PRO polypeptide #49.

XX

KW Human; PRO; secreted polypeptide; transmembrane polypeptide;

KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;

KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;

KW microvascular endothelial cell; endothelial cell tube formation;

KW sports-related joint problem; articular cartilage defect; osteoarthritis;

KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.

XX

OS Homo sapiens.

XX

PN US2003068779-A1.

XX

PD 10-APR-2003.

XX

PF 16-SEP-2002; 2002US-00245107.

PR 09-MAY-2001; 2001US-0290589P.

PR 29- AUG-2001; 2001MO-US027099.
PT 18-JUL-2002; 2002US-00197942.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
XX WPI; 2003-625484/59.
DR N-PSDB; ADA01365.
XX
XX
PT Novel isolated PRO1113, PRO20080 or PRO21383 polypeptide useful for
PT stimulating proliferation of human microvascular endothelial cells, and
PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
PT cells.
XX
XX
XX Claim 11, Fig 98; 307pp; English.
XX
XX The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptides or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for inducing endothelial cell
CC tube formation and for treating sports-related joint problems, articular
CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
CC represents a human PRO polypeptide of the invention.
XX
XX
SQ Sequence 781 AA;
SQ
Query Match 100.0%; Score 180; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-19;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
CY 1 LRTFRSWVWNOFVIEEYAGDEPPLIGKTHSD 33
DB 39 LRTFRSWVWNOFVIEEYAGDEPPLIGKTHSD 71
RESULT 13
ADA43795
ADA43795 standard; protein; 781 AA.
XX
XX ADA43795;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX Human secreted/transmembrane polypeptide PRO34009.
DE
XX
XX Human; PRO; secreted protein; transmembrane protein;
KW endothelial cell tube formation; chondrocyte cell differentiation;
KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
KW liver tumour; cytoslatic; vaccine.
XX
XX Homo sapiens.
OS
XX
XX US2003064474-A1.
PN
XX 03-APR-2003.
PD

PF 16-SEP-2002; 2002US-00245859.
XX
XX 29-AUG-2001; 2001WO-US027099.
RR 18-JUL-2002; 2002US-00197942.
XX
PA (GETH) GENENTECH INC.
XX Baker KP, Raton DU, Filvaroff E, Goddard A, Grimaldi JC;
PI Guney AL, Smith V, Stephan JF, Watanabe CK, Wood WR, Zhang Z;
PI Fong S;
DR WPJ; 2003-605867/57.
XX N-PSSB; ADA43794.
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PR PRO2183, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.

Claim 11; Fig 98; 308pp; English.

The invention relates to an isolated secreted/transmembrane (PRO) polypeptide, having at least 80% sequence identity to a sequence selected from any one of the 57 amino acid sequences given in specification, or to a sequence encoded by a nucleic acid molecule selected from any one of the nucleic acids deposited under any of the ATCC accession numbers given in specification, or a sequence having at least 80% identity to PRO lacking its associated signal peptide, an extracellular domain of PRO with or without its associated signal peptide. Also included are vectors, transformed host cells, anti-PRO antibodies, the nucleic acids encoding PRO, PRO fusion proteins, inducing endothelial cell tube formation (by administering PRO287, PRO1560, PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20993 or PRO34274 polypeptide or its agonist) and an oligonucleotide probe derived from any one of the above nucleotide sequences. PRO6018 polypeptide is useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080 and PRO2183 polypeptides are useful for stimulating the proliferation of human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006 polypeptides are useful for inhibiting the proliferation of human microvascular endothelial cells. PRO polypeptides are useful for detecting the presence of tumour in a mammal, including tumours of lung, colon, breast, prostate, rectal, kidney and liver. PRO287, PRO1560, PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20993 and PRO34274 polypeptides are useful for inducing endothelial cell tube formation. PRO or the antibody are useful in the preparation of a medicament for treating a condition responsive to PRO polypeptide. The oligonucleotide probes are useful for isolating genomic and cDNA nucleotide sequences, for measuring or detecting the expression of an associated gene, and as antisense probes. PRO nucleic acid is useful as a hybridisation probe, in chromosome and gene mapping, in the generation of antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The present sequence represents a PRO protein.

Sequence 781 AA;

Query Match 100.0%; Score 180; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e+19;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 LLTRRSWMNQFEVIEYAGEPEVLIGKTHSD 33
DB 39 LLTRRSWMNQFEVIEYAGEPEVLIGKTHSD 71

RESULT 14
ADA43563
ID ADA43563 standard; protein; 781 AA.
XX
AC ADA43563;
XX
DT 20-NOV-2003 (first entry)
XX

DE Human secreted/transmembrane polypeptide PRO34009.
 XX
 XX Human; PRO, secreted protein; transmembrane protein;
 KW endothelial cell tube formation; chondrocyte cell differentiation;
 KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KW liver tumour; cytoskeletal; vaccine.
 XX
 OS Homo sapiens.
 XX
 XX US2003073196-A1.
 PN
 XX
 XX 17-APR-2003.
 PD
 XX
 XX 18-SEP-2002; 2002US-00246210.
 PF
 XX
 XX 04-APR-2001; 2001US-0282199P.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX
 XX (GENENTECH INC.
 PA
 XX Baker KP, Baton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S,
 PI
 XX WPI; 2003-743814/70.
 DR N-PSDB; ADA43562.
 DR
 PT New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
 PT PRO21383 useful for stimulating the proliferation or differentiation of
 PT chondrocyte cells and detecting the presence of a tumor in a mammal.
 PT
 XX
 XX Claim 11; Fig 98; 307pp; English.
 PS
 XX
 XX The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acids deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide. Also included are vectors,
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO189, PRO499, PRO308, PRO600,
 CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
 CC and PRO21383 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6071, PRO4987 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumour in a mammal, including tumours of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence represents a PRO protein.
 CC
 XX Sequence 781 AA.

QY 1 LKTRRSWMWNOFYIEEYAGPEVLIGKLSHD 33
 DB 39 LKTRRSWMWNOFYIEEYAGPEVLIGKLSHD 71
 RESULT 15
 ADA01238
 ID ADA01238 strandand; protein; 781 AA.
 XX
 AC ADA01238;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human PRO polypeptide #49.
 XX
 KW Human; PRO, secreted polypeptide; transmembrane polypeptide;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
 KW cancer; lung; colon; breast; prostate; rectum; kidney; liver;
 KW microvascular endothelial cell; endothelial cell tube formation.
 XX
 OS Homo sapiens.
 XX
 XX US2003068782-A1.
 PN
 XX 10-APR-2003.
 PD
 XX
 XX 16-SEP-2002; 2002US-00245851.
 PF
 XX
 XX 27-APR-1999; 99US-0131271P.
 PR 29-OCT-1999; 99US-0162506P.
 PR 02-DEC-1999; 99WO-US028551.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX
 XX (GENENTECH INC.
 PA
 XX Baker KP, Baton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S,
 PI
 XX WPI; 2003-625487/59.
 DR N-PSDB; ADA01237.
 DR
 PT Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
 PT preparation of a medicament for treating a condition responsive to PRO
 PT polypeptide, and as therapeutic agents e.g. vaccines.
 PT
 XX
 XX Claim 11; Fig 98; 308pp; English.
 PS
 XX
 XX The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
 CC prostate, rectal, kidney and liver tumours). The polynucleotides are
 CC useful in molecular biology, including uses as hybridisation probes, in
 CC chromosome and gene mapping, in generating antisense RNA and DNA and in
 CC gene therapy. The polynucleotides may also be used in preparing PRO
 CC transgenic animals or knock-out animals which are useful either
 CC development and screening of therapeutically useful reagents. The PRO
 CC polypeptides or antibodies are used in preparing a medicament for
 CC treating a condition responsive to the polypeptides or antibodies, such
 CC as tumours, for stimulating and inhibiting proliferation of human
 CC microvascular endothelial cells and for inducing endothelial cell tube
 CC formation. This sequence represents a human PRO polypeptide of the
 CC invention.
 CC
 XX Sequence 781 AA.

Query Match 100.0%; Score 180; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 1,5e-19;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Wed Dec 8 11:46:16 2004

us-09-788-051-10.rag

Page 11

Query Match 100.0%; Score 180; DB 6; Length 781;
Best Local Similarity 100.0%; Pred.No.1.5e-19;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKTRRSWVWNOFVIEEYAGPEPVLIGKLHSD 33
Db 39 LKTRRSWVWNOFVIEEYAGPEPVLIGKLHSD 71

Search completed: December 8, 2004, 10:13:05
Job time : 13.6558 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 10:13:18 ; Search time 33.7208 Seconds
(without alignments)

349,544 Million cell updates/sec

Title: US-09-788-051-10

Perfect score: 180
Sequence: 1 LRTRRSWWNOFVIEYAGPEPVLIGKLSHD 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/prodata/1/pubppaa/PCIT_NEW_PUB.pep:*
- 3: /cgn2_6/prodata/1/pubppaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/prodata/1/pubppaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/prodata/1/pubppaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/prodata/1/pubppaa/PCITUS_PUBCOMB.pep:*
- 7: /cgn2_6/prodata/1/pubppaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/prodata/1/pubppaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/prodata/1/pubppaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/prodata/1/pubppaa/US10C_PUBCOMB.pep:*
- 15: /cgn2_6/prodata/1/pubppaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/prodata/1/pubppaa/US10C_PUBCOMB.pep:*
- 17: /cgn2_6/prodata/1/pubppaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/prodata/1/pubppaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/prodata/1/pubppaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/prodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	180	100.0	33	US-09-788-051-10	Sequence 10, Appl
2	180	100.0	493	US-10-072-012-482	Sequence 482, App
3	180	100.0	607	US-10-258-951-74	Sequence 74, Appl
4	180	100.0	620	US-09-788-051-7	Sequence 7, Appl
5	180	100.0	636	US-09-788-051-4	Sequence 4, Appl
6	180	100.0	781	US-09-860-868-2	Sequence 2, Appl
7	180	100.0	781	US-10-245-752-98	Sequence 98, Appl
8	180	100.0	781	US-10-245-859-98	Sequence 98, Appl
9	180	100.0	781	US-10-245-103-98	Sequence 98, Appl
10	180	100.0	781	US-10-245-107-98	Sequence 98, Appl
11	180	100.0	781	US-10-245-143-98	Sequence 98, Appl
12	180	100.0	781	US-10-245-771-98	Sequence 98, Appl
13	180	100.0	781	US-10-245-851-98	Sequence 98, Appl

14	180	100.0	781	US-10-245-883-98	Sequence 98, Appl
15	180	100.0	781	US-10-237-535-98	Sequence 98, Appl
16	180	100.0	781	US-10-238-183-98	Sequence 98, Appl
17	180	100.0	781	US-10-238-283-98	Sequence 98, Appl
18	180	100.0	781	US-10-238-370-98	Sequence 98, Appl
19	180	100.0	781	US-10-245-055-98	Sequence 98, Appl
20	180	100.0	781	US-10-245-147-98	Sequence 98, Appl
21	180	100.0	781	US-10-245-730-98	Sequence 98, Appl
22	180	100.0	781	US-10-245-739-98	Sequence 98, Appl
23	180	100.0	781	US-10-246-210-98	Sequence 98, Appl
24	180	100.0	781	US-10-239-196-98	Sequence 98, Appl
25	180	100.0	781	US-10-243-024-98	Sequence 98, Appl
26	180	100.0	781	US-10-243-809-98	Sequence 98, Appl
27	180	100.0	781	US-10-245-621-98	Sequence 98, Appl
28	180	100.0	781	US-10-245-880-98	Sequence 98, Appl
29	180	100.0	781	US-10-245-033-98	Sequence 98, Appl
30	180	100.0	781	US-10-243-095-98	Sequence 98, Appl
31	180	100.0	781	US-10-245-185-98	Sequence 98, Appl
32	180	100.0	781	US-10-245-427-98	Sequence 98, Appl
33	180	100.0	781	US-10-245-473-98	Sequence 98, Appl
34	180	100.0	781	US-10-245-770-98	Sequence 98, Appl
35	180	100.0	781	US-10-245-877-98	Sequence 98, Appl
36	180	100.0	781	US-10-246-976-98	Sequence 98, Appl
37	180	100.0	781	US-10-243-320-98	Sequence 98, Appl
38	180	100.0	781	US-10-162-435-13	Sequence 13, Appl
39	180	100.0	781	US-10-242-743-98	Sequence 98, Appl
40	180	100.0	781	US-10-242-845-98	Sequence 98, Appl
41	180	100.0	781	US-10-237-636-98	Sequence 98, Appl
42	180	100.0	781	US-10-238-325-98	Sequence 98, Appl
43	180	100.0	781	US-10-238-446-98	Sequence 98, Appl
44	180	100.0	781	US-10-238-411-98	Sequence 98, Appl
45	180	100.0	781	US-10-243-124-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-09-788-051-10
Sequence 10, Application US/09788051
Publication No. US20030144491A1
GENERAL INFORMATION:
APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chaiyuan
APPLICANT: Arterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Drmanac, Radcoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES A
FILE REFERENCE: HYS-39
CURRENT APPLICATION NUMBER: US/09/788,051
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10
LENGTH: 33
TYPE: PR
ORGANISM: Homo sapiens
US-09-788-051-10
Query Match 100.0% Score 180 DB 10 Length 33
Best Local Similarity 100.0% Pred. No. 9.86-15
Matches 33 Conservative 0 Mismatches 0 Indels 0 Gaps 0
1 LRTRRSWWNOFVIEYAGPEPVLIGKLSHD 33
|||||

Db 1 LLRTSRWVWVQFVIEVYAGPEPVILGKLHSD 33

RESULT 2

US-10-072-012-482

; Sequence 482, Application US/10072012
; Publication No. US20040033493A1

GENERAL INFORMATION:

; APPLICANT: Tchervnev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zernusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangoli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Futak, Katarzyna
; APPLICANT: Grose, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 482
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-482

Query Match 100.0%; Score 180; DB 15; Length 493;
Best Local Similarity 100.0%; Pred. No. 1,7e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLRTSRWVWVQFVIEVYAGPEPVILGKLHSD 33
Db 39 LLRTSRWVWVQFVIEVYAGPEPVILGKLHSD 71

RESULT 3

US-10-258-951-74

; Sequence 74, Application US/10258951
; Publication No. US20040033504A1

GENERAL INFORMATION:

; APPLICANT: Agarwal, Parraj
; APPLICANT: Mardock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kahnick, Karen
; APPLICANT: Lal, Ying-Ta
; APPLICANT: Xie, Qing
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50025
; CURRENT APPLICATION NUMBER: US/10/258,951
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/13360
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/199,963
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/203,336
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 60/207,087
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/207,546
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-951-74

Query Match 100.0%; Score 180; DB 15; Length 607;
Best Local Similarity 100.0%; Pred. No. 2.1e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLRTSRWVWVQFVIEVYAGPEPVILGKLHSD 33
Db 39 LLRTSRWVWVQFVIEVYAGPEPVILGKLHSD 71

RESULT 4

US-09-788-051-7

; Sequence 7, Application US/09788051
; Publication No. US20030144491A1

GENERAL INFORMATION:

; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaeyun
; APPLICANT: Atteburun, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dimanac, Radoje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AND
; FILE REFERENCE: HVS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-7

Query Match 100.0%; Score 180; DB 10; Length 620;
Best Local Similarity 100.0%; Pred. No. 2.2e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLRTSRWVWNOFVIEEYAGPEPVLIGKLHSD 33
DB 23 LLRTSRWVWNOFVIEEYAGPEPVLIGKLHSD 55

RESULT 5
US-09-788-051-4
; Sequence 4, Application US/09788051
; Publication No. US2003014491A1
; GENERAL INFORMATION:

APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chiaoyun
APPLICANT: Arterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Dumanac, Radjoe T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AND
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: HYS-39
CURRENT APPLICATION NUMBER: US/09/788,051
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 636
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-4

Query Match 100.0%; Score 180; DB 10; Length 636;
Best Local Similarity 100.0%; Pred. No. 2.2e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLRTSRWVWNOFVIEEYAGPEPVLIGKLHSD 33
DB 39 LLRTSRWVWNOFVIEEYAGPEPVLIGKLHSD 71

RESULT 6
US-09-860-868-2
; Sequence 2, Application US/09860868
; Patent No. US20020076757A1
; GENERAL INFORMATION:

APPLICANT: Curtis, Rory A.J.
TITLE OF INVENTION: 57805, A NOVEL HUMAN CADHERIN FAMILY
FILE REFERENCE: 10448-050001
CURRENT FILING DATE: US/09/860,868
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 60/205,674
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-860-868-2

Query Match 100.0%; Score 180; DB 9; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.7e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLRTSRWVWNOFVIEEYAGPEPVLIGKLHSD 33
DB 39 LLRTSRWVWNOFVIEEYAGPEPVLIGKLHSD 71

RESULT 7
US-10-245-752-98
; Sequence 98, Application US/10245752
; Publication No. US20030064473A1
; GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C66
CURRENT APPLICATION NUMBER: US/10/245,752
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-752-98

Query Match 100.0%; Score 180; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.7e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLRTSRWVWNOFVIEEYAGPEPVLIGKLHSD 33
DB 39 LLRTSRWVWNOFVIEEYAGPEPVLIGKLHSD 71

RESULT 8
US-10-245-859-98
; Sequence 98, Application US/10245859
; Publication No. US20030064474A1
; GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen

PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-107-98

Query Match 100.0%; Score 180; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.7e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 LLRTSRWVWNOFFVIEEYAGPEPVILGKLHSD 33
Db 39 LLRTSRWVWNOFFVIEEYAGPEPVILGKLHSD 71

RESULT 11

US-10-245-143-98
Sequence 98, Application US/10245143
Publication No. US20030068780A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C98
CURRENT APPLICATION NUMBER: US/10/245,143
CURRENT FILING DATE: 2002-09-15
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-143-98

Query Match 100.0%; Score 180; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.7e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 LLRTSRWVWNOFFVIEEYAGPEPVILGKLHSD 33
Db 39 LLRTSRWVWNOFFVIEEYAGPEPVILGKLHSD 71

RESULT 12

US-10-245-771-98
Sequence 98, Application US/10245771
Publication No. US20030068781A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C98
CURRENT APPLICATION NUMBER: US/10/245,771
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-771-98

Query Match 100.0%; Score 180; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.7e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 LLRTSRWVWNOFFVIEEYAGPEPVILGKLHSD 33
Db 39 LLRTSRWVWNOFFVIEEYAGPEPVILGKLHSD 71

RESULT 13
US-10-245-851-98
Sequence 98, Application US/10245851
Publication No. US20030068782A1
GENERAL INFORMATION:

```

; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Wacande, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C93
; CURRENT APPLICATION NUMBER: US/10/245,851
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-851-98

Query Match      100.0%; Score 180; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.7e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLRTRSWVWVNFVIEYAGPEPVLIGKLHSD 33
Db 39 LLRTRSWVWVNFVIEYAGPEPVLIGKLHSD 71

RESULT 14
US-10-245-863-98
; Sequence 98, Application US/10245883
; Publication No. US20030068783A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Wacande, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
```

```

; FILE REFERENCE: P3630R1C70
; CURRENT APPLICATION NUMBER: US/10/245,883
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-883-98

Query Match      100.0%; Score 180; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.7e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLRTRSWVWVNFVIEYAGPEPVLIGKLHSD 33
Db 39 LLRTRSWVWVNFVIEYAGPEPVLIGKLHSD 71

RESULT 15
US-10-237-535-98
; Sequence 98, Application US/10237535
; Publication No. US20030073188A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Wacande, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C3
; CURRENT APPLICATION NUMBER: US/10/237,535
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
```


Wed Dec 8 11:46:17 2004

us-09-788-051-10.rapb

Page 7

;; PRIOR FILING DATE: 1998-05-22
;; PRIOR APPLICATION NUMBER: 60/087607
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/089801
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090689
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/091358
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/099803
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/106932
;; PRIOR FILING DATE: 1998-11-03
;; PRIOR APPLICATION NUMBER: 60/115554
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/119342
;; PRIOR FILING DATE: 1999-02-09
;; PRIOR APPLICATION NUMBER: 60/123957
;; PRIOR FILING DATE: 1999-03-12
;; PRIOR APPLICATION NUMBER: 60/123972
;; PRIOR FILING DATE: 1999-03-11
;; PRIOR APPLICATION NUMBER: 60/127372
;; PRIOR FILING DATE: 1999-04-01
;; PRIOR APPLICATION NUMBER: 60/131271
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/133459
;; PRIOR FILING DATE: 1999-05-11
;; PRIOR APPLICATION NUMBER: 60/135725
;; PRIOR FILING DATE: 1999-05-25
;; PRIOR APPLICATION NUMBER: 60/135729
;; PRIOR FILING DATE: 1999-05-25
;; PRIOR APPLICATION NUMBER: 60/135750
;; PRIOR FILING DATE: 1999-05-25
;; PRIOR APPLICATION NUMBER: 60/138385
;; PRIOR FILING DATE: 1999-06-09
;; PRIOR APPLICATION NUMBER: 60/140653
;; PRIOR FILING DATE: 1999-06-22
;; PRIOR APPLICATION NUMBER: 60/141037
;; PRIOR FILING DATE: 1999-06-23
;; PRIOR APPLICATION NUMBER: 60/144732
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/144758
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/144790
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/145228
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/145698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: 60/146222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: 60/146843
;; PRIOR FILING DATE: 1999-08-03
;; PRIOR APPLICATION NUMBER: 60/148188
;; PRIOR FILING DATE: 1999-08-10
;; PRIOR APPLICATION NUMBER: 60/148513
;; PRIOR FILING DATE: 1999-08-12
;; PRIOR APPLICATION NUMBER: 60/149327
;; PRIOR FILING DATE: 1999-08-17
;; PRIOR APPLICATION NUMBER: 60/149395
;; PRIOR FILING DATE: 1999-08-17
;; PRIOR APPLICATION NUMBER: 60/150114
;; PRIOR FILING DATE: 1999-08-20
;; PRIOR APPLICATION NUMBER: 60/151700
;; PRIOR FILING DATE: 1999-08-31
;; PRIOR APPLICATION NUMBER: 60/151734
;; PRIOR FILING DATE: 1999-08-31
;; PRIOR APPLICATION NUMBER: 60/162506
;; PRIOR FILING DATE: 1999-10-29

;; PRIOR APPLICATION NUMBER: 60/170262
;; PRIOR FILING DATE: 1999-12-09
;; PRIOR APPLICATION NUMBER: 60/177118
;; PRIOR FILING DATE: 2000-01-20
;; PRIOR APPLICATION NUMBER: 60/179851
;; PRIOR FILING DATE: 2000-02-02
;; PRIOR APPLICATION NUMBER: 60/180921
;; PRIOR FILING DATE: 2000-02-08
;; PRIOR APPLICATION NUMBER: 60/187202
;; PRIOR FILING DATE: 2000-03-03
;; PRIOR APPLICATION NUMBER: 60/198587
;; PRIOR FILING DATE: 2000-04-18
;; PRIOR APPLICATION NUMBER: 60/199614
;; PRIOR FILING DATE: 2000-04-25
;; PRIOR APPLICATION NUMBER: 60/206330
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/206368
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/209832
;; PRIOR FILING DATE: 2000-06-05
;; PRIOR APPLICATION NUMBER: 60/218371
;; PRIOR FILING DATE: 2000-07-13
;; PRIOR APPLICATION NUMBER: 60/222695
;; PRIOR FILING DATE: 2000-08-02
;; PRIOR APPLICATION NUMBER: 60/229896
;; PRIOR FILING DATE: 2000-09-01
;; PRIOR APPLICATION NUMBER: 60/230621
;; PRIOR FILING DATE: 2000-09-05
;; PRIOR APPLICATION NUMBER: 60/232887
;; PRIOR FILING DATE: 2000-09-15
;; PRIOR APPLICATION NUMBER: 60/235147
;; PRIOR FILING DATE: 2000-09-22
;; PRIOR APPLICATION NUMBER: 60/261878
;; PRIOR FILING DATE: 2001-01-12
;; PRIOR APPLICATION NUMBER: 60/261910
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: 60/261939
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: 60/262150
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: 60/264395
;; PRIOR FILING DATE: 2001-01-25
;; PRIOR APPLICATION NUMBER: 60/266421
;; PRIOR FILING DATE: 2001-02-02
;; PRIOR APPLICATION NUMBER: 60/267623
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/274399
;; PRIOR FILING DATE: 2001-03-09
;; PRIOR APPLICATION NUMBER: 60/280982
;; PRIOR FILING DATE: 2001-04-03
;; PRIOR APPLICATION NUMBER: 60/282129
;; PRIOR FILING DATE: 2001-04-04
;; PRIOR APPLICATION NUMBER: 60/282199
;; PRIOR FILING DATE: 2001-04-04
;; PRIOR APPLICATION NUMBER: 60/290589
;; PRIOR FILING DATE: 2001-05-09
;; PRIOR APPLICATION NUMBER: 09/180997
;; PRIOR FILING DATE: 1998-11-19
;; PRIOR APPLICATION NUMBER: 09/267213
;; PRIOR FILING DATE: 1999-03-12
;; PRIOR APPLICATION NUMBER: 09/380137
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/380138
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/403297
;; PRIOR FILING DATE: 1999-10-18
;; PRIOR APPLICATION NUMBER: 09/423741
;; PRIOR FILING DATE: 1999-11-10
;; PRIOR APPLICATION NUMBER: 09/709238
;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: 09/802706
;; PRIOR FILING DATE: 2001-03-09
;; PRIOR APPLICATION NUMBER: 09/872035

/ PRIOR FILING DATE: 2001-06-01
/ PRIOR APPLICATION NUMBER: 09/918585
/ PRIOR FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: 09/924419
/ PRIOR FILING DATE: 2001-08-06
/ PRIOR APPLICATION NUMBER: 09/927796
/ PRIOR FILING DATE: 2001-08-09
/ PRIOR APPLICATION NUMBER: 09/929404
/ PRIOR FILING DATE: 2001-08-13
/ PRIOR APPLICATION NUMBER: 09/931836
/ PRIOR FILING DATE: 2001-08-16
/ PRIOR APPLICATION NUMBER: 09/941932
/ PRIOR FILING DATE: 2001-08-28
/ PRIOR APPLICATION NUMBER: 09/946374
/ PRIOR FILING DATE: 2001-09-04
/ PRIOR APPLICATION NUMBER: 10/001054
/ PRIOR FILING DATE: 2001-11-30
/ PRIOR APPLICATION NUMBER: 10/052586
/ PRIOR FILING DATE: 2002-01-15
/ PRIOR APPLICATION NUMBER: 10/081056
/ PRIOR FILING DATE: 2002-02-20
/ PRIOR APPLICATION NUMBER: 10/119480
/ PRIOR FILING DATE: 2002-04-09

Query Match 100.0%; Score 180; DB 14; Length 751;
Best Local Similarity 100.0%; Pred. No. 2.7e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTRTRSWVMNQFVIEBYAGPEPVYIGKLHSD 33
Db 39 LTRTRSWVMNQFVIEBYAGPEPVYIGKLHSD 71

Search completed: December 8, 2004, 11:34:29
Job time : 34.7208 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13, Search time 3.93506 Seconds
(without alignments)
556.152 Million cell updates/sec

Title: US-09-788-051-10

Perfect score: 180
Sequence: 1 LKTRRSWMNQFVIEYAGPEVILGKHSD 33

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A COMB .pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB .pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB .pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB .pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB .pep.*
6: /cgn2_6/ptodata/1/iaa/backlist1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	152	84.4	615	2	US-08-738-349-12
2	152	84.4	693	2	US-08-738-349-6
3	152	84.4	693	4	US-09-919-487-55
4	152	84.4	796	1	US-08-188-228-58
5	152	84.4	796	1	US-08-332-643-52
6	152	84.4	796	1	US-08-332-638-58
7	152	84.4	796	2	US-08-738-349-2
8	152	84.4	796	2	US-08-738-349-4
9	152	84.4	796	4	US-09-654-378-2
10	150	83.3	110	3	US-09-187-859-4
11	150	83.3	110	4	US-09-839-542B-4
12	150	83.3	110	4	US-09-535-852-4
13	142	78.9	110	3	US-09-187-859-10
14	142	78.9	110	4	US-09-839-542B-10
15	142	78.9	110	4	US-09-535-852-10
16	139	77.2	532	1	US-08-188-228-44
17	139	77.2	532	1	US-08-332-638-44
18	139	77.2	793	1	US-08-188-228-54
19	139	77.2	793	1	US-08-332-643-48
20	139	77.2	793	1	US-08-332-638-54
21	139	77.2	799	1	US-08-188-228-42
22	139	77.2	799	1	US-08-332-638-42
23	139	76.7	110	3	US-09-187-859-13
24	138	76.7	110	4	US-09-839-542B-13
25	138	76.7	110	4	US-09-535-852-13
26	137	76.1	106	3	US-09-187-859-44
27	137	76.1	106	3	US-09-187-859-45

28	137	76.1	106	4	US-09-305-927-1	Sequence 1, Appl
29	137	76.1	106	4	US-09-305-927-2	Sequence 2, Appl
30	137	76.1	106	4	US-09-305-927-3	Sequence 3, Appl
31	137	76.1	106	4	US-09-073-040-12	Sequence 12, Appl
32	137	76.1	106	4	US-09-073-040-13	Sequence 13, Appl
33	137	76.1	106	4	US-09-839-542B-44	Sequence 44, Appl
34	137	76.1	106	4	US-09-839-542B-45	Sequence 45, Appl
35	137	76.1	106	4	US-09-264-516A-1	Sequence 1, Appl
36	137	76.1	106	4	US-09-264-516A-2	Sequence 2, Appl
37	137	76.1	106	4	US-09-264-516A-3	Sequence 3, Appl
38	137	76.1	106	4	US-09-234-395-4	Sequence 4, Appl
39	137	76.1	106	4	US-09-234-395-5	Sequence 5, Appl
40	137	76.1	106	4	US-09-305-928-4	Sequence 4, Appl
41	137	76.1	106	4	US-09-305-928-5	Sequence 5, Appl
42	136	75.6	110	3	US-09-187-859-22	Sequence 22, Appl
43	136	75.6	110	4	US-09-839-542B-22	Sequence 22, Appl
44	136	75.6	110	4	US-09-535-852-22	Sequence 22, Appl
45	134	74.4	110	3	US-09-187-859-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-738-349-12
Sequence 12, Application US/08738349
Patent No. 5669638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amano, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
PROCESS FOR ITS PRODUCTION
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-738-349-12

Query Match 84.4%; Score 152; DB 2; Length 615;
Best Local Similarity 75.8%; Pred. No. 8.3e-16;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLRTSRSMWNQPFVIEEYAGPEPVLIGKLHSD 33
Db 42 LQSKRGWVNQPFVIEEYTGPDVLVGRHSD 74

RESULT 2
US-08-738-349-6
Sequence 6, Application US/08738349
Patent No. 5869638

GENERAL INFORMATION:

APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amano, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 693 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-738-349-6

Query Match 84.4%; Score 152; DB 2; Length 693;
Best Local Similarity 75.8%; Pred. No. 9.5e-16;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLRTSRSMWNQPFVIEEYAGPEPVLIGKLHSD 33
Db 48 LQSKRGWVNQPFVIEEYTGPDVLVGRHSD 80

RESULT 3

US-09-919-497-55
Sequence 55, Application US/09919497
Patent No. 6773883
GENERAL INFORMATION:

APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.0
SEQ ID NO 55
LENGTH: 693
TYPE: PRT
ORGANISM: Homo sapiens
US-09-919-497-55

Query Match 84.4%; Score 152; DB 4; Length 693;
Best Local Similarity 75.8%; Pred. No. 9.5e-15;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLRTSRSMWNQPFVIEEYAGPEPVLIGKLHSD 33
Db 48 LQSKRGWVNQPFVIEEYTGPDVLVGRHSD 80

RESULT 4

US-08-188-228-58
Sequence 58, Application US/08188228
Patent No. 5597725

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-58

Query Match 84.4%; Score 152; DB 1; Length 796;
Best Local Similarity 75.8%; Pred. No. 1.1e-15;

Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 LKTRRSWVWNOFVIEEYAGPEPVLIGKLHSD 33
DB 48 LQSKRGWVWNOFVIEEYTGPDVVLVGRHSD 80

RESULT 5
US-08-332-643-52

Sequence 52, Application US/08332643

Patent No. 5639634

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

STREET: Bicknell

STREET: Two First National Plaza, 20 South Clark

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/332,643

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/872,643

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: No. 5639634and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/30795

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 346-5750

TELEFAX: (312) 984-9740

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:

LENGTH: 796 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-332-643-52

QY 1 LKTRRSWVWNOFVIEEYAGPEPVLIGKLHSD 33
DB 48 LQSKRGWVWNOFVIEEYTGPDVVLVGRHSD 80

RESULT 6
US-08-332-638-58

Sequence 58, Application US/08332638

Patent No. 5646250

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

STREET: Bicknell

STREET: Two First National Plaza, 20 South Clark

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/738,349

FILING DATE: 25-OCT-1996

CLASSIFICATION: 435

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/332,638

FILING DATE: 01-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/872,643

FILING DATE: 17 APR 1992

APPLICATION NUMBER: US/08/049,460

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: No. 5646250and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31340

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:

LENGTH: 796 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-332-638-58

QY 1 LKTRRSWVWNOFVIEEYAGPEPVLIGKLHSD 33
DB 48 LQSKRGWVWNOFVIEEYTGPDVVLVGRHSD 80

RESULT 7
US-08-738-349-2

Sequence 2, Application US/08738349

Patent No. 5869638

GENERAL INFORMATION:

APPLICANT: Takeshita, Sunao

APPLICANT: Okazaki, Makoto

APPLICANT: Kawai, Shinji

APPLICANT: Tsujimura, Atsushi

APPLICANT: Asanum, Egon

TITLE OF INVENTION: Bone-Related Cadherin-like Protein and

PROCESS FOR ITS PRODUCTION

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/738,349

FILING DATE: 25-OCT-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-2

Query Match
Best Local Similarity 84.4%; Score 152; DB 2; Length 796;
Best Local Similarity 75.8%; Pred. No. 1.1e-15;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 LRTSRWVWNOFVIEEYAGPEPYLIGKLHSD 33
DB 48 LQSKRGWVWNOFVIEEYTGDPDVLVGRHSD 80

RESULT 8
US-08-738-349-4
Sequence 4, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amano, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-4

Query Match
Best Local Similarity 84.4%; Score 152; DB 2; Length 796;
Best Local Similarity 75.8%; Pred. No. 1.1e-15;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 LRTSRWVWNOFVIEEYAGPEPYLIGKLHSD 33
DB 48 LQSKRGWVWNOFVIEEYTGDPDVLVGRHSD 80

RESULT 9
US-09-654-328-2
Sequence 2, Application US/09654328
Patent No. 6787136
GENERAL INFORMATION:
APPLICANT: Brenner, Michael B.
APPLICANT: Valencia, Xavier
TITLE OF INVENTION: Methods and Compositions for Treatment
TITLE OF INVENTION: of Inflammatory Disease Using Cadherin-11 Modulating Agents
FILE REFERENCE: B0801/7187/BRP/MAT
CURRENT APPLICATION NUMBER: US/09/654,328
CURRENT FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/152,456
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: US 60/153,490
PRIOR FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 796
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-654-328-2

Query Match
Best Local Similarity 84.4%; Score 152; DB 4; Length 796;
Best Local Similarity 75.8%; Pred. No. 1.1e-15;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 LRTSRWVWNOFVIEEYAGPEPYLIGKLHSD 33
DB 48 LQSKRGWVWNOFVIEEYTGDPDVLVGRHSD 80

RESULT 10
US-09-187-859-4
Sequence 4, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 4
LENGTH: 110
TYPE: PRT
ORGANISM: Homo sapiens
US-09-187-859-4

Query Match
Best Local Similarity 83.3%; Score 150; DB 3; Length 110;
Best Local Similarity 77.4%; Pred. No. 2.3e-16;
Matches 24; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 RTRSRWVWNOFVIEEYAGPEPYLIGKLHSD 33

Db 1 RSKRGWVWNOFVLEETGPPVLVGRHSD 31

RESULT 11
US-09-839-542B-4

; Sequence 4, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-839-542B-4

Query Match 83.3%; Score 150; DB 4; Length 110;
Best Local Similarity 77.4%; Pred. No. 2,3e-16;
Matches 24; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 RTRRSWVWNOFVLEETGPPVLVGRHSD 33
Db 1 RSKRGWVWNOFVLEETGPPVLVGRHSD 31

RESULT 12

US-09-535-852-4
; Sequence 4, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-852-4

Query Match 83.3%; Score 150; DB 4; Length 110;
Best Local Similarity 77.4%; Pred. No. 2,3e-16;
Matches 24; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 RTRRSWVWNOFVLEETGPPVLVGRHSD 33
Db 1 RSKRGWVWNOFVLEETGPPVLVGRHSD 31

RESULT 13
US-09-187-859-10
; Sequence 10, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-187-859-10

Query Match 78.9%; Score 142; DB 3; Length 110;
Best Local Similarity 74.2%; Pred. No. 4.5e-15;
Matches 23; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 RTRRSWVWNOFVLEETGPPVLVGRHSD 33
Db 1 RSKRGWVWNOFVLEETGPPVLVGRHSD 31

RESULT 14
US-09-839-542B-10

; Sequence 10, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-839-542B-10

Query Match 78.9%; Score 142; DB 4; Length 110;
Best Local Similarity 74.2%; Pred. No. 4.5e-15;
Matches 23; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 RTRRSWVWNOFVLEETGPPVLVGRHSD 33
Db 1 RSKRGWVWNOFVLEETGPPVLVGRHSD 31

RESULT 15
US-09-535-852-10

; Sequence 10, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-535-852-10

Query Match 78.9%; Score 142; DB 4; Length 110;
Best Local Similarity 74.2%; Pred. No. 4.5e-15;

	Matches	23;	Conservative	5;	Mismatches	3;	Indels	0;	Gaps	0;
Qy	3	RTRRSWVWNOFFVIEEYAGPEPVLIGKLSHD	33							
Db	1	RTKRSWVWNOFFVLEEWGSDPLYVGKLSHD	31							

Search completed: December 8, 2004, 10:01:13
Job time : 3.93506 secs